

From: Leffers, Gerald
Sent: Thursday, May 01, 2003 3:12 PM
To: STIC-Biotech/ChemLib
Subject: FW: 09/846,456

Thanks for your help. gerry leffers

Gerald G. Leffers Jr., PhD
Examiner, Art Unit 1636
Crystal Mall 1, Room 11A09
703-308-6232

-----Original Message-----

From: Fredman, Jeffrey
Sent: Thursday, May 01, 2003 2:47 PM
T : Leffers, Gerald
Subject: RE: 09/846,456

Gerald,

I don't think you need approval unless it is a rush. You are under the 10,000 nucleotide limit.

Jeff

-----Original Message-----

From: Leffers, Gerald
Sent: Thursday, May 01, 2003 2:00 PM
To: Fredman, Jeffrey
Subject: 09/846,456

Hi Jeff, please approve the following searches for this application. Total nucleic acid length is ~7 kb. SEQ ID NO: 1 (3.2kb), SEQ ID NO: 2 (357 nts), SEQ ID NO: 3 (2.8 kb), SEQ ID NO: 5 (159 nts). Claims drawn to 30 contiguous nucleotides of SEQ ID NOS: 3 & 5; 300 contiguous nucleotides of SEQ ID NO: 1. Other claims to nucleic acids comprising all of SEQ ID NO: 1 or SEQ ID NO: 2. Thanks, Gerry Leffers

Gerald G. Leffers Jr., PhD
Examiner, Art Unit 1636
Crystal Mall 1, Room 11A09
703-308-6232

11E12
MB

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 5/2
Date Completed: 5/12
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
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AL359182 96717 bp LNA linear PRI 11-JAN-2002
 Human DNA sequence from clone RP11-217B7 on chromosome 9, complete
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 AL359182
 AL359182.20 GI:18151453
 WTC.
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Chordata; Craniota; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 96717)
 Skuce, C.
 Direct Submission
 Submitted (11-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquery@sanger.ac.uk
 On Jan 15, 2002 this sequence version replaced gi:18121486.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 clone; and the
 assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: EMBL, SWISSPROT,
 TrEMBL, Wp, WORMPEP; Information on the WORMPEP
 database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
 Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr9
 RP11-217B7 is from the library RP11-11.1 constructed by the group
 of Pietet de Jong. For further details see
 http://www.chori.org/bacpac/home.htm
 VECTOR: pPR4c3.6
 IMPORTANT: This sequence is not the entire insert of clone
 RP11-217B7. It may be shorter because we sequence overlapping
 sections only once, except for a short overlap.
 The true right end of clone RP11-217B7 is at 96717 in this
 sequence. The true left end of clone RP11-122F10 is at 72980 in
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VERSION AF287262.1 GI:13876612
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SOURCE Homo sapiens.
ORGANISM Homo sapiens.
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AUTHORS Qiu,Y., Cavellier,L., Chiu,S., Yang,X., Kubit,E. and Chetani,J.F.
TITLE Human and mouse ABCA1 comparative sequencing and transgenesis studies revealing novel regulatory sequences
JOURNAL Genomics 73 (1), 66-76 (2001)
MEDLINE 21251004
PubMed 1132567
REFERENCE 2 (bases 1 to 201144)
AUTHORS Qiu,Y., Cavellier,L., Chiu,S., Kubit,E. and Chetani,J.F.
TITLE Direct submission
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Berkeley National Laboratory, 1 Cyclotron Rd, MS R4-171, Berkeley,
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SOURCE Homo sapiens
ORGANISM Homo sapiens
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AUTHORS Santamarina-Fojo, S., Peterson, K., Knepper, C., Qiu, Y., Freeman, J., Cheng, J. F., Osorio, J., Remaley, A. A., Yang, X. P., Haudenschild, C., Prades, C., Chimini, G., Blackmon, E., Francois, T., Duverger, M., Rubin, E. M., Rosier, M., Deneff, P., Fredrickson, D. S. and Brewer, H. B. Jr.
TITLE Complete genomic sequence of the human ABCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
MEDLINE 20345099
PUBMED 10884428
REFERENCE 2 (bases 1 to 149034)
AUTHORS Santamarina-Fojo, S., Peterson, K. M., Knapper, C. L., Freeman, L. A., Remaley, A. T., Yang, X. P., Haudenschild, C. C., Blackmon, E. E., Francois, T. L. and Brewer, H. B. Jr.
TITLE Direct Submission
JOURNAL Submitted (08-JUN-2000) Molecular Disease Branch, National Institutes of Health, National Heart, Lung and Blood Institute, Bethesda, MD 20892, USA

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ORGANISM: Homo sapiens.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 175064)
AUTHORS: Birren, B., Linton, L., Nusbaum, C. and Lander, E.
JOURNAL: Unpublished
REFERENCE
2 (bases 1 to 175064)
AUTHORS: Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckert, R., Boquslavsky, L., Bouckgalter, B.,
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Wyman, B., Ye, W.J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 22, 2000 this sequence version replaced at:6454033.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WtBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L2510
Center clone name: L_M10
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Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.965731
Consensus quality: 117571 bases at least: Q43
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Quality coverage: 2.9 in Q20 bases; average: 1p
Quality coverage: 3.2 in Q20 bases; sum-of-reads: 1p
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 39 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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AUTHORS	Pallinger,C.R., Hakamata,H., Duchateau,P.N., Eng,C., Aouizerat,B.E., Fielding,C.J. and Kane,J.P.				
TITLE	Analysis of ABCA1 gene 5' end: additional peptide sequence, promoter region, and four polymorphisms				
JOURNAL	Biochem. Biophys. Res. Commun. 271 (2000) In press				
REFERENCE	2 (bases 224 to 1167)				
AUTHORS	Pallinger,C.R., Hakamata,H., Duchateau,P.N., Eng,C., Aouizerat,B.E., Fielding,C.J. and Kane,J.P.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-APR-2000) Cardiovascular Research Institute, University of California, San Francisco, 505 Parnassus Avenue, San Francisco, CA 94143-0130, USA				
REFERENCE	3 (bases 1 to 1167)				
AUTHORS	Pallinger,C.R., Hakamata,H., Duchateau,P.N., Eng,C., Aouizerat,B.E., Fielding,C.J. and Kane,J.P.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-JUN-2000) Cardiovascular Research Institute, University of California, San Francisco, 505 Parnassus Avenue, San Francisco, CA 94143-0130, USA				
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TITLE
Kaminski, W.E., Drobnik, W., Honer, C., Schumacher, C., and Schmitz, G.
The zinc finger protein 202 (ZNF202) is a transcriptional repressor
of ATP binding cassette transporter A1 (ABCA1) and ABCG1 gene
expression and a modulator of cellular lipid efflux

JOURNAL
J. Biol. Chem. 276 (15), 12427-12433 (2001)

MECLINE
21192304

PUBMED
11279031

REFERENCE
2 (bases 1 to 1167)

AUTHORS
Porsch-Oezuerumez, M.K.

TITLE
Direct Submission

JOURNAL
Submitted (05-JAN-2000)

FEATURES
Porsch-Oezuerumez, M.K., Institute for
Clinical Chemistry, University of Regensburg,
Franz-Josef-Strauss-Allee 11, 93042 Regensburg, GERMANY

Location/Qualifiers
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/db_xref="taxon:9606"

/chromosome="9"

/map="9q22-31"

/cell_type="leukocyte"

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/gene="ABC-1"

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/function="cholesterol efflux regulatory protein"

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1148..1167

/gene="ABC-1"

/function="cholesterol efflux regulatory protein"

BASE COUNT 278 a 315 c 327 g 247 t

ORIGIN

Query Match 35.08; Score 1140.4; DB 9; Length 1167;
Best Local Similarity 98.78; Pred. No. 1.4e-294;
Matches 1165; Conservative 0; Mismatches 1; Indels 14; Gaps 2;

QY 1955 AAGTGGAGGCTGAGTGGCTGATATATTTACAGACAGTCCAAATCTCTGGTGGACTT 2014

DB 2 AAGTGGAGGCTGAGTGGCTGATATATTTACAGACAGTCCAAATCTCTGGTGGACTT 61

QY 2015 CACAATGATACAACTAAATACAAGTCTGTGTTTATACAGAGAGAGCTGATCAAT 2574

DB 62 CACAATGATACAACTAAATACAAGTCTGTGTTTATACAGAGAGAGCTGATCAAT 122

QY 2075 ATAATGAATTAAGGGGGTGTGTATATGTTCTGTGTTTCTGTTTCTGTTTCTGTT 2154

DB 122 ATAATGAATTAAGGGGGTGTGTATATGTTCTGTGTTTCTGTTTCTGTTTCTGTTT 172

QY 2135 TIGTTCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 2194

DB 174 TIGTTCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 242

QY 2195 ATGTTCTCTCTGGTCTCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 2254

DB 243 ATGTTCTCTCTGGTCTCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 292

QY 2255 TAGTCTGCTATCAAAATCAAGTCCAGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2314

DB 293 TAGTCTGCTATCAAAATCAAGTCCAGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTT 352

QY 2315 ACCGAGAGACTGTCGGCTCTCCCTCAGCCAGCTAGGCTTGAAGAGAAACAAAG 2374

DB 353 ACCGAGAGACTGTCGGCTCTCCCTCAGCCAGCTAGGCTTGAAGAGAAACAAAG 412

QY 2375 ACAAGACAAATGATTGGGTCCTGAGGAGATTTAGGCTAGAGCTGTTCTGTTCTGTT 2414

DB 413 ACAAGACAAATGATTGGGTCCTGAGGAGATTTAGGCTAGAGCTGTTCTGTTCTGTT 472

QY 2435 CCTCTCTCTGCTGAGGAACTTAAAGGAAAGAAAGAAATTTGTAAGAGTAAAGTAA 2494

DB 473 CCTCTCTCTGCTGAGGAACTTAAAGGAAAGAAAGAAATTTGTAAGAGTAAAGTAA 532

QY 2495 AGGAAGCAAAATTCACAGTGGTCTGCTGCGGAAACGTGGACTAGAGAGTCTGCGGC 2554

DB 533 AGGAAGCAAAATTCACAGTGGTCTGCTGCGGAAACGTGGACTAGAGAGTCTGCGGC 592

QY 2555 GAGGCTCCGAGTCCAGAGCTTCCGCGCGCTTTAGGCGGCGGCGGCGGCGGGAAGG 2614

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DB 768 GGGGCGGCGTCCAGCTGCTTCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 827

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QY 2855 GCGCAATCTATAAAGGAAGTGTAGTCCCGGCAAAACCCCGTAACTGCGAGAGAGTGA 2914

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DB 1068 CCGGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1127

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RESULT 12
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KEYWORDS
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Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 69570)
AUTHORS
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Becker, R., Beda, F.,
Bohuslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Chapel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArrelano, K., Dewar, K., Domino, M., Doyle, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J., Johnson, R., Jones, C., Kahn, L., Karatas, A., Klein, J.,
Lauders, T., Lehotzky, J., Levine, R., Liep, C., Liu, G., Locke, K.,
McDonald, P., Marquis, N., McEwan, P., McKernan, K.,
McPherson, R., Moldrim, J., Meneus, L., Morrow, J., Naylor, J.,
Norman, C., O'Connor, T., O'Donnell, P., Oliver, T., Peterson, K.,

Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, K., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thornann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W., Zimmer, A., and Zody, M.

Direct Submission

TITLE

JOURNAL

COMMENT

Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced at: 6765871.

All repeats were identified using RepeatMasker:

Smith, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/km/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L2512

Center clone name: L_N_10

* NOTE: This record contains 73 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will

* be preserved.

1 871: contig of 871 bp in length

872 971: gap of 100 bp

972 1834: contig of 861 bp in length

1835 1934: gap of 100 bp

1935 2804: contig of 870 bp in length

2805 2904: gap of 100 bp

2905 3745: contig of 841 bp in length

3746 3845: gap of 100 bp

3846 4636: contig of 851 bp in length

4637 4790: gap of 100 bp

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5641 5740: gap of 100 bp

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VERSION	AC012230.3		
KEYWORDS	HTG: HTGS_PHASE1; HTGS_DRAFT.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

1 (bases 1 to 175064)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-BM10
Unpublished
2 (bases 1 to 175064)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,I., Boukhalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A., Doyle,M.,
Cooke,P., DeRellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Gallagan,J., Gardyna,S., Grant,G., Hagos,B., Heathford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
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McWan,P., Glick,A., McKernan,K., McDonald,P., Meidrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tefaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 22, 2000 this sequence version replaced gi:6454033.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L2510
Center clone name: 1-M-10
----- Summary Statistics
Sequencing vector: M13: M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 117571 bases at least Q40
Consensus quality: 145749 bases at least Q30
Consensus quality: 160940 bases at least Q20
Insert size: 185000; agarose-fp
Quality coverage: 2.9 in Q20 bases; agarose-fp


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Query Match      17.1%; Score 553.8; DB 2; Length 175064;
Best Local Similarity 84.0%; Pred. No. 1.1e-137;
Matches 569; Conservative 0; Mismatches 107; Indels 1; Gaps 1;

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DB 1198 CCGTGTCTTACAAAAAATAGGAAATATAGATGGGTGCTGTGGATGCACTGCTGCTG 1139
QY 542 CCAGCTACTTGGAGGCTAAGGTGGAGGATCGCTTGAGCTGAGCTGAGGAGTCAAGTACAG 601
DB 1118 CCAGCTACTTGGAGGCTAAGGTGGAGGATCGCTTGAGCTGAGCTGAGGAGTCAAGTACAG 1080
QY 602 TGAGCCATGATTTGATCACTGCACCTCCAGCTGGTATGACAGAGTAAGAGCTGCTGCA 661
DB 1079 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1020
QY 662 AAAAAAGAAATGAAGA 678
DB 1019 NNNNNNNNNNNNNNNNA 1003

RESULT 14
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AC021246.2 GI:9119882
KEYWORDS HTG: HTGS_PHASE0.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 69570)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Albertson,A., Allen,N.,
TITLE Homo sapiens chromosome 1 clone RP11-1N10
JOURNAL
REFERENCE 2 (bases 1 to 69570)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Albertson,A., Allen,N.,
Anderson,S., Baldwin,J., Batra,N., Beckert,T., Binkley,E., Borker,N.,
Boguslavsky,I., Boukhvalter,B., Brown,A., Burkett,D., Busby,A.,

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Choepe,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
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Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheters,R., Meidrim,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rotman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo.A., Wu.X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (15-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6705871.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L2512
Center clone name: L_N10
-----
* NOTE: This record contains 73 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*
* 1 871: contig of 871 bp in length
* 872 971: gap of 100 bp
* 972 1834: contig of 863 bp in length
* 1835 1934: gap of 100 bp
* 1935 2804: contig of 870 bp in length
* 2805 2904: gap of 100 bp
* 2905 3745: contig of 841 bp in length
* 3746 3845: gap of 100 bp
* 3846 4696: contig of 851 bp in length
* 4697 4796: gap of 100 bp
* 4797 5640: contig of 844 bp in length
* 5641 5740: gap of 100 bp
* 5741 6540: contig of 800 bp in length
* 6541 6640: gap of 100 bp
* 6641 7569: contig of 869 bp in length
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* 9531 10376: contig of 846 bp in length
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* 10477 11322: contig of 846 bp in length
* 11323 11422: gap of 100 bp
* 11423 12302: contig of 880 bp in length
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* 12403 13280: contig of 878 bp in length
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* 16224 17072: contig of 849 bp in length
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* 18142 19009: contig of 868 bp in length
* 19010 19109: gap of 100 bp
* 19110 19966: contig of 857 bp in length
* 19967 20066: gap of 100 bp
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* 41914 42013: gap of 100 bp
* 42014 42824: contig of 811 bp in length
* 42825 42924: gap of 100 bp
* 42925 43776: contig of 852 bp in length
* 43777 43876: gap of 100 bp
* 43877 44752: contig of 876 bp in length
* 44753 44852: gap of 100 bp
* 44853 45724: contig of 872 bp in length
* 45725 45824: gap of 100 bp
* 45825 46643: contig of 819 bp in length
* 46644 46743: gap of 100 bp
* 46744 47599: contig of 856 bp in length
* 47600 47699: gap of 100 bp
* 47700 48551: contig of 852 bp in length
* 48552 48651: gap of 100 bp
* 48652 49485: contig of 894 bp in length
* 49486 49585: gap of 100 bp
* 49586 50440: contig of 855 bp in length

* 50441 50540: gap of 100 bp
* 50541 51404: contig of 864 bp in length
* 51405 51504: gap of 100 bp
* 51505 52372: contig of 868 bp in length
* 52373 52472: gap of 100 bp
* 52473 53328: contig of 856 bp in length
* 53329 53428: gap of 100 bp
* 53429 54268: contig of 840 bp in length
* 54269 54368: gap of 100 bp
* 54369 55229: contig of 861 bp in length
* 55230 55329: gap of 100 bp
* 55330 56197: contig of 868 bp in length
* 56198 56297: gap of 100 bp
* 56298 57163: contig of 866 bp in length
* 57164 57263: gap of 100 bp
* 57264 58130: contig of 867 bp in length
* 58131 58230: gap of 100 bp
* 58231 59082: contig of 852 bp in length
* 59083 59182: gap of 100 bp
* 59183 60020: contig of 838 bp in length
* 60021 60120: gap of 100 bp
* 60121 60983: contig of 863 bp in length
* 60984 61083: gap of 100 bp
* 61084 61935: contig of 852 bp in length
* 61936 62035: gap of 100 bp
* 62036 62866: contig of 831 bp in length
* 62867 62966: gap of 100 bp
* 62967 63827: contig of 861 bp in length
* 63828 63927: gap of 100 bp
* 63928 64783: contig of 856 bp in length
* 64784 64883: gap of 100 bp
* 64884 65740: contig of 857 bp in length
* 65741 65840: gap of 100 bp
* 65841 66684: contig of 844 bp in length
* 66685 66784: gap of 100 bp
* 66785 67651: contig of 867 bp in length
* 67652 67751: gap of 100 bp

Query Match: 15.38; Score 494; DB 2; Length 69570;

Best Local Similarity 92.2%; Pred. No. 1.2e-121;

Matches 518; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 2663 CCCCAGCCGACCCACCTCCGCCCAAGTCCTAGATGTGCTGGGGCGGTGAACGTGCGC 2722
DB 67642 CCCCCNNCCGACACCTCCGCAANTATAAGATGTGCTGGGGCGGTGAACGTGCGC 67583
QY 2723 CGTTTAAGGGCGGGGCGGCTCCAGCTGCTTTCCTGCTAGTGAAGTGAACCTAT 2782
DB 67582 CGTATAAGGGCGGGGCGGCTTGTGCTGCTAGTGAAGTGAACCTAT 67523
QY 2783 AGAGGCTGCGCAAGGCGGGGAGGAGGAGCAGCAGGCTTTGACCGATAGTAACTCT 2842
DB 67522 AGAGCCCGGAAAGGGCGGCGGAGGAGGAGCAGCAGGCTTTGATGATAGTAACTCT 67463
QY 2843 GCCTCGGTGACCGCAATCTATAAAGGAAGTGTCCCGGCAAAACCCGTAATGCG 2902
DB 67462 GCCTCGGTGACCGCAATCTATAAAGGAAGTGTCCCGGCAAAACCTGTGTAATGCG 67403
QY 2903 ACCGAGAGTGAAGTGGGGCGGAGCCCGCAGAGCCGAGCGAGCCCTTCTCTCCCGGCTGC 2962
DB 67402 AGCGAGAGTGAAGTGGGGCGGAGCCCGCAGAGCCGAGCGAGCCCTTCTCTCCCGGCTGC 67343
QY 2963 GGCAGGCGAGGGGGGAGCTCGGCGCACACAGAGCGGTTCTCAGGCGGCTTTGGCTC 3022
DB 67342 GACAGGACAGGGCGGGAGCTCGGCGCACACAGAGCGGTTCTCAGGCGGCTTTGGCTC 67283
QY 3023 CTTGTTTTTCCCGGTTCTGTTTTCTCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGA 3082
DB 67282 CGTGTTTTTTCCCGGTTGTTTTCTCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGA 67223
QY 3083 GAAAGAGAGGAAACACAAAAGTGAAGAGGCTCTCCAGTGACTTACCTTGG 3142
DB 67222 GAAAGAGAGGAAACAGTGAAGAGGCTCTCCAGTGACTTACCTTGG 67163

37523 38402: contig of 880 bp in length
38403 38502: gap of 100 bp
38503 39380: contig of 878 bp in length
39381 39480: gap of 100 bp
39481 40407: contig of 927 bp in length
40408 40507: gap of 100 bp
40508 41405: contig of 898 bp in length
41406 41505: gap of 100 bp
41506 42399: contig of 894 bp in length
42400 42499: gap of 100 bp
42500 43357: contig of 858 bp in length
43358 43457: gap of 100 bp
43458 44356: contig of 899 bp in length
44357 44456: gap of 100 bp
44457 45325: contig of 869 bp in length
45326 45425: gap of 100 bp
45426 46305: contig of 880 bp in length
46306 46405: gap of 100 bp
46406 47302: contig of 897 bp in length
47303 47402: gap of 100 bp
47403 48293: contig of 891 bp in length
48294 48393: gap of 100 bp
48394 49280: contig of 887 bp in length
49281 49380: gap of 100 bp
49381 50250: contig of 870 bp in length
50251 50350: gap of 100 bp
50351 51209: contig of 859 bp in length
51210 51309: gap of 100 bp
51310 52221: contig of 912 bp in length
52222 52321: gap of 100 bp
52322 53205: contig of 884 bp in length
53206 53305: gap of 100 bp
53306 54225: contig of 920 bp in length
54226 54325: gap of 100 bp
54326 55206: contig of 881 bp in length
55207 55306: gap of 100 bp
55307 56165: contig of 859 bp in length
56166 56265: gap of 100 bp
56266 57124: contig of 859 bp in length
57125 57224: gap of 100 bp
57225 58121: contig of 897 bp in length
58122 58221: gap of 100 bp
58222 59075: contig of 854 bp in length
59076 59175: gap of 100 bp
59176 60058: contig of 893 bp in length
60059 60158: gap of 100 bp
60159 61067: contig of 909 bp in length
61068 61167: gap of 100 bp
61168 62051: contig of 884 bp in length
62052 62151: gap of 100 bp
62152 63022: contig of 871 bp in length
63023 63122: gap of 100 bp
63123 64026: contig of 904 bp in length
64027 64126: gap of 100 bp
64127 65015: contig of 889 bp in length
65016 65115: gap of 100 bp
65116 65975: contig of 863 bp in length
65976 66075: gap of 100 bp
66076 66954: contig of 879 bp in length
66955 67054: gap of 100 bp
67055 67947: contig of 893 bp in length
67948 68047: gap of 100 bp
68048 68934: contig of 887 bp in length
68935 69034: gap of 100 bp
69035 69910: contig of 876 bp in length
69911 70010: gap of 100 bp

Query Match 14.8% Score 478.87 38 21 Length 906982
Best Local Similarity 90.8% Prod. No. 16e-117
Matches 543, Conservative 0, Mismatches 49, Indels 5, Gaps 2
2 CAGGCGATGGTGGCAGGTGCTGTAATCTCAGTACTCGGAGGTGGAGGTTCCATGAG 41
1 |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 10144 CCGGCGATGGTGGCAGGTGCTGTAATCTCAGTACTCGGAGGTGGAGGTTCCATGAG 10203
Qy 62 CCCAGATCGCACCATTCGACTCCAGCCTGGCGACACAAAAGGTGAATCCCATCAATTA 121
|||||
Db 10204 CCCAGATCGCACCATTCGACTCCAGCCTGGCGACACAAAAGGTGAATCCCATCAATTA 10263
Qy 122 AAAAAAAGAAATATTTTGGTGGTCGACTTCAATAGTAGGAGAGAGAGAGAGGA 181
|||||
Db 10264 AAAAAAATATGATTTTGGTGGTCGACTTCAATAGTAGGAGAGAGAGAGAGGA 10323
Qy 182 GATGAGGCTCAGGAGATCTAATTTACTCTCTAAATCATGCTAGGAAAGATAACACCTT 241
|||||
Db 10324 GATGAGGCTCAGGAGATCTAATTTACTCTCTAAATCATGCTAGGAAAGATAACACCTT 10383
Qy 242 TTAATAACACTCTCTGCTTTTATACATCATCTCTGCCAAGAGCTCAAGGTTTCAACAA 301
|||||
Db 10384 TTAATAACACTCTCTGCTTTTATACATCATCTCTGCCAAGAGCTCAAGGTTTCAACAA 10443
Qy 302 AGTTCACTTTTCAGAAAACCCCTTTTGAGGAAGACAGAAATATACATCTTCTCTCCATTTAA 361
|||||
Db 10444 AGTTCACTTTTCAGAAAACCCCTTTTGAGGAAGACAG-ATATACATCTTCTCTCCATTTAA 10502
Qy 362 AGATGAAGAAACAGCCCGGCACATGCTTAATGCCTGTATCCAGGACTTTGGGAGGC 421
|||||
Db 10503 AGATGAAGAAACAGCCCGGCACATGCTTAATGCCTGTATCCAGGACTTTGGGAGGC 10562
Qy 422 TGAGGCCAGAGCATGCTTGAGCTCCAGAGTTTGAGACCCAGCCTGGATAACATGGCAAAA 481
|||||
Db 10563 TGAGGCCAGAGATCCCTTGAGCTCCAAGTTTGAGACCCAGCCTG--ATACATGCCAAA 10620
Qy 482 CCTCTCTCTACAAAAAATAACAAAAATAGATGGGTGTGGTGATGACACCTGCTGGTC 541
|||||
Db 10621 CCTCTCTCTACAAAAAATA---CGAAATTAATGGGGGGGGGAATGCCCTGTGGTC 10677
Qy 542 CCAAGCTACTTGGCAGGCTTAAGGTGGAGGATCGCTTGAGCCCGAGGAGTCAAGTCTAC 599
|||||
Db 10678 CCAAGCTACTTGGAGGCTAAGGGGGGAGGAGACCCCTTTACCCCGGGGACAAATCTAC 10735

Search completed: May 9, 2003, 16:18:12
Job time : 10636 sec

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2003, 16:10:46 : Search time 8408.31 Seconds
(without alignments)
10013.236 Million cell updates/sec

Title: US-09-846-456-3
Perfect score: 2893
Sequence: 1 acaggcagtggtgcaggtg.....ctagtcgcgaacaccc 2893

Scoring table: OLIGO_NUC
Gapox 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 30
Total number of hits satisfying chosen parameters: 90539

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Listing first 1000 summaries

Database :

- GenEmbl:*
- 1: gb_ba:*
 - 2: gb_htg:*
 - 3: gb_in:*
 - 4: gb_om:*
 - 5: gb_ov:*
 - 6: gb_pat:*
 - 7: gb_ph:*
 - 8: gb_pl:*
 - 9: gb_pr:*
 - 10: gb_ro:*
 - 11: gb_sts:*
 - 12: gb_sy:*
 - 13: gb_un:*
 - 14: gb_vi:*
 - 15: em_ba:*
 - 16: em_fun:*
 - 17: em_hum:*
 - 18: em_in:*
 - 19: em_mu:*
 - 20: em_om:*
 - 21: em_or:*
 - 22: em_ov:*
 - 23: em_pat:*
 - 24: em_ph:*
 - 25: em_pl:*
 - 26: em_ro:*
 - 27: em_sts:*
 - 28: em_un:*
 - 29: em_vi:*
 - 30: em_htg_hum:*
 - 31: em_htg_inv:*
 - 32: em_htg_other:*
 - 33: em_htg_mus:*
 - 34: em_htg_pln:*
 - 35: em_htg_rod:*
 - 36: em_htg_man:*
 - 37: em_htg_vrt:*
 - 38: em_sy:*
 - 39: em_htgo_hum:*
 - 40: em_htgo_mus:*
 - 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2893	100.0	2893	6	AX351031	Sequence
2	2893	100.0	3231	6	AX351029	Sequence
3	1749	60.5	201144	9	AF287262	Homo sapi
4	1149	39.7	149034	9	AF275948	Homo sapi
5	891	30.8	96717	9	AL359182	Human DNA
6	814	28.1	183999	6	AX092589	Sequence
7	541	18.7	1167	9	AF258623	Homo sapi
8	541	18.7	1167	9	HS252201	Homo sapi
9	541	18.7	1643	6	AX060715	Sequence
10	541	18.7	1643	6	AX060894	Sequence
11	541	18.7	175064	2	AC012230	Homo sapi
12	344	11.9	175064	2	AC012230	Homo sapi
13	156	5.4	69570	2	AC021246	Homo sapi
14	152	5.3	90698	2	AC021345	Homo sapi
15	82	2.8	697	9	AF258627	Homo sapi
16	65	2.2	126285	9	AC004139	Homo sapi
17	61	2.1	186889	2	AL807243	Mus muscu
18	61	2.1	206966	9	AC021850	Homo sapi
19	61	2.1	278572	10	AF287263	Mus muscu
20	59	2.0	44897	2	AC103824	Homo sapi
21	58	2.0	57662	2	AC107969	Homo sapi
22	58	2.0	81874	9	HS931815	Human DNA
23	58	2.0	98360	9	HSJ247C2	Human DNA
24	58	2.0	141273	9	AL611933	Human DNA
25	58	2.0	145264	9	AC107939	Homo sapi
26	58	2.0	146312	2	AC015494	Homo sapi
27	58	2.0	155982	2	AC015495	Homo sapi
28	58	2.0	158071	2	AC018988	Homo sapi
29	58	2.0	158450	2	AC068082	Homo sapi
30	58	2.0	162419	2	AC093737	Homo sapi
31	58	2.0	166011	2	AC019307	Homo sapi
32	58	2.0	177533	2	AC069120	Homo sapi
33	58	2.0	188820	2	AC013281	Homo sapi
34	58	2.0	192396	9	AC012668	Homo sapi
35	58	2.0	193314	2	AC087478	Homo sapi
36	58	2.0	194433	9	HSBA425M5	Human DNA
37	58	2.0	195386	2	AL805961	Homo sapi
38	58	2.0	196520	2	AC083830	Homo sapi
39	58	2.0	201197	2	HS424J12	Homo sapien
40	58	2.0	292703	2	AC027176	Homo sapi
41	57	2.0	2532	9	AK094822	Homo sapi
42	57	2.0	4261	9	AB037785	Homo sapi
43	57	2.0	58958	9	AC091813	Homo sapi
44	57	2.0	91907	9	AC131566	Homo sapi
45	57	2.0	104906	9	AC069314	Homo sapi
46	57	2.0	116148	9	AC026423	Homo sapi
47	57	2.0	116650	9	AC004003	Homo sapi
48	57	2.0	117026	9	HS329A5	Human DNA
49	57	2.0	118603	2	AL360017	Homo sapi
50	57	2.0	121600	9	AP003555	Homo sapi
51	57	2.0	125146	9	AL512770	Human DNA
52	57	2.0	134036	9	AC007845	Homo sapi
53	57	2.0	140020	2	AC046162	Homo sapi
54	57	2.0	152558	2	AC013487	Homo sapi
55	57	2.0	154130	9	HS657E11	Human DNA
56	57	2.0	155691	9	AC016868	Homo sapi
57	57	2.0	163437	9	AC092606	Homo sapi
58	57	2.0	174711	9	AC026639	Homo sapi
59	57	2.0	175594	2	AC011134	Homo sapi
60	57	2.0	176212	2	AC084015	Homo sapi
61	57	2.0	177303	2	AC026576	Homo sapi
62	57	2.0	179641	9	AC098591	Homo sapi
63	57	2.0	182427	2	AC061992	Homo sapi
64	57	2.0	184444	9	AL359091	Human DNA
65	57	2.0	185979	9	AC091296	Pan trogl

C 66	57	2.0	187587	9	AC016026	Homo sapi	C 139	55	1.9	162746	9	AC006050	Homo sapi
C 67	57	2.0	189427	30	AC037439	Homo sapi	C 140	55	1.9	163825	2	AC016669	Homo sapi
C 68	57	2.0	190428	30	AC017012	Homo sapi	C 141	55	1.9	163904	9	AP003070	Homo sapi
C 69	57	2.0	196622	9	AC125218	Homo sapi	C 142	55	1.9	163948	9	AC101463	Homo sapi
C 70	57	2.0	196622	9	AC016543	Homo sapi	C 143	55	1.9	169649	9	HS862K6	Homo sapi
C 71	57	2.0	199496	2	AF235096	Homo sapi	C 144	55	1.9	171140	9	AC090685	Homo sapi
C 72	57	2.0	203003	9	AL731556	Human DNA	C 145	55	1.9	171966	2	AC092516	Papio cyn
C 73	57	2.0	206839	2	AC093539	Pan trogl	C 146	55	1.9	172949	2	AC124068	Homo sapi
C 74	57	2.0	217981	9	AC074051	Homo sapi	C 147	55	1.9	173016	2	AC019123	Homo sapi
C 75	57	2.0	259685	2	AC063928	Homo sapi	C 148	55	1.9	173785	9	AP000355	Homo sapi
C 76	57	2.0	280140	2	AC055751	Homo sapi	C 149	55	1.9	173864	9	AL365364	Human DNA
C 77	57	2.0	303717	2	AC063930	Homo sapi	C 150	55	1.9	175986	2	AC023071	Homo sapi
C 78	56	1.9	48522	2	AC105112	Homo sapi	C 151	55	1.9	176926	9	AC009078	Homo sapi
C 79	56	1.9	51815	2	AC068454	Homo sapi	C 152	55	1.9	177402	9	AC007406	Homo sapi
C 80	56	1.9	139737	9	HS228013	Human DNA	C 153	55	1.9	179947	2	AC021467	Homo sapi
C 81	56	1.9	144627	2	AC015710	Homo sapi	C 154	55	1.9	180760	2	AC130435	Homo sapi
C 82	56	1.9	150812	9	AC004765	Homo sapi	C 155	55	1.9	181683	2	AC021618	Homo sapi
C 83	56	1.9	155125	9	AC024361	Homo sapi	C 156	55	1.9	182374	2	AP003968	Homo sapi
C 84	56	1.9	157871	9	AC104365	Homo sapi	C 157	55	1.9	182839	2	AC022619	Homo sapi
C 85	56	1.9	165036	9	AC100835	Homo sapi	C 158	55	1.9	184515	9	AC010653	Homo sapi
C 86	56	1.9	166279	9	CNS010835	Human chr	C 159	55	1.9	186010	2	AC073083	Homo sapi
C 87	56	1.9	171296	9	CNS060686	Human chr	C 160	55	1.9	186981	9	AC006459	Homo sapi
C 88	56	1.9	173354	2	AC027354	Homo sapi	C 161	55	1.9	194211	2	AL442633	Sequence
C 89	56	1.9	173692	2	AC025994	Homo sapi	C 162	55	1.9	194955	9	AC084198	Homo sapi
C 90	56	1.9	176850	2	AC103736	Homo sapi	C 163	55	1.9	203134	9	AC021077	Homo sapi
C 91	56	1.9	178035	2	AC068680	Homo sapi	C 164	55	1.9	211001	9	AC018695	Homo sapi
C 92	56	1.9	181637	9	AC117451	Homo sapi	C 165	55	1.9	219017	9	AP000936	Homo sapi
C 93	56	1.9	183083	9	AC007600	Homo sapi	C 166	55	1.9	246240	6	AR036572	Sequence
C 94	56	1.9	184396	9	AC010853	Homo sapi	C 167	55	1.9	246240	6	AR036573	Sequence
C 95	56	1.9	194198	2	AC013298	Homo sapi	C 168	55	1.9	246240	6	AR036574	Sequence
C 96	56	1.9	194627	9	AC096596	Homo sapi	C 169	55	1.9	246282	9	HSU91328	Human
C 97	56	1.9	195840	9	CNS000066	Human chr	C 170	55	1.9	318488	9	AC005529	Homo sapi
C 98	56	1.9	201861	9	AC067796	Homo sapi	C 171	55	1.9	328439	2	AL590137	Homo sapi
C 99	56	1.9	216902	2	AC018475	Homo sapi	C 172	54	1.9	8216	9	AP001617	Homo sapi
C 100	56	1.9	227008	2	AP001771	Homo sapi	C 173	54	1.9	23599	9	AP001504	Homo sapi
C 101	56	1.9	227430	2	AC091590	Homo sapi	C 174	54	1.9	43147	9	AP002955	Homo sapi
C 102	56	1.9	279308	2	AC091918	Homo sapi	C 175	54	1.9	44663	9	AC093518	Homo sapi
C 103	55	1.9	13646	9	HUMRBP4	L34219 Homo sapien	C 176	54	1.9	44913	9	AC005786	Homo sapi
C 104	55	1.9	39915	2	AC010512	Homo sapi	C 177	54	1.9	50334	9	HS995112	Human DNA
C 105	55	1.9	51891	2	AC074103	Homo sapi	C 178	54	1.9	69537	2	AC107379	Homo sapi
C 106	55	1.9	55627	9	AL589951	Human DNA	C 179	54	1.9	88738	9	AL513343	Human DNA
C 107	55	1.9	64360	2	AC104349	Homo sapi	C 180	54	1.9	94343	9	AC005255	Homo sapi
C 108	55	1.9	81971	9	AC018753	Homo sapi	C 181	54	1.9	95930	9	AC106033	Homo sapi
C 109	55	1.9	84841	9	AL391813	Human DNA	C 182	54	1.9	96075	9	AL590639	Human DNA
C 110	55	1.9	85500	9	HS199816	Human DNA	C 183	54	1.9	102349	9	AL161671	Human DNA
C 111	55	1.9	87925	9	AC005318	Homo sapi	C 184	54	1.9	142116	9	AC034215	Homo sapi
C 112	55	1.9	88238	9	AL353780	Human DNA	C 185	54	1.9	145833	2	AC125837	Rattus no
C 113	55	1.9	94882	2	AC002317	Homo sapi	C 186	54	1.9	147345	9	AL158824	Human DNA
C 114	55	1.9	110000	2	AC135900_1	Continuation (2 of	C 187	54	1.9	152867	9	AC027671	Homo sapi
C 115	55	1.9	119082	9	AP000903	294020 Human DNA S	C 188	54	1.9	153716	9	AL590631	Human DNA
C 116	55	1.9	125686	9	HS503616	Human DNA	C 189	54	1.9	155699	9	AL360176	Human DNA
C 117	55	1.9	127145	9	HS111947	Human DNA	C 190	54	1.9	157381	9	AC007606	Homo sapi
C 118	55	1.9	127286	2	AC025246	Homo sapi	C 191	54	1.9	160069	2	AC064867	Homo sapi
C 119	55	1.9	135405	9	AC000025	Homo sapi	C 192	54	1.9	163739	2	AC012406	Homo sapi
C 120	55	1.9	136098	9	AC006970	Homo sapi	C 193	54	1.9	165375	2	AC073357	Homo sapi
C 121	55	1.9	136646	9	AL138726	Human DNA	C 194	54	1.9	166297	2	AC011271	Homo sapi
C 122	55	1.9	138532	2	AL139222	Homo sapi	C 195	54	1.9	166500	9	AC007785	Homo sapi
C 123	55	1.9	140834	2	AC007460	Homo sapi	C 196	54	1.9	168230	2	AC010624	Homo sapi
C 124	55	1.9	141456	9	AL355300	Human DNA	C 197	54	1.9	170517	9	AC010545	Homo sapi
C 125	55	1.9	143583	9	HS467016	Human DNA	C 198	54	1.9	170919	9	CNS01DX3	Human chr
C 126	55	1.9	145173	9	AC005599	Homo sapi	C 199	54	1.9	170970	9	AL354707	Human DNA
C 127	55	1.9	147594	9	AC013829	Homo sapi	C 200	54	1.9	172462	2	AC091147	Homo sapi
C 128	55	1.9	148750	9	AC002426	Genomic s	C 201	54	1.9	173389	2	AC048385	Homo sapi
C 129	55	1.9	148975	2	AC012145	Homo sapi	C 202	54	1.9	173484	2	AC021145	Homo sapi
C 130	55	1.9	149308	9	AC005527	Homo sapi	C 203	54	1.9	174230	9	AC024073	Homo sapi
C 131	55	1.9	154772	9	AL138764	Human DNA	C 204	54	1.9	175618	2	AC046167	Homo sapi
C 132	55	1.9	155138	9	AL139260	Human DNA	C 205	54	1.9	175831	2	AC015720	Homo sapi
C 133	55	1.9	156619	2	AC013361	Homo sapi	C 206	54	1.9	175999	2	AC021154	Homo sapi
C 134	55	1.9	157566	9	AC022517	Homo sapi	C 207	54	1.9	176092	2	AC068222	Homo sapi
C 135	55	1.9	158193	2	AC010828	Homo sapi	C 208	54	1.9	182659	9	AC023830	Homo sapi
C 136	55	1.9	160450	2	AC087388	Homo sapi	C 209	54	1.9	185145	9	AC087433	Homo sapi
C 137	55	1.9	161054	9	AC104444	Homo sapi	C 210	54	1.9	188769	2	AP002809	Homo sapi
C 138	55	1.9	161355	2	AC011154	Homo sapi	C 211	54	1.9	189757	9	AC023593	Homo sapi

C 212	54	1.9 190776	2	AC064813	AC064813 Homo sapi	C 285	53	1.8 174711	2	AC025515	AC025515 Homo sapi
C 213	54	1.9 193020	9	AL138759	AL138759 Human DNA	C 286	53	1.8 174903	2	AC124039	AC124039 Macaca mu
C 214	54	1.9 203228	9	AC092718	AC092718 Homo sapi	C 287	53	1.8 177045	2	AC015970	AC015970 Homo sapi
C 215	54	1.9 203773	9	AC097369	AC097369 Homo sapi	C 288	53	1.8 179220	9	AC114493	AC114493 Homo sapi
C 216	54	1.9 207961	2	AC014282	AC014282 Homo sapi	C 289	53	1.8 180133	9	AL138885	AL138885 Human DNA
C 217	54	1.9 211422	9	AC073493	AC073493 Homo sapi	C 290	53	1.8 183487	2	AC068628	AC068628 Homo sapi
C 218	54	1.9 219256	9	AP001743	AP001743 Homo sapi	C 291	53	1.8 184118	9	AC016580	AC016580 Homo sapi
C 219	54	1.9 219635	2	AL390207	AL390207 Homo sapi	C 292	53	1.8 184313	9	AL445584	AL445584 Human DNA
C 220	53	1.8 2638	9	AK026796	AK026796 Homo sapi	C 293	53	1.8 185351	9	AC015801	AC015801 Homo sapi
C 221	53	1.8 4452	9	AK074112	AK074112 Homo sapi	C 294	53	1.8 186052	9	AC104187	AC104187 Homo sapi
C 222	53	1.8 4734	9	HSPD4CG7	AL157415 Homo sapi	C 295	53	1.8 187274	2	AL391096	AL391096 Homo sapi
C 223	53	1.8 34688	9	AC005759	AC005759 Homo sapi	C 296	53	1.8 188065	2	AC018689	AC018689 Homo sapi
C 224	53	1.8 36284	9	HSATJ9610	AL1009510 Homo sapi	C 297	53	1.8 189048	2	AC090739	AC090739 Homo sapi
C 225	53	1.8 36852	9	AC106891	AC106891 Homo sapi	C 298	53	1.8 189148	2	AC068262	AC068262 Homo sapi
C 226	53	1.8 42133	9	AP001060	AP001060 Homo sapi	C 299	53	1.8 192307	9	AC005971	AC005971 Homo sapi
C 227	53	1.8 44296	9	AC004471	AC004471 Homo sapi	C 300	53	1.8 193076	2	AC090617	AC090617 Homo sapi
C 228	53	1.8 62930	2	AC106017	AL106017 Homo sapi	C 301	53	1.8 193690	2	AC118559	AC118559 Homo sapi
C 229	53	1.8 66254	9	AL137791	AL137791 Human DNA	C 302	53	1.8 197676	2	AC022344	AC022344 Homo sapi
C 230	53	1.8 73516	2	AC041001	AC041001 Homo sapi	C 303	53	1.8 197748	2	AC026283	AC026283 Homo sapi
C 231	53	1.8 74509	2	AF260012	AF260012 Homo sapi	C 304	53	1.8 198557	2	AC025250	AC025250 Homo sapi
C 232	53	1.8 74999	9	AC008960	AC008960 Homo sapi	C 305	53	1.8 199579	9	AC093536	AC093536 Homo sapi
C 233	53	1.8 75148	9	AC091545	AC091545 Homo sapi	C 306	53	1.8 200458	2	AC019237	AC019237 Homo sapi
C 234	53	1.8 81514	9	HSATJ9616	AL099616 Homo sapi	C 307	53	1.8 20542	2	CNS01863	CNS01863 Homo sapi
C 235	53	1.8 83306	9	AC062021	AC062021 Homo sapi	C 308	53	1.8 206537	9	AC099777	AC099777 Homo sapi
C 236	53	1.8 89690	9	AC106864	AC106864 Homo sapi	C 309	53	1.8 218047	30	AC068624	AC068624 Homo sapi
C 237	53	1.8 90434	2	AC007952	AC007952 Homo sapi	C 310	53	1.8 221909	2	AC021705	AC021705 Homo sapi
C 238	53	1.8 91938	2	AC129838	AC129838 Pan trogl	C 311	53	1.8 340000	9	AP001712	AP001712 Homo sapi
C 239	53	1.8 94074	9	HSBC17A95	AL450224 Homo sapi	C 312	53	1.8 340000	9	AP001753	AP001753 Homo sapi
C 240	53	1.8 96975	9	AC004975	AC004975 Homo sapi	C 313	52	1.8 475	6	AX390668	AX390668 Sequence
C 241	53	1.8 96995	9	AC008149	AC008149 Homo sapi	C 314	52	1.8 2544	9	AK094363	AK094363 Homo sapi
C 242	53	1.8 101098	9	AC002427	AC002427 Homo sapi	C 315	52	1.8 3527	9	AK090951	AK090951 Homo sapi
C 243	53	1.8 103476	9	AC123912	AC123912 Homo sapi	C 316	52	1.8 5072	9	AK090406	AK090406 Homo sapi
C 244	53	1.8 108400	9	HUMDGCRCEN	L75750 Homo sapi	C 317	52	1.8 5987	11	HS50024T	HS50024T H. sapiens
C 245	53	1.8 110000	2	AC003656	AC003656 Homo sapi	C 318	52	1.8 14475	9	AC007078	AC007078 Homo sapi
C 246	53	1.8 113148	9	AC093241	AC093241 Homo sapi	C 319	52	1.8 48103	9	AL356282	AL356282 Human DNA
C 247	53	1.8 115710	2	AL139015	AL139015 Homo sapi	C 320	52	1.8 54405	2	AC111158	AC111158 Homo sapi
C 248	53	1.8 115928	9	AC037475	AC037475 Homo sapi	C 321	52	1.8 56415	9	HSJ994024	HSJ994024 Human DNA
C 249	53	1.8 116103	9	AL606465	AL606465 Human DNA	C 322	52	1.8 63578	9	AC109356	AC109356 Homo sapi
C 250	53	1.8 117946	9	AC023513	AC023513 Homo sapi	C 323	52	1.8 64214	9	AL512408	AL512408 Human DNA
C 251	53	1.8 119580	9	AP000466	AP000466 Homo sapi	C 324	52	1.8 66008	9	AC024582	AC024582 Homo sapi
C 252	53	1.8 120825	9	HSJ733M16	AL109627 Human DNA	C 325	52	1.8 66887	9	AF411057	AF411057 Homo sapi
C 253	53	1.8 133284	2	AC104231	AC104231 Homo sapi	C 326	52	1.8 66954	2	AL591214	AL591214 Human DNA
C 254	53	1.8 136589	2	AC090319	AC090319 Homo sapi	C 327	52	1.8 67412	2	AC131573	AC131573 Homo sapi
C 255	53	1.8 143456	9	AL513365	AL513365 Human DNA	C 328	52	1.8 71166	2	AC099819	AC099819 Homo sapi
C 256	53	1.8 146463	9	AC114971	AC114971 Homo sapi	C 329	52	1.8 72159	9	AL160161	AL160161 Homo sapi
C 257	53	1.8 146878	2	AC011174	AC011174 Homo sapi	C 330	52	1.8 80527	9	AC092290	AC092290 Homo sapi
C 258	53	1.8 150013	2	AC010780	AC010780 Homo sapi	C 331	52	1.8 93403	9	AC073261	AC073261 Homo sapi
C 259	53	1.8 150684	9	AL442445	AL442445 Human DNA	C 332	52	1.8 94718	9	AC026770	AC026770 Homo sapi
C 260	53	1.8 154918	9	AL138781	AL138781 Human DNA	C 333	52	1.8 98647	2	AC025777	AC025777 Homo sapi
C 261	53	1.8 155025	9	AC034246	AC034246 Homo sapi	C 334	52	1.8 97716	9	AL512454	AL512454 Human DNA
C 262	53	1.8 155125	9	AC024561	AC024561 Homo sapi	C 335	52	1.8 104140	9	AC008122	AC008122 Homo sapi
C 263	53	1.8 157193	9	AL355315	AL355315 Human DNA	C 336	52	1.8 106539	9	AF225859	AF225859 Homo sapi
C 264	53	1.8 157672	9	AC113114	AC113114 Homo sapi	C 337	52	1.8 108625	9	AL356773	AL356773 Homo sapi
C 265	53	1.8 157929	9	AL593644	AL593644 Homo sapi	C 338	52	1.8 108907	9	AL135911	AL135911 Human DNA
C 266	53	1.8 158838	9	CNS050TDN	AL566825 Human chr	C 339	52	1.8 110000	2	AC112773	AC112773 Homo sapi
C 267	53	1.8 158840	9	AC091577	AC091577 Homo sapi	C 340	52	1.8 111998	9	AC011509	AC011509 Homo sapi
C 268	53	1.8 160569	9	AC015878	AC015878 Homo sapi	C 341	52	1.8 112748	9	AC007242	AC007242 Homo sapi
C 269	53	1.8 160957	9	AC114487	AC114487 Homo sapi	C 342	52	1.8 123004	9	AC073846	AC073846 Homo sapi
C 270	53	1.8 162820	9	AC138765	AC138765 Human DNA	C 343	52	1.8 126368	9	HS104333	HS104333 Homo sapi
C 271	53	1.8 162921	2	AC093367	AC093367 Homo sapi	C 344	52	1.8 126543	2	AC026156	AC026156 Homo sapi
C 272	53	1.8 162976	9	AC114301	AC114301 Homo sapi	C 345	52	1.8 129435	9	AL391314	AL391314 Human DNA
C 273	53	1.8 164473	2	AP001108	AP001108 Homo sapi	C 346	52	1.8 131345	9	AC069023	AC069023 Homo sapi
C 274	53	1.8 166309	9	AC011944	AC011944 Homo sapi	C 347	52	1.8 133246	2	AC091026	AC091026 Homo sapi
C 275	53	1.8 166717	2	AC125612	AC125612 Homo sapi	C 348	52	1.8 133258	9	AC004944	AC004944 Homo sapi
C 276	53	1.8 167390	9	AC067263	AC067263 Homo sapi	C 349	52	1.8 133614	2	AC025433	AC025433 Homo sapi
C 277	53	1.8 168080	2	AC009047	AC009047 Homo sapi	C 350	52	1.8 133690	9	AL158074	AL158074 Human DNA
C 278	53	1.8 169646	9	AL160269	AL160269 Human DNA	C 351	52	1.8 134308	9	AC011488	AC011488 Homo sapi
C 279	53	1.8 169758	2	AL356139	AL356139 Homo sapi	C 352	52	1.8 135964	9	AC005914	AC005914 Homo sapi
C 280	53	1.8 170245	9	AC092814	AC092814 Homo sapi	C 353	52	1.8 137473	2	AC015944	AC015944 Homo sapi
C 281	53	1.8 170783	2	AC024943	AC024943 Homo sapi	C 354	52	1.8 137718	9	AL137066	AL137066 Human DNA
C 282	53	1.8 171274	2	AC026476	AC026476 Homo sapi	C 355	52	1.8 137945	2	AL133508	AL133508 Homo sapi
C 283	53	1.8 172200	2	AC022626	AC022626 Homo sapi	C 356	52	1.8 138063	9	AC092473	AC092473 Homo sapi
C 284	53	1.8 172657	9	AC015963	AC015963 Homo sapi	C 357	52	1.8 138839	9	HUAC002400	HUAC002400 Human Chr

C 358	1.8 140179	2	AC084688	AC084688 Homo sapi	C 431	52	1.8 183619	9	AC007339	AC007339 Homo sapi
C 359	1.8 140919	9	AC110747	AC110747 Homo sapi	C 432	52	1.8 185316	9	AP002797	AP002797 Homo sapi
C 360	1.8 143423	9	AC116192	AC116192 Human DNA	C 433	52	1.8 185367	2	AC092977	AC092977 Homo sapi
C 361	1.8 144620	9	AC023787	AC023787 Homo sapi	C 434	52	1.8 186109	2	AP001890	AP001890 Homo sapi
C 362	1.8 145242	9	AC008610	AC008610 Homo sapi	C 435	52	1.8 186524	2	AC024465	AC024465 Homo sapi
C 363	1.8 145579	2	AC015737	AC015737 Homo sapi	C 436	52	1.8 186920	9	AP000824	AP000824 Homo sapi
C 364	1.8 145616	9	HS108K11	285986 Human DNA S	C 437	52	1.8 189174	9	AC092687	AC092687 Homo sapi
C 365	1.8 147461	9	AC027348	AC027348 Homo sapi	C 438	52	1.8 189219	9	AC092982	AC092982 Homo sapi
C 366	1.8 147565	2	AC080145	AC080145 Homo sapi	C 439	52	1.8 189355	2	AC053539	AC053539 Homo sapi
C 367	1.8 148278	9	AC006101	AC006101 c11b_3p_	C 440	52	1.8 190253	2	AC090500	AC090500 Homo sapi
C 368	1.8 148507	9	AC008784	AC008784 Homo sapi	C 441	52	1.8 191717	2	AC104115	AC104115 Homo sapi
C 369	1.8 148656	9	AC005482	AC005482 Homo sapi	C 442	52	1.8 192420	2	AC129804	AC129804 Homo sapi
C 370	1.8 149401	2	AC074932	AC074932 Homo sapi	C 443	52	1.8 194486	2	AC016771	AC016771 Homo sapi
C 371	1.8 149563	9	AC116348	AC116348 Homo sapi	C 444	52	1.8 195723	2	AC087732	AC087732 Homo sapi
C 372	1.8 150377	2	AC102797	AC102797 Homo sapi	C 445	52	1.8 195782	9	AC074389	AC074389 Homo sapi
C 373	1.8 150573	9	AC097473	AC097473 Homo sapi	C 446	52	1.8 196263	2	AC131385	AC131385 Homo sapi
C 374	1.8 150573	9	AC097473	AC097473 Homo sapi	C 447	52	1.8 196852	2	AC084866	AC084866 Homo sapi
C 375	1.8 151008	2	AC035146	AC035146 Homo sapi	C 448	52	1.8 198567	9	AL157877	AL157877 Human DNA
C 376	1.8 152555	9	AL354830	AC135456 Human DNA	C 449	52	1.8 200881	2	AC116566	AC116566 Homo sapi
C 377	1.8 152786	9	AL135778	AL135778 Human DNA	C 450	52	1.8 201764	2	AL359818	AL359818 Homo sapi
C 378	1.8 154882	2	AC025346	AC025346 Homo sapi	C 451	52	1.8 202768	2	AC092345	AC092345 Homo sapi
C 379	1.8 155951	2	AL445495	AL445495 Human DNA	C 452	52	1.8 204504	2	AC022487	AC022487 Homo sapi
C 380	1.8 156043	2	AC013631	AC013631 Homo sapi	C 453	52	1.8 208410	9	AC091043	AC091043 Homo sapi
C 381	1.8 156288	2	AC116561	AC116561 Homo sapi	C 454	52	1.8 209401	2	AC106885	AC106885 Homo sapi
C 382	1.8 157288	2	AC116561	AC116561 Homo sapi	C 455	52	1.8 209907	2	AC078778	AC078778 Homo sapi
C 383	1.8 157435	9	HS500224	AL034850 Human DNA	C 456	52	1.8 106417	2	AC034201	AC034201 Homo sapi
C 384	1.8 158482	2	AC025346	AC025346 Homo sapi	C 457	52	1.8 212753	9	HS21242	295114 Human DNA S
C 385	1.8 159365	9	AL392111	AL392111 Human DNA	C 458	52	1.8 213613	2	AC013405	AC013405 Homo sapi
C 386	1.8 159562	9	AC034205	AC034205 Homo sapi	C 459	52	1.8 217929	2	AL133395	AL133395 Human DNA
C 387	1.8 159637	2	AC007990	AC007990 Homo sapi	C 460	52	1.8 220581	2	AC015918	AC015918 Homo sapi
C 388	1.8 159713	9	AC087190	AC087190 Homo sapi	C 461	52	1.8 223735	9	AC096677	AC096677 Homo sapi
C 389	1.8 160301	2	AC130417	AC130417 Homo sapi	C 462	52	1.8 240379	9	AC005077	AC005077 Homo sapi
C 390	1.8 160915	2	AC001084	AC001084 Homo sapi	C 463	52	1.8 260967	2	AC068769	AC068769 Homo sapi
C 391	1.8 161179	2	AC083954	AC083954 Homo sapi	C 464	52	1.8 299301	2	AC098584	AC098584 Homo sapi
C 392	1.8 161538	9	AL139188	AC083954 Homo sapi	C 465	51	1.8 567	9	HS038671	U38671 Human Alu r
C 393	1.8 162805	2	AC020565	AC020565 Homo sapi	C 466	51	1.8 1025	9	HS342941	AJ342941 Homo sapi
C 394	1.8 162901	9	AL512656	AC020565 Homo sapi	C 467	51	1.8 1159	9	F272846S06	AF272846 Homo sapi
C 395	1.8 163689	9	AL451065	AL451065 Human DNA	C 468	51	1.8 1479	9	AK098617	F4098617 Homo sapi
C 396	1.8 163731	9	AC008949	AC008949 Homo sapi	C 469	51	1.8 3407	9	HOMOTSP1	AF136270 Homo sapi
C 397	1.8 164302	9	AC122457	AC122457 Homo sapi	C 470	51	1.8 3423	9	HS0591P1	AF135120 Homo sapi
C 398	1.8 165554	2	AC025144	AC025144 Homo sapi	C 471	51	1.8 3926	9	HSUDGF2	AF135120 Homo sapi
C 399	1.8 165596	2	AC091588	AC091588 Homo sapi	C 472	51	1.8 3994	9	AL358173	Y09998 H.sapiens T
C 400	1.8 165749	2	AC015102	AC015102 Homo sapi	C 473	51	1.8 4360	9	AR018045	AL358173 Human DNA
C 401	1.8 166606	2	AC020685	AC020685 Homo sapi	C 474	51	1.8 5190	9	HS1ADNAG	AB018045 Homo sapi
C 402	1.8 166839	2	AL359391	AL359391 Homo sapi	C 475	51	1.8 13996	9	AC112722	X76775 H.sapiens H
C 403	1.8 166839	2	AC079468	AC079468 Homo sapi	C 476	51	1.8 14699	9	AF351120	AC112722 Homo sapi
C 404	1.8 167656	9	AC022576	AC022576 Homo sapi	C 477	51	1.8 26303	9	HSF536	AF351120 Homo sapi
C 405	1.8 167985	2	AC022576	AC022576 Homo sapi	C 478	51	1.8 20303	9	HS094788	X54156 Human p53 g
C 406	1.8 168513	2	AC011982	AC011982 Homo sapi	C 479	51	1.8 24119	9	HS447E6	U94789 Human p53 g
C 407	1.8 169612	2	AC027493	AC027493 Homo sapi	C 480	51	1.8 24813	9	AL357632	AL0311724 Human DNA
C 408	1.8 169825	9	AC012452	AC012452 Homo sapi	C 481	51	1.8 28409	9	AL354930	..L357632 Human DNA
C 409	1.8 170761	9	CNS05TER	AC012452 Homo sapi	C 482	51	1.8 30652	9	AC004753	AL354930 Human DNA
C 410	1.8 171541	2	AC048482	AC048482 Homo sapi	C 483	51	1.8 48491	9	AC006049	AC004753 Homo sapi
C 411	1.8 171978	2	AC009649	AC009649 Homo sapi	C 484	51	1.8 48598	9	AC013531	AC006049 Homo sapi
C 412	1.8 172853	9	AC064363	AC064363 Homo sapi	C 485	51	1.8 38629	9	AC114267	AC013531 Homo sapi
C 413	1.8 172964	9	AC069413	AC069413 Homo sapi	C 486	51	1.8 38902	9	HS027	AC114267 Homo sapi
C 414	1.8 173117	2	AL357885	AL357885 Homo sapi	C 487	51	1.8 39004	9	HSE90C2	296104 Human DNA S
C 415	1.8 173677	9	AC084768	AC084768 Homo sapi	C 488	51	1.8 39236	9	AC004510	282182 Human DNA S
C 416	1.8 173728	9	AC018507	AC018507 Homo sapi	C 489	51	1.8 39261	9	AC000387	AC004510 Homo sapi
C 417	1.8 174144	2	AC091765	AC091765 Homo sapi	C 490	51	1.8 39569	9	AC000084	AC000387 Gemic s
C 418	1.8 174311	2	AL365319	AL365319 Homo sapi	C 491	51	1.8 41081	9	AC003048	AC000084 Homo sapi
C 419	1.8 174527	2	AC092859	AC092859 Homo sapi	C 492	51	1.8 42304	9	AC002491	AC003048 Homo sapi
C 420	1.8 174741	9	AC040977	AC040977 Homo sapi	C 493	51	1.8 42616	9	AC005566	AC002491 Homo sapi
C 421	1.8 175162	9	AL590103	AL590103 Human DNA	C 494	51	1.8 43516	9	AP000041	AC005566 Homo sapi
C 422	1.8 176153	9	AC006287	AC006287 Homo sapi	C 495	51	1.8 43715	9	AC092298	AP000041 Homo sapi
C 423	1.8 176967	2	AC022742	AC022742 Homo sapi	C 496	51	1.8 43759	9	AB015355	AC092298 Homo sapi
C 424	1.8 178494	9	AC009481	AC009481 Homo sapi	C 497	51	1.8 44090	9	AC000080	AB015355 Homo sapi
C 425	1.8 178710	2	AC106766	AC106766 Homo sapi	C 498	51	1.8 45416	9	AC000090	AC000080 Homo sapi
C 426	1.8 179655	9	AC018740	AC018740 Homo sapi	C 499	51	1.8 46465	2	AC006183	AC000090 Homo sapi
C 427	1.8 179969	9	AC016643	AC016643 Homo sapi	C 500	51	1.8 47480	9	AL356354	AC006183 Homo sapi
C 428	1.8 180531	9	AC068745	AC068745 Homo sapi	C 501	51	1.8 51146	2	AC090342	AL356354 Human DNA
C 429	1.8 180533	2	AC119427	AC119427 Homo sapi	C 502	51	1.8 51480	9	AP000261	AC090342 Homo sapi
C 430	1.8 181636	2	AC025138	AC025138 Homo sapi	C 503	51	1.8 51923	9	AL356983	AP000261 Homo sapi

c 504	1.8	53157	9	AL136302	AC136402 Human DNA	517	51	1.8	112484	9	AP002336	AP002336 Homo sapi
c 505	1.8	54982	2	AL100814	AL100814 Homo sapi	578	51	1.8	112898	2	AC008552	AC008552 Homo sapi
c 506	1.8	56570	2	AL153194	AL153194 Human DNA	c 579	51	1.8	114231	2	HS390C10	HS390C10 Human DNA
c 507	1.8	56737	2	AC025208	AC025208 Homo sapi	c 580	51	1.8	114584	2	AF252827	AF252827 Homo sapi
c 508	1.8	56940	9	AC105427	AC105427 Homo sapi	c 581	51	1.8	115278	9	AL119819	AL119819 Human DNA
c 509	1.8	59012	9	HSABLOC2	U 75F2 Human ABL	c 582	51	1.8	115583	9	HS1351K20	HS1351K20 Human DNA
c 510	1.8	63945	9	AC091979	AC091979 Homo sapi	c 583	51	1.8	117264	2	AC127024	AC127024 Homo sapi
c 511	1.8	64470	2	AC103400	AC103400 Mus muscu	c 584	51	1.8	117431	2	HS850H21	HS850H21 Human DNA
c 512	1.8	66686	2	AC087659	AC087659 Homo sapi	c 585	51	1.8	117493	9	HSJ654H19	HSJ654H19 Human DNA
c 513	1.8	67188	2	AC104364	AC104364 Homo sapi	c 586	51	1.8	117893	9	HS109M1	HS109M1 Human DNA
c 514	1.8	67289	2	AC040394	AC040394 Homo sapi	c 587	51	1.8	117952	9	AL133541	AL133541 Human DNA
c 515	1.8	67445	9	AL1591486	AL1591486 Human DNA	c 588	51	1.8	117962	9	AF312032	AF312032 Homo sapi
c 516	1.8	68037	9	AY046055	AY046055 Homo sapi	c 589	51	1.8	118819	9	AP000647	AP000647 Homo sapi
c 517	1.8	68662	9	AL133293	AL133293 Human DNA	c 590	51	1.8	119875	2	AL108051	AL108051 Homo sapi
c 518	1.8	69570	2	AC021246	AC021246 Homo sapi	c 591	51	1.8	120015	2	AL354860	AL354860 Homo sapi
c 519	1.8	69912	2	AC010322	AC010322 Homo sapi	c 592	51	1.8	120030	9	AC002075	AC002075 Homo sapi
c 520	1.8	71627	9	AC004851	AC004851 Homo sapi	c 593	51	1.8	121739	9	AC006084	AC006084 Homo sapi
c 521	1.8	73686	9	AP000280	AP000280 Homo sapi	c 594	51	1.8	121856	2	AC022575	AC022575 Homo sapi
c 522	1.8	76702	9	HS756674	AL135072 Human DNA	c 595	51	1.8	122186	6	AX051112	AX051112 Sequence
c 523	1.8	76850	9	AC003109	AC003109 Human DNA	c 596	51	1.8	122186	9	AC004466	AC004466 Homo sapi
c 524	1.8	77888	9	AL1590611	AL1590611 Human DNA	c 597	51	1.8	122591	9	AL157786	AL157786 Human DNA
c 525	1.8	79611	9	AC002486	AC002486 Human DNA	c 598	51	1.8	122717	2	AP001186	AP001186 Homo sapi
c 526	1.8	79914	9	AC005159	AC005159 Homo sapi	c 599	51	1.8	122889	9	HSDA204F4	HSDA204F4 Human DNA
c 527	1.8	80914	9	AC007959	AC007959 Homo sapi	c 600	51	1.8	123004	9	AC087892	AC087892 Homo sapi
c 528	1.8	81768	9	AL662825	AL662825 Human DNA	c 601	51	1.8	123554	9	AB023049	AB023049 Homo sapi
c 529	1.8	81826	9	HS078645	U75F2 Human COL1A	c 602	51	1.8	124001	9	HS886K2	HS886K2 Human DNA
c 530	1.8	82976	9	AC005031	AC005031 Homo sapi	c 603	51	1.8	125549	9	AL645941	AL645941 Human DNA
c 531	1.8	83332	9	AL138665	AL138665 Human DNA	c 604	51	1.8	125878	2	AC108924	AC108924 Homo sapi
c 532	1.8	84686	9	AL138665	AL138665 Human DNA	c 605	51	1.8	126045	9	HS1010E17	HS1010E17 Human DNA
c 533	1.8	85538	9	HS751022	AL049645 Human DNA	c 606	51	1.8	126290	2	AC099483	AC099483 Homo sapi
c 534	1.8	86130	9	AC005365	AC005365 Homo sapi	c 607	51	1.8	126380	2	AP000714	AP000714 Homo sapi
c 535	1.8	86299	9	AL359358	AL359358 Human DNA	c 608	51	1.8	126503	9	AC008114	AC008114 Homo sapi
c 536	1.8	86719	9	HSJ906P16	AL075349 Human DNA	c 609	51	1.8	126956	2	HS881	HS881 Human DNA
c 537	1.8	87424	9	AC006377	AC006377 Homo sapi	c 610	51	1.8	127335	2	AC068083	AC068083 Homo sapi
c 538	1.8	89874	30	AL356483	AL356483 Human DNA	c 611	51	1.8	128473	9	AC004241	AC004241 Homo sapi
c 539	1.8	90476	9	AC015910	AC015910 Homo sapi	c 612	51	1.8	129643	9	AC011507	AC011507 Homo sapi
c 540	1.8	91202	2	AC006186	AC006186 Homo sapi	c 613	51	1.8	130278	9	AC005664	AC005664 Homo sapi
c 541	1.8	92118	9	AC074484	AC074484 Homo sapi	c 614	51	1.8	131078	9	HSU80017	HSU80017 Homo sapien
c 542	1.8	94224	9	HS661120	AL131669 Human DNA	c 615	51	1.8	131602	2	AC034263	AC034263 Homo sapi
c 543	1.8	94535	2	HS1141E20	AL109512 Homo sapi	c 616	51	1.8	131602	2	AC034263	AC034263 Homo sapi
c 544	1.8	95218	9	AC019066	AC019066 Homo sapi	c 617	51	1.8	131673	9	HS336H9	HS336H9 Human DNA
c 545	1.8	95782	9	AC025775	AC025775 Homo sapi	c 618	51	1.8	132433	9	HS0321081	HS0321081 Human DNA
c 546	1.8	96202	9	AL138664	AL138664 Human DNA	c 619	51	1.8	132755	9	AC008670	AC008670 Homo sapi
c 547	1.8	96963	9	AC015855	AC015855 Homo sapi	c 620	51	1.8	133516	9	AL591409	AL591409 Human DNA
c 548	1.8	96978	9	AC024075	AC024075 Homo sapi	c 621	51	1.8	133801	9	AC092540	AC092540 Homo sapi
c 549	1.8	97128	9	AL662845	AL662845 Human DNA	c 622	51	1.8	134245	9	HS1052M9	HS1052M9 Human DNA
c 550	1.8	98309	2	AL671924	AL671924 Homo sapi	c 623	51	1.8	135305	9	HSJ1112D6	HSJ1112D6 Homo sapi
c 551	1.8	100000	9	AP000035	AP000035 Homo sapi	c 624	51	1.8	135618	2	AL359965	AL359965 Homo sapi
c 552	1.8	100000	9	AP000039	AP000039 Homo sapi	c 625	51	1.8	135996	2	AL356007	AL356007 Homo sapi
c 553	1.8	100000	9	AP000109	AP000109 Homo sapi	c 626	51	1.8	137217	2	HS4211L10	HS4211L10 Homo sapi
c 554	1.8	100000	9	AP000197	AP000197 Homo sapi	c 627	51	1.8	137343	9	AP000946	AP000946 Homo sapi
c 555	1.8	100000	9	AP000176	AP000176 Homo sapi	c 628	51	1.8	138093	9	AL606467	AL606467 Human DNA
c 556	1.8	100000	9	AP000144	AP000144 Homo sapi	c 629	51	1.8	138879	9	AC124210	AC124210 Homo sapi
c 557	1.8	100000	9	AP000514	AP000514 Homo sapi	c 630	51	1.8	138928	9	AC064847	AC064847 Homo sapi
c 558	1.8	102151	9	HS979N1	AL075659 Human DNA	c 631	51	1.8	139035	9	AL356102	AL356102 Human DNA
c 559	1.8	103122	9	AC005663	AC005663 Homo sapi	c 632	51	1.8	139173	9	AC009140	AC009140 Homo sapi
c 560	1.8	103146	9	HS187N21	HS0303 Human DNA	c 633	51	1.8	139776	9	AL160165	AL160165 Human DNA
c 561	1.8	103179	9	AP000619	AP000619 Homo sapi	c 634	51	1.8	139966	9	AC004820	AC004820 Homo sapi
c 562	1.8	103186	9	AL158218	AL158218 Human DNA	c 635	51	1.8	140476	9	AC104465	AC104465 Homo sapi
c 563	1.8	103370	9	AL161656	AL161656 Human DNA	c 636	51	1.8	141073	9	AC100827	AC100827 Homo sapi
c 564	1.8	103930	9	AL358234	AL358234 Human DNA	c 637	51	1.8	141848	2	AC107980	AC107980 Homo sapi
c 565	1.8	104429	9	AP003787	AP003787 Homo sapi	c 638	51	1.8	141991	2	HSJ3821D9	HSJ3821D9 Human DNA
c 566	1.8	104892	9	AL589664	AL589664 Human DNA	c 639	51	1.8	142273	9	AL391994	AL391994 Human DNA
c 567	1.8	106658	9	AL606468	AL606468 Human DNA	c 640	51	1.8	142634	2	AC018778	AC018778 Homo sapi
c 568	1.8	107381	2	AC115093	AC115093 Homo sapi	c 641	51	1.8	142830	9	AC007097	AC007097 Homo sapi
c 569	1.8	108836	9	AC069137	AC069137 Homo sapi	c 642	51	1.8	143409	2	AP001787	AP001787 Homo sapi
c 570	1.8	109018	9	HSJ1129A6	AL069673 Human DNA	c 643	51	1.8	143618	9	AL137856	AL137856 Human DNA
c 571	1.8	109378	9	AC022143	AC022143 Homo sapi	c 644	51	1.8	144098	9	AC104967	AC104967 Homo sapi
c 572	1.8	109891	9	HS112K5	HS0987 Human DNA	c 645	51	1.8	144588	2	AC012239	AC012239 Homo sapi
c 573	1.8	109902	9	HS0346C2	AL132275 Human DNA	c 646	51	1.8	145063	2	AC027069	AC027069 Homo sapi
c 574	1.8	110816	9	AC002404	AC002404 Human DNA	c 647	51	1.8	145066	2	AP002418	AP002418 Homo sapi
c 575	1.8	111293	9	HS156L9	AL213222 Human Chr	c 648	51	1.8	145133	2	AC013822	AC013822 Homo sapi
c 576	1.8	111344	9	AL1354C3	AL135403 Human DNA	c 649	51	1.8	145206	9	AC026170	AC026170 Homo sapi

c 650	51	1.8 145442	9	AC004859	AC004859 Homo sapi	c 723	51	1.8 164057	9	AL590138	AL590138 Human DNA
c 651	51	1.8 146083	9	AC009480	AC009480 Homo sapi	c 724	51	1.8 164519	9	AL138712	AL138712 Human DNA
c 652	51	1.8 146250	2	AC074240	AC074240 Homo sapi	c 725	51	1.8 164587	2	AC023001	AC023001 Homo sapi
c 653	51	1.8 147244	9	AC005969	AC005969 Homo sapi	c 726	51	1.8 164604	9	AL138682	AL138682 Human DNA
c 654	51	1.8 147767	2	AC105030	AC105030 Homo sapi	c 727	51	1.8 165077	2	AC024493	AC024493 Homo sapi
c 655	51	1.8 148068	9	CNS01RHN	AL161873 Human chr	c 728	51	1.8 165483	2	AL591362	AL591362 Homo sapi
c 656	51	1.8 148271	9	AL392046	AL392046 Human DNA	c 729	51	1.8 165868	2	AC021719	AC021719 Homo sapi
c 657	51	1.8 149188	9	AC114781	AC114781 Homo sapi	c 730	51	1.8 166124	9	AF238375	AF238375 Homo sapi
c 658	51	1.8 149244	9	AL683842	AL683842 Human DNA	c 731	51	1.8 166181	9	HS37E16	HS37E16 Human DNA
c 659	51	1.8 149324	2	AL157822	AL157822 Homo sapi	c 732	51	1.8 166206	2	AC009668	AC009668 Homo sapi
c 660	51	1.8 149710	2	AC022563	AC022563 Homo sapi	c 733	51	1.8 166254	9	AL359983	AL359983 Human DNA
c 661	51	1.8 150397	2	CNS05TD2	AL355423 Homo sapi	c 734	51	1.8 166765	9	AC112496	AC112496 Homo sapi
c 662	51	1.8 151031	9	AC112222	AC112222 Homo sapi	c 735	51	1.8 166837	2	AC087895	AC087895 Homo sapi
c 663	51	1.8 151228	9	AL662800	AL662800 Human DNA	c 736	51	1.8 166941	2	AC008049	AC008049 Homo sapi
c 664	51	1.8 151302	9	AC073617	AC073617 Homo sapi	c 737	51	1.8 166989	2	AC013554	AC013554 Homo sapi
c 665	51	1.8 151712	9	AC008385	AC008385 Homo sapi	c 738	51	1.8 167185	9	AC093132	AC093132 Homo sapi
c 666	51	1.8 151976	9	AC024588	AC024588 Homo sapi	c 739	51	1.8 167390	9	AC007263	AC007263 Homo sapi
c 667	51	1.8 153702	9	AL645730	AL645730 Human DNA	c 740	51	1.8 167479	9	AL445235	AL445235 Human DNA
c 668	51	1.8 154066	9	HS24018	AL621808 Human DNA	c 741	51	1.8 167594	2	AC100791	AC100791 Homo sapi
c 669	51	1.8 154068	9	AL356292	AL356292 Human DNA	c 742	51	1.8 167631	2	AC016032	AC016032 Homo sapi
c 670	51	1.8 154405	9	AC009275	AC009275 Homo sapi	c 743	51	1.8 167633	9	AL513534	AL513534 Human DNA
c 671	51	1.8 154604	2	AC104974	AC104974 Homo sapi	c 744	51	1.8 167671	2	AC090081	AC090081 Homo sapi
c 672	51	1.8 154935	2	AL356781	AL356781 Homo sapi	c 745	51	1.8 167749	2	AC016416	AC016416 Homo sapi
c 673	51	1.8 154994	9	AC099755	AC099755 Homo sapi	c 746	51	1.8 167831	2	AC027723	AC027723 Homo sapi
c 674	51	1.8 154994	9	AC099755	AC099755 Homo sapi	c 747	51	1.8 168063	2	AC090699	AC090699 Homo sapi
c 675	51	1.8 155085	2	AC104112	AC104112 Homo sapi	c 748	51	1.8 168481	2	AC025094	AC025094 Homo sapi
c 676	51	1.8 155308	2	AC109487	AC109487 Homo sapi	c 749	51	1.8 168613	9	AC091133	AC091133 Homo sapi
c 677	51	1.8 155439	9	AC008626	AC008626 Homo sapi	c 750	51	1.8 168872	2	AC019036	AC019036 Homo sapi
c 678	51	1.8 155521	9	AC069335	AC069335 Homo sapi	c 751	51	1.8 168900	2	AC024418	AC024418 Homo sapi
c 679	51	1.8 156089	2	AC013750	AC013750 Homo sapi	c 752	51	1.8 168981	9	AC126347	AC126347 Homo sapi
c 680	51	1.8 156399	9	AC002456	AC002456 Homo sapi	c 753	51	1.8 169007	9	AC034193	AC034193 Homo sapi
c 681	51	1.8 156503	9	AC011511	AC011511 Homo sapi	c 754	51	1.8 169347	9	AC007327	AC007327 Homo sapi
c 682	51	1.8 156580	9	AP003493	AP003493 Homo sapi	c 755	51	1.8 170048	2	AC025240	AC025240 Homo sapi
c 683	51	1.8 156633	2	AC113431	AC113431 Homo sapi	c 756	51	1.8 170056	2	AC087643	AC087643 Homo sapi
c 684	51	1.8 156733	9	AP000640	AP000640 Homo sapi	c 757	51	1.8 170336	2	AC011244	AC011244 Homo sapi
c 685	51	1.8 157289	9	AC069421	AC069421 Homo sapi	c 758	51	1.8 170392	9	AC060765	AC060765 Homo sapi
c 686	51	1.8 157299	2	AC083932	AC083932 Homo sapi	c 759	51	1.8 170722	2	AC087847	AC087847 Homo sapi
c 687	51	1.8 157358	9	AC016745	AC016745 Homo sapi	c 760	51	1.8 170772	2	AC016454	AC016454 Homo sapi
c 688	51	1.8 157545	2	AL163535	AL163535 Homo sapi	c 761	51	1.8 170823	2	AC092294	AC092294 Homo sapi
c 689	51	1.8 158405	9	AC009753	AC009753 Homo sapi	c 762	51	1.8 171068	9	AL356281	AL356281 Human DNA
c 690	51	1.8 158424	9	CNS01R13	AL162832 Human chr	c 763	51	1.8 171073	2	AL590609	AL590609 Homo sapi
c 691	51	1.8 158817	9	AP005353	AP005353 Homo sapi	c 764	51	1.8 171099	9	AC092544	AC092544 Homo sapi
c 692	51	1.8 158838	2	CNS05TDN	AL356605 Human chr	c 765	51	1.8 171381	9	AL162730	AL162730 Human DNA
c 693	51	1.8 159098	2	AC016484	AC016484 Homo sapi	c 766	51	1.8 171550	9	AC079322	AC079322 Homo sapi
c 694	51	1.8 159122	2	AC025556	AC025556 Homo sapi	c 767	51	1.8 171606	2	AL591118	AL591118 Homo sapi
c 695	51	1.8 159263	9	AC092544	AC092544 Homo sapi	c 768	51	1.8 171739	9	AC093294	AC093294 Homo sapi
c 696	51	1.8 159351	2	AC018783	AC018783 Homo sapi	c 769	51	1.8 171902	2	AP000846	AP000846 Homo sapi
c 697	51	1.8 159597	9	AC008747	AC008747 Homo sapi	c 770	51	1.8 172217	2	AC068391	AC068391 Homo sapi
c 698	51	1.8 159692	9	AC016727	AC016727 Homo sapi	c 771	51	1.8 172358	9	AC011895	AC011895 Homo sapi
c 699	51	1.8 159787	2	AC016285	AC016285 Homo sapi	c 772	51	1.8 172393	2	AC025740	AC025740 Homo sapi
c 700	51	1.8 160525	2	AC027074	AC027074 Homo sapi	c 773	51	1.8 172403	2	AC017061	AC017061 Homo sapi
c 701	51	1.8 160545	9	AC036214	AC036214 Homo sapi	c 774	51	1.8 172543	9	AP004287	AP004287 Homo sapi
c 702	51	1.8 160656	2	AL592072	AL592072 Homo sapi	c 775	51	1.8 172577	2	AL365174	AL365174 Homo sapi
c 703	51	1.8 160658	9	AC024258	AC024258 Homo sapi	c 776	51	1.8 172588	2	AC007430	AC007430 Homo sapi
c 704	51	1.8 160754	9	AC007611	AC007611 Homo sapi	c 777	51	1.8 172880	9	AC027419	AC027419 Homo sapi
c 705	51	1.8 160994	2	AC004480	AC004480 Homo sapi	c 778	51	1.8 173083	2	AC034272	AC034272 Homo sapi
c 706	51	1.8 161109	2	AC094594	AC094594 Homo sapi	c 779	51	1.8 173087	9	AC010809	AC010809 Homo sapi
c 707	51	1.8 161179	2	AC066661	AC066661 Homo sapi	c 780	51	1.8 173184	9	AC112515	AC112515 Homo sapi
c 708	51	1.8 161499	9	AC015488	AC015488 Homo sapi	c 781	51	1.8 173317	9	AC016637	AC016637 Homo sapi
c 709	51	1.8 161505	9	AP001888	AP001888 Homo sapi	c 782	51	1.8 173359	2	AP000922	AP000922 Homo sapi
c 710	51	1.8 161540	9	AC076972	AC076972 Homo sapi	c 783	51	1.8 173456	9	AC055758	AC055758 Homo sapi
c 711	51	1.8 161788	2	AC025619	AC025619 Homo sapi	c 784	51	1.8 173463	9	AL359092	AL359092 Human DNA
c 712	51	1.8 161976	2	AC012415	AC012415 Homo sapi	c 785	51	1.8 174018	2	AL445311	AL445311 Homo sapi
c 713	51	1.8 161987	9	AC079848	AC079848 Homo sapi	c 786	51	1.8 174074	9	AC018891	AC018891 Homo sapi
c 714	51	1.8 162107	2	AP002423	AP002423 Homo sapi	c 787	51	1.8 174283	2	AC013723	AC013723 Homo sapi
c 715	51	1.8 162314	9	AC061965	AC061965 Homo sapi	c 788	51	1.8 174346	9	AC108173	AC108173 Homo sapi
c 716	51	1.8 162450	6	AK211792	AK211792 Sequence	c 789	51	1.8 174400	9	AC011603	AC011603 Homo sapi
c 717	51	1.8 163338	9	AL162426	AL162426 Human DNA	c 790	51	1.8 175028	9	AC066692	AC066692 Homo sapi
c 718	51	1.8 163390	9	AL137058	AL137058 Human DNA	c 791	51	1.8 175053	2	AC023226	AC023226 Homo sapi
c 719	51	1.8 163541	9	AC068954	AC068954 Homo sapi	c 792	51	1.8 175127	2	AC016048	AC016048 Homo sapi
c 720	51	1.8 163891	9	AC092647	AC092647 Homo sapi	c 793	51	1.8 175129	2	AC021490	AC021490 Homo sapi
c 721	51	1.8 163924	2	AL162592	AL162592 Homo sapi	c 794	51	1.8 175265	2	AC063964	AC063964 Homo sapi
c 722	51	1.8 163958	2	AC019303	AC019303 Homo sapi	c 795	51	1.8 175345	9	AC073065	AC073065 Homo sapi

796	51	1.8 175582	9	AC023590	AC023590 Homo sapi	869	51	1.8 190430	2	AC118987	AC118987 Pan trogl
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DEFINITION Sequence 1 from Patent. WO0183746.

ACCESSION AX351029

VERSION AX351029.1 GI:18616385

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Makallia; Eutheria; Primates; Catarrhini; Hominidae; Homo;

TITLE

Koster-Montus, M.F., Prades, C., Lamore, C., Nardone, L., Boudier, P.,

Brewer, B., Duverger, N., Romley, A. and Santalucia, F., 2001.

JOURNAL Regulatory nucleic acid sequences of the above gene.

Patent: WO 0183746-A 1 (08 Nov 2001);

Aventis Pharma S.A. (FR)

FEATURES

Location/Qualifiers

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and SNAP protein genes, complete cds.
ACCESSION
AF287262
VERSION
AF287262.1 GI:13876612
KEYWORDS
Homo sapiens.
SOURCE
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ORGANISM
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 201144)
Oiu.Y., Cavellier.L., Chiu,S., Yang,X., Rubin,E. and Cheng,J.F.
Human and mouse ABCA1 comparative sequencing and transgenesis
studies revealing novel regulatory sequences
Genomics 73 (1), 66-76 (2001)
MEDLINE
21251004
PUBMED
11352567
REFERENCE
2 (bases 1 to 201144)
Oiu.Y., Cavellier.L., Chiu,S., Rubin,E. and Cheng,J.F.
Direct Submission
Submitted (13-JUL-2000) Genome Science Department, Lawrence
Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,
CA 94720, USA
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Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W.-J., Zimmer, A. and Zody, M.

TITLE JOURNAL

Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Apr 22, 2000 this sequence version replaced gi:645433.

All repeats were identified using RepeatMasker.

Smit, A.F.A. & Green, P. (1995-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBK

Web site: <http://www.seq.wi.mit.edu>

Contact: sequence-submissions@genome.wi.mit.edu

----- Project Information

Center project name: L2510

Center clone name: L.M.10

----- Summary Statistics

Sequencing vector: M13; M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960741

Consensus quality: 117571 bases at least Q40

Consensus quality: 145749 bases at least Q35

Consensus quality: 160940 bases at least Q20

Insert size: 185000; agarose-1p

Insert size: 171264; sum-of-contigs

Quality coverage: 2.9 in Q20 bases; agarose-1p

Quality coverage: 3.2 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 39 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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63762 68437: contig of 4676 bp in length
68438 68537: gap of 100 bp
68538 71458: contig of 2921 bp in length
71459 71558: gap of 100 bp
71559 76888: contig of 5330 bp in length
76889 76988: gap of 100 bp
76989 82113: contig of 5125 bp in length
82114 82213: gap of 100 bp
82214 88220: contig of 6007 bp in length
88221 88320: gap of 100 bp
88321 93499: contig of 5173 bp in length
93500 93599: gap of 100 bp
93600 97901: contig of 4302 bp in length
97902 98001: gap of 100 bp
98002 103016: contig of 5615 bp in length
103017 103116: gap of 100 bp
103117 109178: contig of 6362 bp in length
109179 109278: gap of 100 bp
109279 117307: contig of 8029 bp in length
117308 117407: gap of 100 bp
117408 124079: contig of 6672 bp in length
124080 124179: gap of 100 bp
124180 131281: contig of 7102 bp in length
131282 131381: gap of 100 bp
131382 138059: contig of 6678 bp in length
138060 138159: gap of 100 bp
138160 145491: contig of 7432 bp in length
145492 145591: gap of 100 bp
145592 157391: contig of 11800 bp in length
157392 157491: gap of 100 bp
157492 175064: contig of 17573 bp in length.
Location/Qualifiers
1. 175064
/organism="Homo sapiens"

FEATURES
Source

/db_xref="taxon:9606"
/clone_lib="RP11-IM10"
/clone_lib="RP11-11 Human Male BAC"
1. 1003
/note="assembly_fragment"
1104. 2634
/note="assembly_fragment"
2735. 4415
/note="assembly_fragment"
4516. 5785
/note="assembly_fragment"
5886. 7879
/note="assembly_fragment"
7980. 9686
/note="assembly_fragment"
9787. 12253
/note="assembly_fragment"
12354. 15228
/note="assembly_fragment"
15329. 17200
/note="assembly_fragment"
17301. 20131
/note="assembly_fragment"
20232. 22587
/note="assembly_fragment"
22688. 25707
/note="assembly_fragment"
25808. 28184
/note="assembly_fragment"
28285. 31338
/note="assembly_fragment"
31439. 34299
/note="assembly_fragment"
34400. 38318
/note="assembly_fragment"
38419. 42835
/note="assembly_fragment"
42936. 45448
/note="assembly_fragment"
45549. 48116
/note="assembly_fragment"
48217. 52618
/note="assembly_fragment"
52719. 56592
/note="assembly_fragment"
56693. 59635
/note="assembly_fragment"
59736. 63661
/note="assembly_fragment"
63762. 68437
/note="assembly_fragment"
68538. 71458
/note="assembly_fragment"
clone_end:SP6
vector_side:left
71559. 76888
misc_feature

Query Match 11.9%; Score 344; DB 2; Length 175064;
Best Local Similarity 99.7%; Pred. No. 6.1e-182;
Matches 394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 35 TACTCGGAGCTGGAGCTTGCATGAGCCGACATCGCACCATTGCATCCAGCTGGCA 94
DB 1645 TACTCGGAGCTGGAGCTTGCATGAGCCGACATCGCACCATTGCATCCAGCTGGCA 1586
QY 95 ACAAAGGTGAACCTCATCTCAATTAACAAAAAGAAATGATTTGGTGTCGACTTCA 154
DB 1585 ACAAAGGTGAACCTCATCTCAATTAACAAAAAGAAATGATTTGGTGTCGACTTCA 1526
QY 155 ATATAGTAGCAGAGAGAGAGAGAGAGATGGAGGTCAGGAGATCTTAATTACTCTCTA 214
DB 1525 AATAGTAGCAGAGAGAGAGAGAGAGATGGAGGTCAGGAGATCTTAATTACTCTCTA 1466

* 3313 33412: gap of 100 bp
* 33413 34268: contig of 856 bp in length
* 34269 34368: gap of 100 bp
* 34369 35204: contig of 816 bp in length
* 35205 35304: gap of 100 bp
* 35305 36156: contig of 852 bp in length
* 36157 36256: gap of 100 bp
* 36257 37128: contig of 872 bp in length
* 37129 37228: gap of 100 bp
* 37229 38083: contig of 855 bp in length
* 38084 38183: gap of 100 bp
* 38184 39031: contig of 848 bp in length
* 39032 39131: gap of 100 bp
* 39132 40006: contig of 875 bp in length
* 40007 40106: gap of 100 bp
* 40107 40967: contig of 861 bp in length
* 40968 41067: gap of 100 bp
* 41068 41913: contig of 846 bp in length
* 41914 42013: gap of 100 bp
* 42014 42824: contig of 811 bp in length
* 42825 42924: gap of 100 bp
* 42925 43776: contig of 852 bp in length
* 43777 43876: gap of 100 bp
* 43877 44752: contig of 876 bp in length
* 44753 44852: gap of 100 bp
* 44853 45724: contig of 872 bp in length
* 45725 45824: gap of 100 bp
* 45825 46643: contig of 819 bp in length
* 46644 46743: gap of 100 bp
* 46744 47599: contig of 856 bp in length
* 47600 47699: gap of 100 bp
* 47700 48551: contig of 852 bp in length
* 48552 48651: gap of 100 bp
* 48652 49485: contig of 834 bp in length
* 49486 49585: gap of 100 bp
* 49586 50440: contig of 855 bp in length
* 50441 50540: gap of 100 bp
* 50541 51404: contig of 864 bp in length
* 51405 51504: gap of 100 bp
* 51505 52372: contig of 868 bp in length
* 52373 52472: gap of 100 bp
* 52473 53328: contig of 856 bp in length
* 53329 53428: gap of 100 bp
* 53429 54268: contig of 840 bp in length
* 54269 54368: gap of 100 bp
* 54369 55229: contig of 861 bp in length
* 55230 55329: gap of 100 bp
* 55330 56197: contig of 868 bp in length
* 56198 56297: gap of 100 bp
* 56298 57163: contig of 866 bp in length
* 57164 57263: gap of 100 bp
* 57264 58130: contig of 867 bp in length
* 58131 58230: gap of 100 bp
* 58231 59082: contig of 852 bp in length
* 59083 59182: gap of 100 bp
* 59183 60020: contig of 838 bp in length
* 60021 60120: gap of 100 bp
* 60121 60983: contig of 863 bp in length
* 60984 61083: gap of 100 bp
* 61084 61935: contig of 852 bp in length
* 61936 62035: gap of 100 bp
* 62036 62866: contig of 841 bp in length
* 62867 62966: gap of 100 bp
* 62967 63827: contig of 861 bp in length
* 63828 63927: gap of 100 bp
* 63928 64783: contig of 856 bp in length
* 64784 64883: gap of 100 bp
* 64884 65740: contig of 857 bp in length
* 65741 66684: contig of 844 bp in length
* 66685 66784: gap of 100 bp
* 66785 67651: contig of 867 bp in length
* 67652 67751: gap of 100 bp

Query Match 5.4%; Score 156; DB 2; Length 69570;
Best local Similarity 99.5%; Pred. No. 7.6e-76;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2464 GGAAGAAAAATTCGGAAAGCAGGATTAGAGGAAGCAAAATTCACCTGGTGCCTTGGC 2523
|||||
Db 41139 GGAAGAAAAATTCGGAAAGCAGGATTAGAGGAAGCAAAATTCACCTGGTGCCTTGGC 41198
|||||
QY 2524 TGCCGGGAATGTGACCTAGAGAGTCTCCGGCGCAGCCGAGCCGAGCGCTTCCCGCGC 2583
|||||
Db 41199 TGCCGGGAATGTGACCTAGAGAGTCTCCGGCGCAGCCGAGCCGAGCGCTTCCCGCGC 41258
|||||
QY 2584 TCTTAGGCGCGCGCGCGCGCGCGGGAAGGAGCGAGCGCGGAGCCCTAAGACACCT 2643
|||||
Db 41259 TCTTAGGCGCGCGCGCGCGCGCGGGAAGGAGCGAGCGCGGAGCCCTAAGACACCT 41318
|||||
QY 2644 GCTGTACCTCCACCCACCCACCCACCC 2670
|||||
Db 41319 GCTGTACCTCCACCCACCCACCCACCC 41345

RESULT 14

AC021345 90698 bp DNA linear HTG 13-JUL-2000
LOCUS Homo sapiens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC021345
ACCESSION AC021345
VERSION AC021345.2 GI:9130845
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Graniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90698)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-24J9
Unpublished
2 (bases 1 to 90698)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
Choepl,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArellano,K., Dewar,K., Domino,M., Doyle,M., Feneator,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivari,T.M., Peterson,K.,
Pierre,N., Pisanic,C., Pollara,V., Raymond,C., Riley,P., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Tkemann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.

Direct Submission

Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6705761.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www.seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4483
Center clone name: 24_J_9

TITLE

JOURNAL

COMMENT

* NOTE: This record contains 92 individual
* sequencing reads that have not been assembled into

- contigs. Runs of N are used to separate the reads.
- and the order in which they appear is completely
- arbitrary. Low-pass sequence sampling is useful for
- identifying clones that may be generic and allows
- overlap relationships among clones to be deduced.
- However, it should not be assumed that this clone
- will be sequenced to completion. In the event that
- the record is updated, the accession number will
- be preserved.

* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allow
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this alone
* will be sequenced to completion, in the event that
* the record is updated, the accession number will
* be preserved.

1	910:	contig of 910 bp in length.
911	1010:	gap of 100 bp
1011	1873:	contig of 863 bp in length.
1874	1973:	gap of 100 bp
1974	2824:	contig of 851 bp in length.
2825	2924:	gap of 100 bp
2925	3802:	contig of 878 bp in length.
3803	3902:	gap of 100 bp
3903	4816:	contig of 914 bp in length.
4817	4916:	gap of 100 bp
4917	5759:	contig of 843 bp in length.
5760	5859:	gap of 100 bp
5860	6764:	contig of 905 bp in length.
6765	6864:	gap of 100 bp
6865	7747:	contig of 883 bp in length.
7748	7847:	gap of 100 bp
7848	8755:	contig of 908 bp in length.
8756	8855:	gap of 100 bp
8856	9753:	contig of 898 bp in length.
9754	9853:	gap of 100 bp
9854	10757:	contig of 904 bp in length.
10758	10857:	gap of 100 bp
10858	11732:	contig of 875 bp in length.
11733	11832:	gap of 100 bp
11833	12739:	contig of 967 bp in length.
12740	12839:	gap of 100 bp
12840	13710:	contig of 871 bp in length.
13711	13810:	gap of 100 bp
13811	14684:	contig of 874 bp in length.
14685	14784:	gap of 100 bp
14785	15662:	contig of 878 bp in length.
15663	15762:	gap of 100 bp
15763	16677:	contig of 915 bp in length.
16678	16777:	gap of 100 bp
16778	17678:	contig of 901 bp in length.
17679	17778:	gap of 100 bp
17779	18679:	contig of 901 bp in length.
18680	18779:	gap of 100 bp
18780	19632:	contig of 853 bp in length.
19633	19732:	gap of 100 bp
19733	20634:	contig of 922 bp in length.
20635	20734:	gap of 100 bp
20735	21620:	contig of 883 bp in length.
21621	21720:	gap of 100 bp
21721	22579:	contig of 859 bp in length.
22580	22679:	gap of 100 bp
22680	23568:	contig of 889 bp in length.
23569	23668:	gap of 100 bp
23669	24554:	contig of 886 bp in length.
24555	24654:	gap of 100 bp
24655	25521:	contig of 867 bp in length.
25522	25621:	gap of 100 bp
25622	26487:	contig of 865 bp in length.
26488	26587:	gap of 100 bp
26588	27464:	contig of 877 bp in length.
27465	27564:	gap of 100 bp
27565	28466:	contig of 902 bp in length.
28467	28566:	gap of 100 bp
28567	29464:	contig of 898 bp in length.
29465	29564:	gap of 100 bp
29565	30447:	contig of 883 bp in length.
30448	30547:	gap of 100 bp
30548	31453:	contig of 906 bp in length.
31454	31553:	gap of 100 bp

repeat_region complement(36689..37629)

Query Match 2.2% Score 65; DB 9; Length 126295;
Best Local Similarity 100.0%; Pred. No. 1.9e-24;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1017 GAATCGACTACTGAACCTGCTCCGGGTCAAGGATTCCTGCGTACGCTG 1076

||||| 10177 GTGAG 1081

||||| 31175 CTGAG 31179

RESULT 17

AL807243/c

LOCUS 186889 bp DNA linear HTG 30-JUN-2002
DEFINITION Mus musculus chromosome 4 clone RP23-25D17, *** SEQUENCING IN
PROGRESS ***, 24 unordered pieces.

AL807243 GI:21668234

VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
1 (bases 1 to 186889)

McLay, K.

Direct Submission

Submitted (29-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail: enquiries;
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk

on Jul 2, 2002 this sequence version replaced gi:21668136.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Web site: <http://www.sanger.ac.uk>

Contact: humquery@sanger.ac.uk

----- Project Information

Center project name: BM25D17

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Chemistry: Dye-terminator; 100% of reads

Consensus quality: 175959 bases at least Q40

Consensus quality: 179463 bases at least Q30

Consensus quality: 182069 bases at least Q20

Insert size: 184589; sum-of contigs

Insert size: 189466; 5.5% error; adaptor-seq

Quality coverage: 4.72x in 920 bases; sum-of contigs Quality

coverage: 4.82x in 920 bases; adaptor-seq

----- NOTE: This is a 'working draft' sequence. It currently
consists of 24 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 4849: contig of 4849 bp in length

4850 4949: gap of 100 bp

4950 22620: contig of 17671 bp in length

22621 22720: gap of 100 bp

22721 29963: contig of 7243 bp in length

29964 30063: gap of 100 bp

30064 40087: contig of 10024 bp in length

40088 40187: gap of 100 bp

40188 44438: contig of 4251 bp in length

44439 44538: gap of 100 bp

44539 48960: contig of 4422 bp in length

48961 49060: gap of 100 bp

49061 56007: contig of 6947 bp in length

56008 56107: gap of 100 bp

56108 58284: contig of 2177 bp in length

58285 58384: gap of 100 bp

58385 60786: contig of 2402 bp in length

60787 60886: gap of 100 bp

60887 66707: contig of 5821 bp in length

66708 66807: gap of 100 bp

66808 92102: contig of 25295 bp in length

92103 92202: gap of 100 bp

92203 99909: contig of 7707 bp in length

99910 100009: gap of 100 bp

100010 103760: contig of 3751 bp in length

103761 103860: gap of 100 bp

103861 110765: contig of 6905 bp in length

110766 110865: gap of 100 bp

110866 114685: contig of 3820 bp in length

114686 114785: gap of 100 bp

114786 125959: contig of 11174 bp in length

125960 126059: gap of 100 bp

126060 128749: contig of 2690 bp in length

128750 128849: gap of 100 bp

128850 132373: contig of 3524 bp in length

132374 132473: gap of 100 bp

132474 134930: contig of 2457 bp in length

134931 135030: gap of 100 bp

135031 139301: contig of 4271 bp in length

139302 139401: gap of 100 bp

139402 144448: contig of 5047 bp in length

144449 144548: gap of 100 bp

144549 147074: contig of 2526 bp in length

147075 147174: gap of 100 bp

147175 156317: contig of 9143 bp in length

156318 156417: gap of 100 bp

156418 186889: contig of 30472 bp in length.

FEATURES

Source

1..186889

/organism="Mus musculus"

/db_xref="taxon:10090"

/chromosome="4"

/clone "RP23-25D17"

/clone_lib="RPC1-23"

misc_feature

1..4849

/note="assembly fragment:01920

fragment_chain:1"

4950..22620

/note="assembly fragment:01761

fragment_chain:1"

22721..29963

/note="assembly fragment:00140

fragment_chain:1"

30064..40087

/note="assembly fragment:00335

fragment_chain:1"

40188..44438

/note="assembly fragment:00241

fragment_chain:1"

44539..48960

/note="assembly fragment:01430

fragment_chain:1"

49061..56007

/note="assembly fragment:01667

fragment_chain:1"

56108..58284

/note="assembly fragment:00965

fragment_chain:2"

58385..60786

/note="assembly fragment:01660

fragment_chain:2"

60887..66707

/note="assembly fragment:00374

fragment_chain:2"

66808..92102

/note="assembly fragment:01792

```

misc_feature      fragment_chain:2"
92203...99909
/note="assembly_fragment:01082
fragment_chain:2"
100010...103760
/note="assembly_fragment:00358
fragment_chain:2"
103861...110765
/note="assembly_fragment:01182
fragment_chain:3"
110866...114685
/note="assembly_fragment:01582
fragment_chain:3"
114786...125959
/note="assembly_fragment:00043
fragment_chain:3"
126060...128749
/note="assembly_fragment:00352
fragment_chain:3"
128850...132373
/note="assembly_fragment:00217
fragment_chain:4"
132474...134930
/note="assembly_fragment:01737
fragment_chain:4"
135031...139301
/note="assembly_fragment:00487"
139402...144448
/note="assembly_fragment:00557"
144549...147074
/note="assembly_fragment:01342"
147175...156317
/note="assembly_fragment:01564.0"
156418...186889
/note="assembly_fragment:01772"
BASE COUNT      52900 a 39593 c 40710 q 51348 t 2348 others
ORIGIN
Query Match      2.18; Score 61; DB 2; Length 195889;
Best Local Similarity 100.0%; Pred. No. 3,Se-22;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2744 CTCACGTCCTTCCTGCTGACTGACTACATACAGAGCGGGAGAGGGCGGG 2803
|||||
DB 9251 CTCACGTCCTTCCTGCTGACTGACTACATACAGAGCGGGAGAGGGCGGG 99192
QY 2804 G 2804
DB 99191 G 99191

RESULT 18
AC021850/c
LOCUS          AC021850      206966 bp      DNA      linear      PRI 09-MAY-2001
DEFINITION     Homo sapiens BAC clone RP11-389E17 from 4, complete sequence.
ACCESSION      AC021850
VERSION        AC021850.8 GI:12862232
KEYWORDS       HTC.
SOURCE         Homo sapiens.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 206966)
Sulston,J.E. and Waterston,R.
TITLE          Toward a complete human genome sequence
JOURNAL        Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE        99063792
PUBMED         9847074
REFERENCE      2 (bases 1 to 206966)
AUTHORS        Kang,K., Maupin,K. and Ureta-M.
TITLE          The sequence of Homo sapiens BAC clone RP11-389E17
JOURNAL        Unpublished
REFERENCE      3 (bases 1 to 206966)

```

AUTHORS TITLE JOURNAL:

REFERENCE
AUTHORS
TITLE
JOURNAL:

REFERENCE
AUTHORS
TITLE
JOURNAL:

COMMENT

Waterston,R.H.
Direct Submission
Submitted (20-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 206966)
Waterston,R.H.
Direct Submission
Submitted (16-FEB-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 206966)
Waterston,R.
Direct Submission
Submitted (09-MAY-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Feb 16, 2001 this sequence version replaced gi:11761497.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics

Center project name: H_NH0389E17

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e. phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RP11 human BAC library was made from the blood of one male donor, as described by Osogawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateo,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-62B4. Actual start of this clone is at base position 1 of RP11-389E17; actual end is at base position 206966 of RP11-389E17.

FEATURES

```

source
1..206966
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/map="4"
/clone="RP11-389E17"
/clone_lib="RP11"
3..256
/rpt_family="L1"
389..509
/rpt_family="L1"
523..1023
/rpt_family="L1"
repeat_region
repeat_region
repeat_region

```

repeat_region 1088..1319 /rpt_family="L1"
repeat_region 1775..1908 /rpt_family="MIR"
repeat_region 1930..1950 /rpt_family="MIR"
repeat_region 2531..2753 /rpt_family="AT_rich"
repeat_region 2772..2792 /rpt_family="Alu"
repeat_region 2987..3022 /rpt_family="AT_rich"
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repeat_region 9284..9364 /rpt_family="L2"
repeat_region 9388..9734 /rpt_family="L1"
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repeat_region 12620..12715 /rpt_family="L2"
repeat_region 12726..12923 /rpt_family="MER2_type"
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repeat_region 19217..19324 /rpt_family="MIR"
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repeat_region 35013..35078 /rpt_family="L1"
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Query Match 2.1% Score 61; DB 9; Length 206966;
Best Local Similarity 100.0%; Pred. No. 3.5e-22;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1017 GATCTGACATCACTGAACCTCTGCTCCCGGGTTCAAGCGATTCTCTGCGCTCAGCCTC 1076
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DB 45729 GATCTGACATCACTGAACCTCTGCTCCCGGGTTCAAGCGATTCTCTGCGCTCAGCCTC 45670

QY 1077 C 1077
DB 45669 C 45669

RESULT 14

AF287263 AF287263 278572 bp DNA linear ROD 23-APR-2001
LOCUS Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abca1)
DEFINITION gene, complete cds.
ACCESSION AF287263.1 GI:11611824
VERSION AF287263.1
KEYWORDS Mus musculus.
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 278572)
AUTHORS Qiu.Y., Cavelier.L., Chiu.S., Yang.X., Rubin.E. and Cheng.J.F.
TITLE Human and mouse ABCA1 comparative sequencing and transgenesis studies revealing novel regulatory sequences
JOURNAL Genomics 73 (1), 66-76 (2001)
MEDLINE 21251004
PUBMED 11352567
REFERENCE 2 (bases 1 to 278572)
AUTHORS Qiu.Y., Cavelier.L., Chiu.S., Rubin.E. and Cheng.J.F.
TITLE Direct Submission
JOURNAL Submitted (14-JUL-2000) Genome Science Department, Lawrence Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley, CA 94720, USA

AUTHORS

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Bana, N., Bastien, V., Bloom, T., Boquslavsky, L., Boukhalter, B., Canarata, J., Chang, J., Chazaro, B., Choquet, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kellis, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., MacDonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Mencus, L., Mihova, T., Muegg, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Rella, R., Rose, C., Rodoy, P., Roman, J., Roy, A., Schauer, S., Schuback, R., Suman, S., Severy, P., Smith, C., Spencer, B., Stange-Thumann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zalcoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

COMMENT

Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 30, 2002 this sequence version replaced gi:17149709.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1995-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L21813

Center clone name: 2319_g_14

NOTE: This record contains 54 individual

sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be detected. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

1 734: contig of 74 bp in length
735 834: gap of 100 bp
835 1552: contig of 718 bp in length
1553 1652: gap of 100 bp
1653 2405: contig of 754 bp in length
2406 2505: gap of 100 bp
2506 3239: contig of 734 bp in length
3240 3339: gap of 100 bp
3340 4094: contig of 755 bp in length
4095 4194: gap of 100 bp
4195 4930: contig of 736 bp in length
4931 5030: gap of 100 bp
5031 5753: contig of 723 bp in length
5754 5853: gap of 100 bp
5854 6627: contig of 774 bp in length
6628 6727: gap of 100 bp
6728 7449: contig of 722 bp in length
7450 7549: gap of 100 bp
7550 8322: contig of 773 bp in length
8323 8422: gap of 100 bp
8423 9126: contig of 704 bp in length
9127 9226: gap of 100 bp
9227 9973: contig of 747 bp in length
9974 10073: gap of 100 bp
10074 10811: contig of 748 bp in length
10812 10911: gap of 100 bp
10912 11635: contig of 724 bp in length
11636 11735: gap of 100 bp
11736 12489: contig of 754 bp in length
12490 12589: gap of 100 bp
12590 13349: contig of 760 bp in length
13350 13449: gap of 100 bp
13450 14174: contig of 725 bp in length
14175 14274: gap of 100 bp
14275 15022: contig of 748 bp in length
15023 15122: gap of 100 bp
15123 15716: contig of 594 bp in length
15717 15816: gap of 100 bp
15817 16563: contig of 747 bp in length
16564 16663: gap of 100 bp
16664 17387: contig of 724 bp in length
17388 17487: gap of 100 bp
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18228 18327: gap of 100 bp
18328 19058: contig of 731 bp in length
19059 19158: gap of 100 bp
19159 19883: contig of 725 bp in length
19884 19983: gap of 100 bp
19984 20734: contig of 751 bp in length
20735 20834: gap of 100 bp
20835 21541: contig of 707 bp in length
21542 21641: gap of 100 bp
21642 22399: contig of 758 bp in length
22400 22499: gap of 100 bp
22500 23236: contig of 737 bp in length
23237 23336: gap of 100 bp
23337 24091: contig of 755 bp in length
24092 24191: gap of 100 bp
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25027 25760: contig of 734 bp in length
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38307 39038: contig of 732 bp in length
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41539 41638: gap of 100 bp
41639 42396: contig of 758 bp in length


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* 52108 52207: gap of 100 bp
* 52208 52909: contig of 702 bp in length
* 52910 53009: gap of 100 bp
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Best Local Similarity 2.0%; Score 58; DB 2; Length 57662;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGGCTCCAAAGTGCTGGGATTACAGGCATGAGCCACTGGCCGACG 1244
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Db 39017 CTGCCACCTTGGGCTCCAAAGTGCTGGGATTACAGGCATGAGCCACTGGCCGACG 38960

RESULT 22
HS931E15/c
LOCUS
DEFINITION Human DNA sequence from clone 931E15 on chromosome Xq25. Contains
SISS, GSSs and genomic marker DXS8098, complete sequence.
ACCESSION AL023575.1 GI:3618163
VERSION AL023575.1
KEYWORDS HTG; DXS8098.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 81874)
AUTHORS Pavitt,R.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-1998) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonequest@sanger.ac.uk
COMMENT On Sep 18, 1998 this sequence version replaced gi:3550203.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
This sequence was generated from part of bacterial clone cosmids of
human chromosome X, constructed by the Sanger Centre Chromosome X
Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/ChrX>
931E15 is from the library RPiC15 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
details see <http://bacpac.med.buffalo.edu/VECTOR:pcyPAC2>
IMPORTANT: This sequence is not the entire insert of clone 931E15.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
neighbouring submissions.
The true left end of 424J12 (Z82207) is at 36643 in this sequence.
The true right end of 50662 (Z82213) is at 37431.
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repeat_region complement(228..531)
/note="AluX repeat: matches 292..1 of consensus"
repeat_region 569..687

Anderson, S., Barna, N., Bastien, V., Bloom, J., Bloom, J., Boucklavsky, L.,
 Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, L.,
 Chazaro, B., Choepel, Y., Colangelo, M., Collics, S., Collymore, A.,
 Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
 Fato, S., Ferreira, P., FitzHugh, W., Gage, D., Gajanan, J., Gardyna, S.,
 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
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 Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
 Raymond, C., Retta, R., Rieback, M., Riley, K., Risse, C., Rogov, P.,
 Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,
 Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
 Topham, K., Travers, M., Travis, N., Trigglio, J., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
 Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 4 (bases 1 to 145264)

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

Anderson, S., Barna, N., Bastien, V., Bloom, J., Bloom, J., Boucklavsky, L.,
 Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, L.,
 Chazaro, B., Choepel, Y., Colangelo, M., Collics, S., Collymore, A.,
 Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
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 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
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 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
 Submitted (31-MAR-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 31, 2002 this sequence version replaced gi14543475.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996 1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLE
 JOURNAL
 COMMENT

Center: Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www.seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L24018
 Center clone name: 48_Q_9

FEATURES
 Source

Location/Qualifiers
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 repeat_region 16611..16630

NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence. As soon as it is available and the accession number will be preserved.

- * 1732: contig of 1732 bp in length
- * 1733 1812: gap of 100 bp
- * 1833 2945: contig of 1113 bp in length;
- * 2946 3045: gap of 100 bp
- * 3046 4116: contig of 1071 bp in length

4217	5937:	contig of 1541 bp in length
5758	5857:	gap of 100 bp
5858	7545:	contig of 1688 bp in length
7546	7645:	gap of 100 bp
7646	11527:	contig of 3882 bp in length
11628	11627:	gap of 100 bp
11628	55477:	contig of 43850 bp in length
55478	55577:	gap of 100 bp
55578	66767:	contig of 11190 bp in length
66768	66867:	gap of 100 bp
66868	83973:	contig of 17106 bp in length
83974	84073:	gap of 100 bp
84074	107174:	contig of 23101 bp in length
107175	107274:	gap of 100 bp
107275	137395:	contig of 30121 bp in length
137496	137495:	gap of 100 bp
137496	146312:	contig of 8817 bp in length

* 11628 55477: contig of 43850 bp in length
* 55478 55577: gap of 100 bp
* 55578 66767: contig of 11190 bp in length
* 66768 68667: gap of 100 bp
* 68668 83973: contig of 17106 bp in length
* 83974 84073: gap of 100 bp
* 84074 107174: contig of 23101 bp in length
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* 107275 137395: contig of 30121 bp in length
* 137396 137495: gap of 100 bp
* 137496 446312: contig of 8817 bp in length.

66768 66867: gap of 100 bp in length.
66768 66868 83973: contig of 17106 bp in length.
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83974 84074 107174: contig of 100 bp in length.
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Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, R.,
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
 Testaye, S., Theodore, J., Tirrell, A., Travers, M., Triguillo, J.,
 Vassiliev, H., Viel, R., Vo, A., Wilson, R., Wu, X., Wyman, D., Ye, W., J.,
 Young, G., Zainoun, J., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (28-APR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jun 4, 2000 this sequence version replaced at 768456.
 All repeats were identified using RepeatMasker:
 Smith, A.F.A. & Green, P. (1996) 1997
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center:
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIRB
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: t10095
 Center clone name: 21_M_2

----- Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 146955 bases at least Q40
 Consensus quality: 151080 bases at least Q30
 Consensus quality: 155108 bases at least Q20
 Insert size: 163000; agarose-1p
 Insert size: 156250; sum-of-ctnigs
 Quality coverage: 3.6 in Q20 bases; agarose-1p
 Quality coverage: 3.8 in Q20 bases; sum-of-ctnigs

NOTE: This is a 'working draft' sequence. It currently
 consists of 23 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1
 1750 1849: contig of 1749 bp in length
 1850 3169: contig of 1320 bp in length
 3170 3269: gap of 100 bp
 3270 4573: contig of 1304 bp in length
 4574 4673: gap of 100 bp
 4674 7997: contig of 3324 bp in length
 7998 8097: gap of 100 bp
 8098 13045: contig of 4948 bp in length
 13046 13145: gap of 100 bp
 13146 16766: contig of 3621 bp in length
 16767 16866: gap of 100 bp
 16867 20859: contig of 4993 bp in length
 20860 20959: gap of 100 bp
 20960 23743: contig of 2784 bp in length
 23744 23843: gap of 100 bp
 23844 27652: contig of 3809 bp in length
 27653 27752: gap of 100 bp
 27753 31395: contig of 3643 bp in length
 31396 31495: gap of 100 bp
 31496 36408: contig of 4913 bp in length
 36409 36508: gap of 100 bp
 36509 42265: contig of 5757 bp in length
 42266 42365: gap of 100 bp
 42366 47307: contig of 4942 bp in length
 47308 47407: gap of 100 bp
 47408 52438: contig of 5041 bp in length
 52439 52538: gap of 100 bp
 52539 60035: contig of 7497 bp in length
 60036 60135: gap of 100 bp
 60136 68356: contig of 8221 bp in length
 68357 68456: gap of 100 bp
 68457 76898: contig of 8442 bp in length

* 76899 76998: gap of 100 bp
 * 85827: contig of 8829 bp in length
 * 85828 85927: gap of 100 bp
 * 85928 96327: contig of 10400 bp in length
 * 96328 96427: gap of 100 bp
 * 96428 108928: contig of 12501 bp in length
 * 108929 109028: gap of 100 bp
 * 109029 121274: contig of 12246 bp in length
 * 121275 121474: gap of 100 bp
 * 121375 141287: contig of 19913 bp in length
 * 141288 141387: gap of 100 bp
 * 141388 158450: contig of 17063 bp in length.

FEATURES
 source
 1. 158450
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="2"
 /map="2"
 /clone_lib="RPC1-11 Human Male BAC"
 1. 1749

misc_feature
 1850..3169
 /note="assembly_fragment"

misc_feature
 3270..4573
 /note="assembly_fragment"

misc_feature
 4674..7997
 /note="assembly_fragment"

misc_feature
 8098..13045
 /note="assembly_fragment"

misc_feature
 13146..16766
 /note="assembly_fragment"

misc_feature
 16867..20859
 /note="assembly_fragment"

misc_feature
 20960..23743
 /note="assembly_fragment"

misc_feature
 vector_side:left
 clone_end:SP6

misc_feature
 23844..27652
 /note="assembly_fragment"

misc_feature
 vector_side:left
 clone_end:17

misc_feature
 27753..31395
 /note="assembly_fragment"

misc_feature
 31496..36408
 /note="assembly_fragment"

misc_feature
 36509..42265
 /note="assembly_fragment"

misc_feature
 42466..47307
 /note="assembly_fragment"

misc_feature
 47408..52438
 /note="assembly_fragment"

misc_feature
 52539..60035
 /note="assembly_fragment"

misc_feature
 60136..68356
 /note="assembly_fragment"

misc_feature
 68457..76898
 /note="assembly_fragment"

misc_feature
 76999..85827
 /note="assembly_fragment"

misc_feature
 85928..96327
 /note="assembly_fragment"

misc_feature
 96428..108928
 /note="assembly_fragment"

misc_feature
 109029..121274
 /note="assembly_fragment"

misc_feature
 121375..141287
 /note="assembly_fragment"

misc_feature
 141388..158450
 /note="assembly_fragment"

misc_feature
 29527 c 30211 g 48215 t

BASE COUNT 48293 a 29527 c 30211 g 48215 t

ORIGIN

```

Query Match          2.0%  Score 58:  DB 2:  Length 15645r;
Best Local Similarity 100.0%:  Pred. No. 1.7e-20;
Matches 58:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:

QY 1187 CTGCCACCTTGCCCTCCCAAGTGTGGGATTACAGGATGAGCACTGCGGCTAGC 1244
|||||
DB 64066 CTGCCACCTTGCCCTCCCAAGTGTGGGATTACAGGATGAGCACTGCGGCTAGC 64066

RESULT 30
AC093737
LOCUS
DEFINITION
Homo sapiens chromosome 2 clone RP11-21M2, WORKING DRAFT SEQUENCE,
2 unordered pieces.
ACCESSION
AC093737.1 GI:15529775
VERSION
AC093737.1 GI:15529775
KEYWORDS
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLIOP.
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 162419)
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 162419)
Waterston,R.H.
Direct Submission
Submitted (10-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/qsc/index.shtml
----- Project Information -----
Center project name: H.MH0021M02
Drafting center: QC core
----- Summary Statistics -----
Sequencing vector: M13; 36%
Chemistry: Dye-primer ET; 0% of reads
Assembly program: Phrap; version 0.960319
Consensus quality: 162004 bases at least Q40
Consensus quality: 162155 bases at least Q30
Consensus quality: 162211 bases at least Q20
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 70250: contig of 70250 bp in length
* 70251 70350: gap of unknown length
* 70351 162419: contig of 92069 bp in length.
FEATURES
    source
        1..162419
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="2"
            /clone="RP11-21M2"
    misc-feature
        1..70250
            /note="assembly_name:Contig13
            clone_end:7
            vector_side:right"
        70351..162419
            misc-feature

```

```

/note="assembly_name:Contig14
clone_end:SP6
vector_side:right"
BASE COUNT  50019 a 30933 c 30950 g 50417 t 100 others
ORIGIN

Query Match          2.0%  Score 58:  DB 2:  Length 162419;
Best Local Similarity 100.0%:  Pred. No. 1.7e-20;
Matches 58:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:

QY 1187 CTGCCACCTTGCCCTCCCAAGTGTGGGATTACAGGATGAGCACTGCGGCTAGC 1244
|||||
DB 52046 CTGCCACCTTGCCCTCCCAAGTGTGGGATTACAGGATGAGCACTGCGGCTAGC 52103

RESULT 31
AC019307
LOCUS
DEFINITION
Homo sapiens chromosome 8 clone RP11-359P11 map 8, WORKING DRAFT
SEQUENCE, 33 unordered pieces.
ACCESSION
AC019307.3 GI:7249157
VERSION
AC019307.3 GI:7249157
KEYWORDS
HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 166011)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguslavsky,L., Bouckgalter,B., Brown,A., Burkett,G., Castle,A.,
Choquel,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P.,
DeArillano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lebecky,J., Levine,R., Liu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrum,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severi,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo.A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (31-DEC-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 16, 2000 this sequence version replaced gi:6721260.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center -----
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: L5223
Center clone name: 359_P11
----- Summary Statistics -----
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 150247 bases at least Q40
Consensus quality: 157501 bases at least Q30
Consensus quality: 159942 bases at least Q20
Insert size: 177000; agarose-fp
Insert size: 162811; sum-of-contigs

```

Quality coverage: 3.9 in Q20 bases; agarose-gp
Quality coverage: 4.3 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1042: contig of 1042 bp in length
1043 1142: gap of 100 bp
1143 2142: contig of 1000 bp in length
2143 2242: gap of 100 bp
2243 3710: contig of 1468 bp in length
3711 3810: gap of 100 bp
3811 5057: contig of 1247 bp in length
5058 5157: gap of 100 bp
5158 6697: contig of 1540 bp in length
6698 6797: gap of 100 bp
6798 7389: contig of 592 bp in length
7390 7489: gap of 100 bp
7490 8708: contig of 1219 bp in length
8709 8808: gap of 100 bp
8809 10176: contig of 1368 bp in length
10177 10276: gap of 100 bp
10277 11738: contig of 1462 bp in length
11739 11838: gap of 100 bp
11839 14084: contig of 2246 bp in length
14085 14184: gap of 100 bp
14185 15991: contig of 1807 bp in length
15992 16091: gap of 100 bp
16092 18991: contig of 2890 bp in length
18992 18991: gap of 100 bp
18992 21414: contig of 2423 bp in length
21415 21514: gap of 100 bp
21515 23808: contig of 2394 bp in length
23809 23908: gap of 100 bp
23909 25419: contig of 1511 bp in length
25420 25519: gap of 100 bp
25520 28063: contig of 2544 bp in length
28064 28163: gap of 100 bp
28164 32741: contig of 4578 bp in length
32742 32841: gap of 100 bp
32842 37294: contig of 4453 bp in length
37295 37394: gap of 100 bp
37395 42230: contig of 4836 bp in length
42231 42330: gap of 100 bp
42331 47685: contig of 5455 bp in length
47686 47785: gap of 100 bp
47786 52553: contig of 4768 bp in length
52554 52653: gap of 100 bp
52654 59378: contig of 6725 bp in length
59379 59478: gap of 100 bp
59479 64583: contig of 5105 bp in length
64584 64683: gap of 100 bp
64684 72618: contig of 7945 bp in length
72619 72718: gap of 100 bp
72719 78416: contig of 5698 bp in length
78417 78516: gap of 100 bp
78517 85048: contig of 6532 bp in length
85049 85148: gap of 100 bp
85149 91596: contig of 6448 bp in length
91597 91696: gap of 100 bp
91697 98785: contig of 7089 bp in length
98786 98885: gap of 100 bp
98886 108615: contig of 9730 bp in length
108616 108715: gap of 100 bp
108716 120908: contig of 12193 bp in length
120909 121008: gap of 100 bp
121009 131478: contig of 10470 bp in length
131479 131578: gap of 100 bp

* 131579 144378: contig of 12800 bp in length
* 144379 144478: gap of 100 bp
* 144479 166011: contig of 21533 bp in length.

FEATURES	Location/Qualifiers	Source
	1..166011	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/chromosome="8"	
	/map="8"	
	/clone="RP11-359P11"	
	/clone_lib="RPC1-11 Human Male BAC"	
	1..1042	
misc_feature	/note="assembly_fragment"	
	1143..2142	
misc_feature	/note="assembly_fragment"	
	2243..3710	
misc_feature	/note="assembly_fragment"	
	3811..5057	
misc_feature	/note="assembly_fragment"	
	5158..6697	
misc_feature	/note="assembly_fragment"	
	6798..7389	
misc_feature	/note="assembly_fragment"	
	clone_end:T7	
	vector_side:right	
	7490..8708	
misc_feature	/note="assembly_fragment"	
	8809..10176	
misc_feature	/note="assembly_fragment"	
	10277..11738	
misc_feature	/note="assembly_fragment"	
	11839..14084	
misc_feature	/note="assembly_fragment"	
	14185..15991	
misc_feature	/note="assembly_fragment"	
	16092..18891	
misc_feature	/note="assembly_fragment"	
	18992..21414	
misc_feature	/note="assembly_fragment"	
	21515..23808	
misc_feature	/note="assembly_fragment"	
	23909..25419	
misc_feature	/note="assembly_fragment"	
	clone_end:SP6	
	vector_side:right	
	25520..28063	
misc_feature	/note="assembly_fragment"	
	28164..32741	
misc_feature	/note="assembly_fragment"	
	32842..37294	
misc_feature	/note="assembly_fragment"	
	37395..42230	
misc_feature	/note="assembly_fragment"	
	42331..47685	
misc_feature	/note="assembly_fragment"	
	47786..52553	
misc_feature	/note="assembly_fragment"	
	52654..59378	
misc_feature	/note="assembly_fragment"	
	59479..64583	
misc_feature	/note="assembly_fragment"	
	64684..72618	
misc_feature	/note="assembly_fragment"	
	72719..78416	
misc_feature	/note="assembly_fragment"	
	78517..85048	
misc_feature	/note="assembly_fragment"	
	85149..91596	
misc_feature	/note="assembly_fragment"	
	91697..98785	
misc_feature	/note="assembly_fragment"	

Query Match

2.0%; Score 58; DB 2; Length 166011;

```

Best Local Similarity 100.0%; Pred. No. 1,7e-20; Gaps 3;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 3;

QY 1187 CTGCCACCTTGGCTCCCAAGTGTGGGATTACAGGATGAGCCACTGCGCCAGC 1244
|||||
Db 51640 CTGCCACCTTGGCTCCCAAGTGTGGGATTACAGGATGAGCCACTGCGCCAGC 51697

RESULT 32
AC069120/c
LOCUS
DEFINITION
Homo sapiens chromosome 8 clone RP11-675F6 map 8, *** SEQUENCING IN
PROGRESS ***, 15 unordered pieces.
AC069120
AC069120.4 GI:16931029
HTG: HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 177533)
Birken, B., Linton, L., Nusbaum, C., Lander, E., Aldred, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedalov, F.,
Bonuskavly, L., Boukhallal, B., Brown, A., Buckett, G.,
Campiano, A., Castle, A., Choquet, Y., Colanquhoun, N., Collins, S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
Galligan, J., Gardy, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Haas, R., Heaford, A., Herton, R.,
Howland, J. C., Iliev, I., Johnson, K., Jones, C., Karn, J., Karatas, A.,
Klein, J., Larocque, K., Lamazares, R., Landers, T., Lebecky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGowan, A., McKernan, K., McKeever, R.,
McLarty, J., Meneus, L., Mihova, T., Miranda, C., Mienda, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, R.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigglio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (18-MAY-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 15, 2001 this sequence version replaced gi:1457522.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Smit, A.F.A. & Green, P. (1996-1997)
Center: Genome Center
Center code: W1BR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
Project Information:
Center project name: L9305
Center clone name: 675_F_6
*****
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved
*
* 1 1253: contig of 1253 bp in length
* 1254 1353: gap of 100 bp
* 1354 26734: contig of 25381 bp in length

```

```

26735 26834: gap of 100 bp
26835 60661: contig of 33827 bp in length
60662 60761: gap of 100 bp
60762 91265: contig of 30504 bp in length
91266 91365: gap of 100 bp
91366 108600: contig of 17235 bp in length
108601 108700: gap of 100 bp
108701 114249: contig of 5549 bp in length
114250 114349: gap of 100 bp
114350 128608: contig of 12459 bp in length
128609 128708: gap of 100 bp
128709 137847: contig of 10939 bp in length
137848 137947: gap of 100 bp
137948 140143: contig of 2196 bp in length
140144 140243: gap of 100 bp
140244 143309: contig of 3066 bp in length
143310 143409: gap of 100 bp
143410 145669: contig of 2260 bp in length
145670 145769: gap of 100 bp
145770 154154: contig of 8385 bp in length
154155 154254: gap of 100 bp
154255 15634: contig of 2180 bp in length
156343 156534: gap of 100 bp
156535 166277: contig of 9743 bp in length
166278 166377: gap of 100 bp
166378 177533: contig of 11156 bp in length.
FEATURES
Location/Qualifiers
1..177533
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="8"
/clone="RP11-675F6"
/cclone.lib="RP11-11 Human Male BAC"
BASE COUNT 46561 a 40970 c 39158 g 49339 t 1505 others
ORIGIN
Query Match 2.0%; Score 58; DB 2: Length 177533;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1187 CTGCCACCTTGGCTCCCAAGTGTGGGATTACAGGATGAGCCACTGCGCCAGC 1244
|||||
Db 123261 CTGCCACCTTGGCTCCCAAGTGTGGGATTACAGGATGAGCCACTGCGCCAGC 123204

RESULT 33
AC013281
LOCUS
DEFINITION
Homo sapiens chromosome 15 clone RP11-528M4, WORKING DRAFT
SEQUENCE, 12 unordered pieces.
AC013281
AC013281.5 GI:10048071
VERSION
HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
Homo sapiens
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 188820)
The sequence of Homo sapiens clone
Waterston, R.H.
Unpublished
2 (bases 1 to 188820)
Waterston, R.H.
Direct Submission
Submitted (05-NOV-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 10, 2000 this sequence version replaced gi:8568902.
COMMENT
*****
Center: Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC

```

Web site: <http://genome.wustl.edu/gsc/index.shtml>
 ----- Project Information -----
 Center project name: H_NH0528N04
 ----- Summary Statistics -----
 Sequencing vector: M13; 76%
 Sequencing: Dye-primer EL: 76% of reads
 Chemistry: Dye-terminator Big Dye; 24% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 179527 bases at least Q40
 Consensus quality: 182913 bases at least Q30
 Consensus quality: 184575 bases at least Q20
 Insert size: 203000; agarose-fp
 Insert size: 189063; sum-of-contigs
 Quality coverage: 4.28 in Q20 bases; agarose-fp
 Quality coverage: 4.60 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 12 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 *
 * 1 2415: contig of 2415 bp in length
 * 2416 2515: gap of unknown length
 * 2516 5539: contig of 3024 bp in length
 * 5540 5639: gap of unknown length
 * 5640 12163: contig of 6524 bp in length
 * 12164 12263: gap of unknown length
 * 12264 22743: contig of 10480 bp in length
 * 22744 22843: gap of unknown length
 * 22844 36050: contig of 13207 bp in length
 * 36051 38150: gap of unknown length
 * 38151 47862: contig of 1712 bp in length
 * 47863 47962: gap of unknown length
 * 47963 62123: contig of 1414 bp in length
 * 62124 62223: gap of unknown length
 * 62224 75585: contig of 13362 bp in length
 * 75586 75685: gap of unknown length
 * 75686 90351: contig of 14666 bp in length
 * 90352 90451: gap of unknown length
 * 90452 110259: contig of 19838 bp in length
 * 110260 110359: gap of unknown length
 * 110360 140334: contig of 24975 bp in length
 * 140335 140435: gap of unknown length
 * 140435 188820: contig of 48385 bp in length.

 Location/Qualifiers
 1..188820
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="15"
 /clone="RP11-528N4"
 1..2415
 /note="assembly_name:Contig15"
 2516..5539
 /note="assembly_name:Contig16"
 5640..12163
 /note="assembly_name:Contig17"
 12264..22743
 /note="assembly_name:Contig18"
 22844..36050
 /note="assembly_name:Contig19
 clone_end:SP6
 vector_side:right
 36151..47862
 /note="assembly_name:Contig10"
 47963..62123
 /note="assembly_name:Contig11"
 62224..75585
 /note="assembly_name:Contig12"
 75686..90351

misc_feature
 90452..110259
 /note="assembly_name:Contig13"
 misc_feature
 110360..140334
 /note="assembly_name:Contig14"
 misc_feature
 140435..188820
 /note="assembly_name:Contig15"
 misc_feature
 188820..44833
 /note="assembly_name:Contig16"
 BASE COUNT 48904 a 45259 c 44833 g 48717 t 1107 others
 ORIGIN
 Query Match 2.0% Score 58; DB 2: Length 188820;
 Best Local Similarity 100.0%; Pred. No. 1.7e-20;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1187 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCCACTGGCCGAGC 1244
 Db 123691 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCCACTGGCCGAGC 123748
 RESULT 34
 AC012668 192396 bp DNA linear PRI 09-JAN-2002
 LOCUS Homo sapiens BAC clone RP11-458D8 from 2, complete sequence.
 DEFINITION AC012668
 ACCESSION AC012668.1 GI:14589741
 VERSION AC012668.1
 KEYWORDS HTG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS Sulston, J.E. and Waterston, R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE 99083742
 PUBMED 9847074
 REFERENCE
 2 (bases 1 to 192396)
 AUTHORS Waligorski, J., Cotton, M. and Elliott, G.
 TITLE The sequence of Homo sapiens BAC clone RP11-458D8
 JOURNAL unpublished (2001)
 REFERENCE
 3 (bases 1 to 192396)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (02-NOV-1999) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 REFERENCE
 4 (bases 1 to 192396)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (03-JUL-2001) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 REFERENCE
 5 (bases 1 to 192396)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Jul 3, 2001 this sequence version replaced gi:13431202.
 COMMENT
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@watson.wustl.edu
 ----- Summary Statistics -----
 Center project name: H_NH0458D08

NOTICE: This sequence may not represent the entire insert of this
 clone. It may be shorter because we only sequence overlapping
 clone sections once, or longer because we provide a small overlap
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., paired quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/qsc>

SOURCE INFORMATION:

The RPCL11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Ziazi, R., Friedgen, E., Tatenoe, M., Catanese, J.J., and de Jong, P.J. (1995) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Priet de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-566F21, 2000 bp overlap; the clone sequenced to the right is RP11-489P15. Actual start of this clone is at base position 1 of RP11-456D8; actual end is at base position 192396 of RP11-458J8.

Data from 97986 to 98116 is covered only by a single plasmid subclone. Data from H_ACO12462 was used to finish this clone, AC012668.

FEATURES

Source

Location/Qualifiers

1..192396

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="2"

/map="2"

/clone="RP11-458J8"

/clone_lib="RPC1-11"

repeat_region

1182..11221

repeat_region

1511..11741

repeat_region

1773..2136

repeat_region

2154..2319

repeat_region

2305..2327

repeat_region

2362..2842

repeat_region

2843..2917

repeat_region

3022..3240

repeat_region

3334..3589

repeat_region

3617..3676

repeat_region

3678..4037

repeat_region

4157..4188

repeat_region

4265..4806

repeat_region

4977..5050

repeat_region

5051..5348

repeat_region

5349..6247

repeat_region

6007..6027

repeat_region

6007..6027

repeat_region

6007..6027

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6007..6027

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6007..6027

repeat_region

6007..6027


```

clone_end:T7
vector_side:right*
BASE COUNT 51569 a 46564 c 45000 g 48977 t 1224 others
ORIGIN

Query Match      2.0%; Score 58; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. NO. 1.7e-20;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGCATGACGACACGTCGACGACG 1244
      |||||||
DB 87925 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGCATGACGACGTCGACGACG 87982

RESULT 36
HSBA425M5/C
LOCUS
DEFINITION
  HSB425M5 194433 bp. DNA linear. 171 14-MAR-2001
  Human DNA sequence from clone RP11-425M5 on chromosome 20. Contains
  a GLRX (glutaredoxin (thioltransferase)) pseudogene, a PPIA
  (peptidylprolyl isomerase A (cyclophilin A)) pseudogene, the NNAT
  gene for neurexin, the BLCAP gene for bladder cancer 10 kD
  protein BC10, a putative novel transcript, BSIs, SSSs, GSSs and
  three putative CpG islands, complete sequence.
ACCESSION
  AL109614
VERSION
  AL109614.28 GI:8745190
KEYWORDS
  HTG; BC10; BLCAP; CpG island; cyclophilin; GLRX; neurexin; NNAT;
  PPIA.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 194433)
  Phillimore, B.
  Direct Submission
  Submitted (06-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
  CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
  requests: clonerequest@sanger.ac.uk
  On Jun 26, 2000 this sequence version replaced gi:7329727.
  During sequence assembly data is compared from overlapping clones.
  Where differences are found these are annotated as variations
  together with a note of the overlapping clone name. Note that the
  variation annotation may not be found in the sequence submission
  corresponding to the overlapping clone, as we submit sequences with
  only a small overlap as described above.
  The following abbreviations are used to associate primary accession
  numbers given in the feature table with their source databases:
  Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WormPeP; Inf,
  on the WormPeP database can be found at
  http://www.sanger.ac.uk/Projects/H/clovas/accomp This sequence
  was generated from part of bacterial clone RP11-425M5 from
  chromosome 20, constructed by the Sanger Centre Human 20
  Mapping Group. Further information can be found at
  http://www.sanger.ac.uk/HGP/Chr20
  This sequence was finished as follows unless otherwise noted: all
  regions were either double-stranded or sequenced with an alternate
  chemistry or covered by high quality data (i.e., phred quality >
  30); an attempt was made to resolve all sequencing problems, such
  as compressions and repeats; all regions were covered by at least
  one plasmid subclone or more than one M13 subclone; and the
  assembly was confirmed by restriction digest. RP11-425M5 is from
  the library RP11-11.2 constructed by the group of Pieter de Jong.
  For further details see
  http://www.chori.org/bacpac/home.htm
  VECTOR: pBAC3.6
  This sequence is the entire insert of clone RP11-425M5. The true
  left end of clone RP4-640H8 is at 176187 in this sequence. The true
  right end of clone RP4-592G19 is at 59744 in this sequence.
FEATURES
  Location/Qualifiers
    1..194433
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /chromosome="20"
      /clone="RP11-425M5"
  /clone_lib="RPC111.2"
  9..86
  /note="AluJ/FLAM repeat: matches 3..80 of consensus"
  424..701
  /note="MLT1-INTERNAL repeat: matches 308..583 of
  consensus"
  901..1251
  /note="MLT1F repeat: matches 170..540 of consensus"
  1528..1827
  /note="AluX repeat: matches 1..299 of consensus"
  1960..2174
  /note="LIME2 repeat: matches 5746..6163 of consensus"
  2175..2513
  /note="AluSg/X repeat: matches 175..308 of consensus"
  2516..2541
  /note="U2 repeat: matches 5..33 of consensus"
  2542..2738
  /note="AluSg repeat: matches 1..201 of consensus"
  2741..4206
  /note="LIME2 repeat: matches 5283..5748 of consensus"
  3207..3525
  /note="AluJb repeat: matches 1..303 of consensus"
  3526..3551
  /note="LIME2 repeat: matches 5258..5283 of consensus"
  3559..3856
  /note="LIM4 repeat: matches 4669..4987 of consensus"
  3857..4157
  /note="AluSg repeat: matches 1..299 of consensus"
  4158..4286
  /note="LIM4 repeat: matches 4541..4669 of consensus"
  4521..4624
  /note="MIR repeat: matches 47..152 of consensus"
  4674..4804
  /note="L2 repeat: matches 581..713 of consensus"
  5823..5850
  /note="L2 repeat: matches 1312..1557 of consensus"
  5861..6031
  /note="FRAM repeat: matches 8..176 of consensus"
  6420..6487
  /note="L2 repeat: matches 2648..2710 of consensus"
  6762..7013
  /note="L16C repeat: matches 133..387 of consensus"
  7292..8014
  /note="LIME1 repeat: matches 5444..6163 of consensus"
  8053..8364
  /note="AluJb repeat: matches 1..302 of consensus"
  8384..8590
  /note="LIME3 repeat: matches 5545..5755 of consensus"
  8770..9137
  /note="LIME3 repeat: matches 5763..6134 of consensus"
  9165..9444
  /note="AluJb repeat: matches 40..312 of consensus"
  9706..10153
  /note="L2 repeat: matches 1057..1554 of consensus"
  10598..10799
  /note="L2 repeat: matches 2111..2358 of consensus"
  10862..10958
  /note="MLTIC repeat: matches 1..98 of consensus"
  10959..11266
  /note="AluX repeat: matches 1..308 of consensus"
  11267..11298
  /note="MLTIC repeat: matches 98..129 of consensus"
  11299..11721
  /note="MSTA repeat: matches 1..426 of consensus"
  11722..12061
  /note="MLTIC repeat: matches 129..466 of consensus"
  12065..12411
  /note="L2 repeat: matches 2389..2706 of consensus"
  13039..13353
  /note="AluJb repeat: matches 1..312 of consensus"
  complement(14182..14645)
  /note="match: GSS: Em:AQ719314"
  14310..14793
  misc_feature
  misc_feature

```

/note="match; GSS: Em:A0812338"
15382..15581
/note="MIR repeat: matches 39..244 of consensus"
15547..15599
/note="L2 repeat: matches 2692..2745 of consensus"
15598..16111
/note="L2 repeat: matches 1119..2029 of consensus"
16314..16444
/note="L2 repeat: matches 2092..2221 of consensus"
16445..16851
/note="L1M4 repeat: matches 5014..5402 of consensus"
16956..17162
/note="L2 repeat: matches 2174..2380 of consensus"
17502..17852
/note="L1M6 repeat: matches 5394..5624 of consensus"
18164..18298
/note="L1P repeat: matches 4879..5012 of consensus"
L1P repeat: matches 4879..5012 of consensus"
18608..18952
/note="match; GSS: Em:A005989"
21158..21213
/note="L2 repeat: matches 2066..2119 of consensus"
21214..21538
/note="AluX repeat: matches 1..312 of consensus"
21539..22081
/note="L2 repeat: matches 2119..2792 of consensus"
22089..22510
/note="L2 repeat: matches 1148..1567 of consensus"
22514..22831
/note="L1M4 repeat: matches 4532..4834 of consensus"
23524..23826
/note="L1M6 repeat: matches 5525..5817 of consensus"
24119..24589
/note="match; GSS: Em:A055890"
24205..24250
/note="L23 copies 2 mer tt 78% conserved"
24271..24576
/note="AluX repeat: matches 1..304 of consensus"
24594..24655
/note="L1 copies 2 mer aa 67% conserved"
24667..24943
/note="L1 repeat: matches 4727..4988 of consensus"
25177..25275
/note="MIR repeat: matches 49..115 of consensus"
25336..25689
/note="L2 repeat: matches 2326..2700 of consensus"
25676..25699
/note="L2 repeat: matches 2151..2172 of consensus"
25700..26011
/note="AluX repeat: matches 1..312 of consensus"
26012..26841
/note="L2 repeat: matches 1249..2151 of consensus"
complement(27254..27711)
/note="match; GSS: Em:A081244"
27511..27796
/note="L2 repeat: matches 1339..1602 of consensus"
27797..28088
/note="AluX repeat: matches 1..293 of consensus"
28089..28720
/note="L2 repeat: matches 1602..2325 of consensus"
28727..28984
/note="AluY repeat: matches 49..307 of consensus"
29196..29339
/note="L2 repeat: matches 2278..2425 of consensus"
29381..29418
/note="L2 repeat: matches 2556..2593 of consensus"
29419..29747
/note="AluJo repeat: matches 1..308 of consensus"
29748..29842
/note="L2 repeat: matches 2593..2687 of consensus"

Query Match 2.0%; Score 58; DB 9; Length 14443;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;

Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1187 CTCCACCTTGCCCTCCCAAGTCTGGATTACAGGCATGAGCCACTGCCGCCAGC 1244
|||||
Db 148147 CTCCACCTTGCCCTCCCAAGTCTGGATTACAGGCATGAGCCACTGCCGCCAGC 148090
|||||

RESULT 37
AL805961/C
LOCUS
DEFINITION Homo sapiens chromosome 1 clone RP11-718D19, *** SEQUENCING IN
PRGRESS ***, in ordered pieces.
ACCESSION AL805961
VERSION AL805961.12 GI:22204675
KEYWORDS HTGS_PHASE2; HTGS_ACTIVIFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 195386)
Van Heilmond, Z.
Direct Submission
Submitted (31-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 11, 2002 this sequence version replaced gi:2200315.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA718D19
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 195288 bases at least Q40
Consensus quality: 195341 bases at least Q30
Consensus quality: 195366 bases at least Q20
Insert size: 195386; sum-of-contigs
Insert size: 181232; 9.2% error; agarose-fp
Quality coverage: 12.04x in Q20 bases; sum-of-contigs Quality
coverage: 13.15x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
source
1..195386
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-718D19"
/clone_lib="RPCT-11.3"
1..195386
/note="assembly fragment:04211"
BASE COUNT 48905 a 47558 c 50028 g 48895 t
ORIGIN

Query Match 2.0%; Score 58; DB 2; Length 195386;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTCCACCTTGCCCTCCCAAGTCTGGATTACAGGCATGAGCCACTGCCGCCAGC 1244
|||||
Db 168811 CTCCACCTTGCCCTCCCAAGTCTGGATTACAGGCATGAGCCACTGCCGCCAGC 168754
|||||

RESULT 38
AC083830/C
LOCUS
DEFINITION Homo sapiens chromosome UL clone RP11-495K24, WORKING DRAFT

misc_feature
 /note=-assembly_fragment:05572.0-
 190925..201197
 /note=-assembly_fragment:03857
 clone_end:T7
 vector_side:right*

BASE COUNT 55207 a 43266 c 43712 g 57504 t 1508 others

ORIGIN
 Query Match 2.0%; Score 58; DB 2; Length 20197;
 Best Local Similarity 100.0%; Pred. No. 1.7e-20;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGCATATAGCATATGTCGACG 1244
 DB 60280 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGCATATAGCATATGTCGACG 1244

RESULT 40
 AC027176 292703 bp DNA linear HTG 19-AUG-2002
 LOCUS Homo sapiens chromosome 20 clone RP11-493E3 map 20. *** SEQUENCING
 IN PROGRESS ***, 6 unordered pieces.

AC027176
 AC027176.11 GI:22297423
 HTG: HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVATED IN
 human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Graciatia; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 292703)
 Birren, B., Nusbaum, C., and Lander, E.

TITLE Homo sapiens chromosome 20, clone RP11-493E3
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 292703)

AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
 Anderson, S., Baldwin, J., Bara, N., Bastien, V., Beck, E.,
 Bonafant, L., Boukhalter, B., Brown, A., Burkett, C.,
 Campione, A., Castiglione, A., Choquet, Y., Choudhury, S., Collins, S.,
 Compagno, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J. S.,
 Dodge, S., Domino, M., Doyle, M., Ferreira, V., Fitzgerald, W., Gage, D.,
 Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
 Grand-Pierre, N., Grant, G., Hades, H., Heath, A., Horton, L.,
 Howland, J. C., Iliev, J., Johnson, K., Jones, G., Kahn, L., Karatas, A.,
 Klein, J., Lacombe, K., Lamazares, K., Landers, T., Lechoczky, J.,
 Levine, R., Lieu, C., Liu, G., Locke, K., Mardian, L., Marquis, N.,
 McCarthy, M., McEwan, P., McGuire, A., McKenna, K., McPherson, R.,
 Melrim, J., Meneus, L., Mihova, I., Miranda, J., Miranda, V., Morrow, J.,
 Murphy, T., Naylor, J., Norman, E. H., O'Connor, T., O'Connor, L.,
 O'Neill, D., Olivier, T. M., Oliver, J., Peterson, K., Pierre, K.,
 Pisani, C., Pollara, V., Raymond, C., Riley, K., Roach, P., Rollman, G.,
 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
 Testaye, S., Theodore, J., Tirrell, A., Travers, M., Triadillo, J.,
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
 Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
 Submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 292703)
 Birren, B., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
 Bara, N., Bastien, V., Bloom, T., Bonafant, L., Boukhalter, B.,
 Camarata, J., Chang, J., Chazaro, B., Choquet, Y., Cullymore, A.,
 Cooke, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
 Faru, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
 Gardyna, S., Ginde, S., Graham, L., Grand-Pierre, N., Hades, H.,
 Horton, L., Hulme, W., Iliev, J., Johnson, K., Jones, G., Kanat, A.,
 Karatas, A., Kells, C., Landers, T., Levine, R., Linton, L.,
 Liu, G., Maclean, C., Macdonald, P., Mardian, L., Matthews, C.,
 McCarthy, M., Melrim, J., Meneus, L., Mihova, I., Miranda, V.,
 Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norman, E. H.,
 O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
 Plunkhang, P., Pierre, N., Raymond, C., Retta, K., Roach, P.,
 Roman, J., Roy, A., Schauer, S., Schupbach, K., Severy, P.,

TITLE
 JOURNAL

COMMENT

Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
 Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
 Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (19-AUG-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Aug 19, 2002 this sequence version replaced gi:22213416.
 All repeats were identified using RepeatMasker:
 Smith, A. F. A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
 Center: Whitehead Institute/MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
 Center project name: L6996
 Center clone name: 493_E_3

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 6 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N. But the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 14452: contig of 14452 bp in length
 * 14453 14552: gap of 100 bp
 * 14554 26924: contig of 12372 bp in length
 * 26925 27024: gap of 100 bp
 * 27025 139971: contig of 112947 bp in length
 * 139972 140071: gap of 100 bp
 * 140072 151044: contig of 10973 bp in length
 * 151045 151144: gap of 100 bp
 * 151145 179656: contig of 28512 bp in length
 * 179657 179757: gap of 100 bp
 * 179757 292703: contig of 112947 bp in length.

----- Location/Qualifiers
 1. 292703
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 /db_xref="taxon:9606"
 /chromosome="20"
 /map="20"
 /clone="RP11-493E3"
 /clone_lib="RP11-11 Human Male BAC"
 BASE COUNT 83142 a 66391 c 66021 g 76579 t 570 others

ORIGIN
 Query Match 2.0%; Score 58; DB 2; Length 292703;
 Best Local Similarity 100.0%; Pred. No. 1.8e-20;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGCATATAGCATATGTCGACG 1244
 DB 9771 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGCATATAGCATATGTCGACG 9828

RESULT 41
 AK094822/c 2532 bp mRNA linear PRI 15-JUL-2002
 LOCUS Homo sapiens cDNA FLJ37503 fis, clone BRAWH2016679.

DEFINITION AK094822
 ACCESSION AK094822
 VERSION 1
 KEYWORDS oligo capping; fis (full insert sequence);
 SOURCE Homo sapiens brain cDNA to mRNA, clone LIB:BRAWH2
 clone: BRAWH2016679.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1
 Suzuki, T., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T.,

FEATURES	Fax: +81-438-52-3914)
source	Location/Qualifiers
	1. .4261
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="fj02442"
	/issue_type="brain"
	/clone_lib="pBluescriptII SK plus"
gene	1. .4261
	/gene="KIAA1364"
CDS	<1. .2436
	/gene="KIAA1364"

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/note-Start codon is not identified.*
/codon_start-1
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/protein_id-"BAA92602.1"
/db_xref-"GI:7243109"
/translation-"LKUVALILGIEIHYNVFQGLIOPEDQENERTGWRALVHPKTH
PVSEYFEVLIIGDGRNLTGCFRPEKPGKLAIAITANFNIRNRTAEAKVEELSGVA
SLEINQKFEQLRATGIDLENIVYYKDOTHFYVTKAKQSLDKGVILHYADTELLE
SRNVDGELTARGAAGFSTQQQLQDFAINHYGQPDVAMFDTCMTGVAENAAVL
REUNGHLLVALLGDSLEPPPMQGTARGFLAAMDAAWNRWSLGSITPLEVLAER
ESYIKLLPTVPNVSKNSQSVIDPVTPIRYNINFLRPSQVRLHYDGTGDKDHL
SINMSKRTPTKLTRNESVARSKSLKRCQRTDGTAGVNTDITMSGWKGLCAIIL
HYHPVLQDFDSLDQENKQNLAFDAEKELGSIPTIKENASVGEQDKLSMYMY
LITUPYEMFKDLSLSTDLNAAEALVIATRSPISPLSKLGVTISKKRSPDKDKE
LQDAGAKRRTISQSEEEAPRGHGRERTPLVSTLDRDMDVAVNONKVKVYMATOLLA

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Query Match 2.0% Score 57: DB 9: Length 4261:

	Matches	57: Conservative	0: Mismatches	0: Indels	0: Gaps
QY	1188	TGCCACCTTGGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGGCCAG	1244		
DB	3878	TGCCCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGGCCAGC	3822		

RESULI 43

EXON	AC091813	Homo sapiens BAC clone RP11-616K2 from 7, complete sequence.	UNL	linear	PKI 09-JAN-2000
DEFINITION	AC091813		35318 bp		
ACCESSION	AC091813				
VERSION	AC091813				
KEYWORDS	HTG.				
SOURCE	AC091813	GI:15809181			
ORGANISM	Homo sapiens.				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1. (bases 1 to 35958)				

REFERENCE	1 (bases 1 to 56938)
AUTHORS	Sulston, J. E. and Waterston, R.
TITLE	Toward a complete human genome sequence
JOURNAL	Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE	99063792
PUBMED	9847074
REFERENCE	2 (bases 1 to 58958)
AUTHORS	Goyea, E. and Kozlowski, A.
TITLE	The sequence of Homo sapiens BAC clone RP11-616K2
JOURNAL	Unpublished (2001)

REFERENCE	3 (bases 1 to 58958)
AUTHORS	Waterston, R.H.
TITLE	Direct Submission
JOURNAL	Submitted (08-JUN-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE	4 (bases 1 to 58958)
AUTHORS	Waterston, R.H.

TITLE

Direct Submission
Submitted (30-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

REFERENCE

Waterston, R.

AUTHORS

Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Sep 30, 2001 this sequence version replaced 4 116778789.

COMMENT

----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/qsc>
Contact: sapiens@watson.wustl.edu
----- Summary Statistics

Center project name: H_NH0616K02

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NUGGI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson at the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/GIB/CHR7>, send <mailto:ogreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/qsc>

SOURCE INFORMATION:

The RPCL11 human BAC library was made from the blood of one male donor, as described by Osoeckwa, K., Woon, Y., Zhang, B., Friedman, E., Tatenio, M., Catanesi, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP5 997A5, 203 bp overlap; the clone sequenced to the right is RP11-757A2, 2036 bp overlap. Actual start of this clone is at base position 1-4273 of RP5-997N5; actual end is at base position 44275 of RP11-54E23.

FEATURES

Source

Location/Qualifiers

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
/map="7"

/clone="RP11-616K2"

/clone_lib="RPCL11"

10..1288

/rpt_family="L2"

2206..2486

/rpt_family="MaLR"

3076..3290

/rpt_family="L2"

3416..3442

/rpt_family="(CTA)?"

repeat_region 3443..3487
/rpt_family="(CA)n"
repeat_region 3527..3778
/rpt_family="L2"
repeat_region 4302..4592
/rpt_family="L2"
repeat_region 4752..5129
/rpt_family="MaLR"
repeat_region 5489..5509
/rpt_family="AT-rich"
repeat_region 6218..6301
/rpt_family="MaLR"
repeat_region 6306..6401
/rpt_family="GA-rich"
repeat_region 6456..6558
/rpt_family="MaLR"
repeat_region 6665..6818
/rpt_family="L2"
repeat_region 7679..7707
/rpt_family="(TG)n"
repeat_region 9052..9381
/rpt_family="Alu"
repeat_region 9170..9216
/rpt_family="(TAAAA)n"
repeat_region 9471..9406
/rpt_family="(TAAA)n"
repeat_region 9446..9521
/rpt_family="MIR"
repeat_region 9514..10111
/rpt_family="MIR"
repeat_region 11924..11974
/rpt_family="(TATATG)n"
repeat_region 12057..12085
/rpt_family="MER2_type"
repeat_region 12086..12393
/rpt_family="Alu"
repeat_region 12394..13529
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repeat_region 12812..12847
/rpt_family="AT-rich"
repeat_region 12882..12905
/rpt_family="AT-rich"
repeat_region 12956..13033
/rpt_family="AT-rich"
repeat_region 13542..13571
/rpt_family="(TA)n"
repeat_region 13574..14658
/rpt_family="L1"
repeat_region 14706..15418
/rpt_family="L1"
repeat_region 15025..15140
/rpt_family="CT-rich"
repeat_region 15604..16018
/rpt_family="ERVL"
repeat_region 17729..17946
/rpt_family="L2"
repeat_region 17818..17867
/rpt_family="(TTTTIG)n"
repeat_region 18111..18285
/rpt_family="L1"
repeat_region 18286..19823
/rpt_family="ERVL"
repeat_region 19864..19893
/rpt_family="(T)n"
repeat_region 20322..20521
/rpt_family="MER1_type"
repeat_region 20580..20619
/rpt_family="(T)n"
repeat_region 20592..20897
/rpt_family="Alu"
repeat_region 23205..23501
/rpt_family="Alu"
repeat_region 23502..23593


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BASE COUNT   26999 a   20814 c   19555 g   24539 t
ORIGIN
Query Match          2.0%; Score 57; DB 9; Length 91907;
Best Local Similarity 100.0%; Pred. No. 6e-20;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1025 CTCACGTGAACCTCGCTCCGGGTCACAGCGATTCTCTCGCTCAGCCTCCCTGAG 1081
|||||
DB 916 CTCACGTGAACCTCGCTCCGGGTCACAGCGATTCTCTCGCTCAGCCTCCCTGAG 860

RESULT 45
AC069314
LOCUS
DEFINITION Homo sapiens BAC clone CTD-2300122 from 2, complete sequence.
ACCESSION AC069314
VERSION AC069314.5 GI:18042324
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 104906)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
PUBMED 9847074
2 (bases 1 to 104906)
Desai, A., Meyer, R. and Boyer, E.
The sequence of Homo sapiens BAC clone CTD-2300122
Unpublished (2001)
3 (bases 1 to 104906)
Waterston, R.H.
Direct Submission
Submitted (26-MAY-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 104906)
Waterston, R.H.
Direct Submission
Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 104906)
Waterston, R.
Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jan 3, 2002 this sequence version replaced gi:16924147.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
-----
Center project name: H_MS2300122

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

```

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/use>

SOURCE INFORMATION:

Clone CTD-2300122 is from a release of the human BAC library CID. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); D.-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (<http://www.resgen.com>).
VECTOR: pBelobAC11
Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-498M11, 2000 bp overlap.
The clone sequenced to the right is AF225899, 2000 bp overlap.
Actual start of this clone is at base position 342435 of RP11-498M11.

FEATURES

Source

Location/Qualifiers
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/chromosome="2"
/map="2"
/clone="CTD-2300122"
/clone_lib="C:D"
607..892
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893..937
/rpt_family="(TG)n"
997..1251
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1376..1424
/rpt_family="MIR"
1599..1909
/rpt_family="Alu"
1880..1902
/rpt_family="(CAAA)n"
2027..2621
/note="Similar to Mus musculus EST B76620.8
(NID:g16496123)"
2737..2760
/rpt_family="AT-rich"
2751..3006
/rpt_family="L1"
3526..3561
/rpt_family="MIR"
4670..4696
/rpt_family="(T)n"
6431..6627
/rpt_family="MIR"
7465..7710
/rpt_family="Alu"
8016..8092
/rpt_family="L2"
8316..8420
/rpt_family="CT-rich"
8380..8415
/note="Similar to Homo sapiens EST S597527
(NID:g12340042)"
8708..8743
/rpt_family="AT-rich"
8874..9191
/rpt_family="Alu"
9177..9221
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9217..9318
/rpt_family="Mariner"
9319..9607
/rpt_family="Alu"
9579..9517

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9608..9737
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repeat_region
10967..10998
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repeat_region
10685..11002
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repeat_region
11040..11347
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repeat_region
11318..11352
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repeat_region
11353..11375
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repeat_region
12077..12096
/rpt_family="(CAAA)n"
repeat_region
12184..12495
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repeat_region
12467..12489
/rpt_family="(TAAA)n"
repeat_region
14337..14615
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14615..14660
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repeat_region
14966..15383
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repeat_region
15535..15577
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repeat_region
15549..15680
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16050..16086
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repeat_region
16302..16354
/rpt_family="(TTCA)n"
repeat_region
16326..16402
/rpt_family="L2"
repeat_region
17576..18132
/rpt_family="ERV1"
repeat_region
18319..18621
/rpt_family="Alu"
repeat_region
19730..19766
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repeat_region
19735..20044
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21134..21154
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repeat_region
22103..22169
/rpt_family="L2"
repeat_region
22191..22306
/rpt_family="Alu"
repeat_region
22364..22386
/rpt_family="AT-rich"
repeat_region
22370..22646
/rpt_family="Alu"
repeat_region
22804..23026
/rpt_family="MIR"
repeat_region
24156..23176
/rpt_family="AT-rich"
repeat_region
24638..24749
/rpt_family="MIR"
repeat_region
24815..24933
/rpt_family="MIR"
repeat_region
24991..25071
/rpt_family="ERV1"
repeat_region
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repeat_region
25189..25484
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repeat_region
25694..25983

Query Match 4.0% Score 57; DB 9; Length 164936;
Best Local Similarity 100.0%; Pred. No. 6e-20;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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repeat_region 150..530
repeat_region /rpt_family="L1"
repeat_region 498..649
repeat_region /rpt_family="L1"
repeat_region 673..1096
repeat_region /rpt_family="MAlR"
repeat_region 3188..3348
repeat_region /rpt_family="L1"
repeat_region 3605..3726
repeat_region /rpt_family="(TA)n"
repeat_region 3845..4563
repeat_region /rpt_family="L1"
repeat_region 5641..6075
repeat_region /rpt_family="Retroviral"
repeat_region 6133..6433
repeat_region /rpt_family="Alu"
misc_feature 7110..8040
gene /note="CpG island (AGC=69.1, o/e=0.80, #pCs 93)"
7872..40218
/genes="WUGSC:H.RG437L15.1"
join(7872..8044,12642..12795,15154..15409,15584..19741,
21552..21601,22478..22639,29862..29975,33555..33944,
36395..36488,39123..39284,39881..40218)
/genes="WUGSC:H.RG437L15.1"
/note="serine/threonine kinase KICK: Match to protein
AF027706 (PID:g3123887) and mRNA AF027706 (NID:g3123886);
H.RG437L15.1"
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/db_xref="GI:3264574"
/translation="MNCEAICSALEPTIPYHKLAIRYLKSGASGIVSSARHADRWQV
AVKHLIHPLDSEKDLKRAEILIKARFVILFILGNEPPEFLGIVTEYMPGS
LNELLIRKTEYPOVAPLRFRIILHETALGVNLYHNTPVLLHDLKTONILLONEFHV
KIDFGLSKWRMSLSQSRSSKSAPEGGTLYMPHPNYEPQKSKAS:KHUIYSYAVI
TWVLSRKOPEDYTNPIQIMYSVSQCHRPVINEESLPYLPEKARM:SLIESCHAQN
PDERPFLKCLIELEPVLRFETITLVAIVCKKTKKGSVSAIHITDKKMKELSEN
IPVNHGQECSSQSOLHENSSEPTSRSLPAQNDFTSRKAQDCYFMKHLHCPSNH
SWDSTISGSORAAFCDHKTPCQSALINPLTAGNSERLQPSIAGQIUSKREDIVNQ
MTACLNQSLDALLKOLINKKEYELVSKPTISKVRQLLITIDTQGEFEKAVIQK
LKONKQMGLOPYEPIILWSRSPSLNLQNSKM"
8463..8770
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repeat_region 10435..10540
repeat_region /rpt_family="MIR"
repeat_region 11433..11538
repeat_region /rpt_family="Alu"
repeat_region 11790..12003
repeat_region /rpt_family="Alu"
repeat_region 12466..12557
repeat_region /rpt_family="MIR"
repeat_region 15579..16292
repeat_region /rpt_family="L1"
repeat_region 16292..16429
repeat_region /rpt_family="L1"
repeat_region 16460..16991
repeat_region /rpt_family="L1"
repeat_region 22863..23483
repeat_region /rpt_family="L2"
repeat_region 23575..23750
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repeat_region /rpt_family="Alu"
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Query Match 2.0% Score 57; DB 9; Length 116650;
Best Local Similarity 100.0%; Prod. No. 6.1e-20;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1025 CTCACHTGTAACCTCTGCTCCCGGTTCAAGCGATTCTCTCCCTCAGCCTCTCTGAG 1081
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DB 44313 CTCACHTGTAACCTCTGCTCCCGGTTCAAGCGATTCTCTCCCTCAGCCTCTCTGAG 44257

RESULT 48
HS329A5/c
LOCUS

HS329A5 117026 bp DNA linear PRI 01-FEB-2000
Human DNA sequence from clone RP3-329A5 on chromosome 6p21.1-21.33
Contains a pseudogene similar to ribosomal protein L35a, ZNF76
(zinc finger protein 76 (expressed in testis)), part of the gene
for KIAA0646 protein, an EST, SIF5, GSSS and CpG Islands.b,
complete sequence.

ACCESSION Z97832
VERSION Z97832.1
KEYWORDS HTG; CpG Island; KIAA0646; ribosomal protein L35a; ZNF76.

SOURCE Homo sapiens.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 117026)
REFERENCE Williams,S.
AUTHORS Direct Submission
TITLE Submitted (01-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
JOURNAL requests: clones@clones.sanger.ac.uk
 On Oct 19, 1999 this sequence version replaced at 15056482.
 This sequence has been finished according to sequence map criteria
 as follows. An attempt is made to resolve all sequencing problems,
 such as compressions and repeats, but not necessarily within known
 annotated human repeat sequence elements (e.g. Alu). Where the
 sequence is ambiguous, there is an annotation using the 'unsure'
 feature key.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information
 on the WormPEP database can be found at
<http://www.sanger.ac.uk/projects/Celegans/wormpep>
 RP3-329A5 is
 from the library RP3-329A5 constructed at the Roswell Park Cancer
 Institute by the group of Pieter de Jong. For further details see
<http://bacpac.med.buffalo.edu/>
VECTOR: pCYPAC2
IMPORTANT: This sequence is not the entire insert of clone
 RP3-329A5. It may be shorter because we only sequence overlapping
 sections once, or longer because we arrange for a small overlap
 between neighbouring submissions.
 The true left end of clone RP3-329A5 is at 116427 in this sequence. The
 true left end of clone RP1-109F14 is at 116427 in this sequence.
 This sequence was generated from part of bacterial clone contigs of
 human chromosome 6, constructed by the Sanger Centre Chromosome 6
 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/chr6>.
 Location/Qualifiers

FEATURES

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 31101..31220
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 41817..41842
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 46481..47711
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 Sw:P04645"
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REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
    Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published Only in Database (2001)
REFERENCE 2 (bases 1 to 121600)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
    Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (27-APR-2001) Masahira Hattori, The Institute of Physical
    and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
    1-7-22 Suhiro-chou,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
    (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
    Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Dec 7, 2001 this sequence version replaced gi:13528404.
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BASE COUNT 30736 a 29421 c 29985 g 31456 t

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 AC AAF24681:
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 DI 20-APR-2003: (first entry)
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 FE Nucleotide sequence of the 5' flanking region of the human ABC1 gene.
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 KW Human: adenosine triphosphate binding cassette protein (ABC1) gene.
 KW apolipoprotein-mediated mobilisation of cholesterol; familial disease
 KW chromosome 9q22-q31; heart disease; hypercholesterolemia;
 KW atherosclerosis; cholesterol transport; ss.
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 PR 13-NOV-1999: 9905-0166573.
 XX
 XX (CVTH-) CV THERAPEUTICS INC.
 XX
 XX Lawn RM. Wade D. Garvin M.
 XX
 XX WPI: 2001-137812/14.
 DB

XX
 PT Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
 PT useful for the development of agents for the treatment of heart disease
 PT and other disorders associated with hypercholesterolemia and
 PT atherosclerosis
 XX
 PS Claim 1: Page 144-144: 215pp; English.
 XX
 CC The present sequence represents the 5' flanking region of the human
 CC adenosine triphosphate (ATP) binding cassette protein (ABC1) gene. ABC1
 CC resides in cell membranes and utilises ATP hydrolysis to transport a wide
 CC variety of substrates across the plasma membrane. ABC1 is a pivotal
 CC protein in the apolipoprotein-mediated mobilisation of intracellular
 CC cholesterol stores. ABC1 is defective in Tangier disease, a genetic
 CC disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1
 CC gene is localised to chromosome 9q22-q31. The ABC1 gene and proteins
 CC are useful for developing pharmaceutical agents for the treatment of
 CC heart disease and other disorders associated with hypercholesterolemia
 CC and atherosclerosis. The genes are useful for developing screening assays
 CC to screen for compounds that regulate the expression of genes associated
 CC with cholesterol transport. The genes and proteins are also useful for
 CC are also useful as diagnostic indicators of cardiovascular disease and
 CC other disorders associated with hypercholesterolemia.
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 DB 1525 ATGATGGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 1534

 QY 1585 TCTGGCTAAAGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTC 1594

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DI 21 NOV-2001 (first entry)
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XX human reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
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28 QY 729 GAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 788
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30 DB 3253 AAATGCGACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3309
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32 QY 789 AGAGGAGAGAGCTTTACTGATAATGTTGATATGATGATGATGATGATGATGATGATG 848
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34 DB 3410 ATATTATCAATTTTGTAGACACATGATGATGATGATGATGATGATGATGATGATG 3469
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KW antiallergic; antidiabetic; antidiuretic; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
XX neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
US Homo sapiens.
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PD 16-AUG-2001.
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Human nervous system related polynucleotide SEQ ID NO 9949.

Human; neotropic; neuroprotective; cytoskeletal; dermatological; vitreous;
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PR 17-NEW-2000: 2000US-0249212.
PR 17-NEW-2000: 2000US-0249213.
PR 17-NEW-2000: 2000US-0249214.
PR 17-NEW-2000: 2000US-0249215.
PR 17-NEW-2000: 2000US-0249216.
PR 17-NEW-2000: 2000US-0249217.
PR 17-NEW-2000: 2000US-0249218.
PR 17-NEW-2000: 2000US-0249244.
PR 17-NEW-2000: 2000US-0249245.
PR 17-NEW-2000: 2000US-0249264.
PR 17-NEW-2000: 2000US-0249265.
PR 17-NEW-2000: 2000US-0249297.
PR 17-NEW-2000: 2000US-0249299.
PR 01-DEC-2000: 2000US-0250391.
PR 01-DEC-2000: 2000US-0251160.
PR 05-DEC-2000: 2000US-0251040.
PR 05-DEC-2000: 2000US-0251988.
PR 05-DEC-2000: 2000US-0256719.
PR 06-DEC-2000: 2000US-0251479.
PR 08-DEC-2000: 2000US-0251856.
PR 08-DEC-2000: 2000US-0251868.
PR 08-DEC-2000: 2000US-0251869.
PR 08-DEC-2000: 2000US-0251984.
PR 08-DEC-2000: 2000US-0251990.
PR 11-DEC-2000: 2000US-0254097.
PR 05-JAN-2001: 2001US-0255678.
PR (HUMA) HUMAN GENOME SCI INC.

XX Rosen CA, Barash SC, Ruben SM;

XX WPI: 2001-041565/60.

XX Nucleic acids encoding 1224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases -

PS Disclosure: SEQ ID NO 9032; 1701pp - Sequence has been English.

XX The invention relates to novel genes (AHL14.4, AHL2154) and proteins
XX (AHL14678-AHL1800) useful for preventing, treating or ameliorating
XX medical conditions e.g. by protein or gene therapy. The genes are
XX isolated from a range of human tissues disclosed in the specification.
XX The nucleic acids, proteins, antibodies and (antibodies) are used in
XX in the diagnosis, treatment and prevention of (a) cancer, e.g. breast
XX and ovarian cancer and other cancers of the adrenal gland, bone, bone
XX marrow, breast, gastrointestinal tract, liver, lung, or thyroid;
XX (b) immune disorders e.g. Addison's disease, allergic autoimmune
XX haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Cushing's
XX disease, multiple sclerosis, rheumatoid arthritis and myeloma.

CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic form directly
XX from WIPO at http://wipo.int/pub/published_pct_sequences.
SQ Sequence 5075 BP: 1417 A: 1054 C: 1187 G: 1397 T: 0 other;

Query Match 10.1%; Score 325.8; DB 22; Length 3075;
Best Local Similarity 64.7%; Pred. No. 2.9e-59;
Matches 584; Conservative 0; Mismatches 302; Indels 17; Gaps 6;

QY 375 GGCGGGGATCAATAGCTATATCCAGCACCTTTGGAGGGCTGAAGCCAGAGGA 434
DB 3221 GGGCTGGTGTATATGCTATGCTGTATATCCAGCACCTTTGGAGGGCTGAAGCCAGAGGA 3162
QY 435 TGCTTTAGCTTCAGAGTTTGGAGCAGCTGGATAGATGCAAAACCTCTCTCTACA 494
DB 3161 TCACCTGATAGTCAGAGTTTGGAGCAGCTGGATAGATGCAAAACCTCTCTCTACA 3103
QY 495 AAAAAAATACAAAAATAGATGGTGTGCTGCAATGCCACCTGTGCTCCACGCTACTTGGG 554
DB 3102 CTAATAAATACAAAAATAGCCAGGATGGTGGAGGGCTGTATATCCAGCACCTACTCAGG 3043
QY 555 AGGCTAAGCTGGAGGATGCTTGAGCCAGGAGTCAAGTCTACACTGAGCCATGATG 614
DB 3042 AGGCTGAGGAGCAAGAAATGCTTGAACCCAGGAGCTGGAGTGGCAGTGGCCAGATCA 2983
QY 615 GATCAGTGCCTCGAGGCTG---GATGACAGAGCAAGACCTGTCTCAAAAAGAAA 671
DB 2982 CCGCACTGCAATCCAGGCTGGATGATAGAGGAGCACTGTCTCTCAAAAAGAGAG 2923
QY 672 TCAGAGAGAAAGAAAGAGAGGAGGAGTCAAGGAGGAGGAGGGAGGGGAG 731
DB 2922 AGAGAGAAAGAAAGAGCTTGCATAGGAACTTGGCTAACTAAATATTTGGAGATAAA 2863
QY 732 GAAGGAGGAG 791
DB 2852 AAGTCAAGGAGAGCTTCAGAGTCTTTTACCAATATTTTAAAGTCAAGTCAACACCA 2803
QY 792 GGCAGAAAGAGCTTGAAGTAAATGCTCATGCTGTGTTGCTCAAGTTCAGCCAAAACCC 851
DB 2802 GCTAGCTAAG 2746
QY 852 AATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 911
DB 2745 GGTGGTAAATTCAGGAGGAGCTTGGCTTTCGGTGGAGGCTCTTCAGGTGAGCTTCTATC 2686
QY 912 GGTTTAGAAAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 971
DB 2685 AACTTTGAGCAAGCTGGGCAAGCTTCTGCTGGAATAATTTTTTTTTTTTTTTTTTTTTT 2626
QY 972 GATACGAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1031
DB 2625 GATACGAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2566
QY 1032 TAAATCT 1083
DB 2565 CAACCT 2506
QY 1084 AATACGAGAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143
DB 2505 TACAGCAATGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2447
QY 1144 TCATGTTGAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1203
DB 2445 CCATGTTGAGAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2387
QY 1204 GCAAGAGTCTGAGATACAG 1262
DB 2386 GCAAGAGTCTGAGATACAG 2327

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run On: May 9, 2003, 12:47:56 : Search time 5422.82 Seconds
(without alignment's)
9649.520 Million (el): updates/sec

Title: US-09-846-456-1
Perfect score: 3231
Sequence: 1 acaggcatgtgagcagtg.....gcccacatccccaccatt 3231

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum Match 100%

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_estc:*
- 9: gb_estl:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_othr:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	336	10.4	763	9	AU121731
2	237.8	7.4	289	10	AW748338
3	221.8	6.9	736	9	AU135588
4	221.2	6.8	457	10	AW816516
5	219.4	6.8	577	17	AQ265389
6	218.6	6.8	544	17	AQ418551

7	217	6.7	620	14	BQ775487
8	216.4	6.7	990	14	BM803650
9	215.2	6.7	719	17	AQ475181
10	214.4	6.6	423	14	BM991096
11	214.2	6.6	581	17	AQ347610
12	213.4	6.6	338	10	AW023111
13	213.4	6.6	666	17	AG075934
14	213.2	6.6	493	17	B50449
15	213.2	6.6	622	17	AQ537948
16	213	6.6	514	9	A1754653
17	213	6.6	739	17	AQ200209
18	213	6.6	827	10	AV755654
19	213	6.6	1183	13	BM564264
20	212.8	6.6	484	17	AQ314669
21	212.8	6.6	487	17	AQ414845
22	212.8	6.6	513	14	BQ082122
23	212.4	6.6	501	17	AQ040260
24	212.2	6.6	416	10	AW341978
25	212.2	6.6	448	17	AQ634562
26	212.2	6.6	521	10	AW970571
27	212	6.6	575	17	AQ587429
28	211.4	6.5	577	10	AW973181
29	211.4	6.5	678	17	AQ387027
30	211.2	6.5	864	12	BG682030
31	211	6.5	1005	9	AL524675
32	210.8	6.5	458	9	A1733856
33	210.8	6.5	844	14	BQ961856
34	210.6	6.5	388	10	AW069227
35	210.6	6.5	437	9	AA644090
36	210.6	6.5	546	14	BM697526
37	210.6	6.5	551	9	AL698703
38	210.6	6.5	605	17	AQ412598
39	210.4	6.5	547	9	AL698654
40	210.4	6.5	552	9	AL712937
41	210.4	6.5	684	17	AG102895
42	210.2	6.5	492	14	BM758113
43	210.2	6.5	570	14	BQ086265
44	210.2	6.5	725	14	BQ181241
45	210.2	6.5	924	12	BG697612

ALIGNMENTS

RESULT 1	AU121731	663 bp	linear	EST 01-AUG-2002
LOCUS	AU121731	MAHMA1 Homo sapiens cDNA clone	MAHMA1000851 5', mRNA	
DEFINITION	AU121731	sequence.		
ACCESSION	AU121731			
VERSION	AU121731.1	GI:10936966		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	1 (bases 1 to 763)			
AUTHORS	Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y., Yamamoto.J., Nakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and Isozaki.T.			
TITLE	HRI human cDNA project			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Takao Isozaki Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix Research Institute: cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.			

FEATURES
Source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ClTBI-EI"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

BASE COUNT 167 a 127 c 137 g 146 t
ORIGIN

Query Match 6.8%; Score 219.4; DB 17; Length 577;
Best Local Similarity 78.0%; Pred. No. 2.5e-15;
Matches 280; Conservative 0; Mismatches 71; Indels 8; Gaps 1;

QY 956 TCTTTTATTTTTCACAGGAGTCTTCTCTCTACACAGCGTGGAGTGCAGTGCACA 1015
DB 436 TTTTTHTTTTTTTTCAGACAGTCTAACTTTGACCCAGGCTAGAGTGCAGTGCACA 371
QY 1016 TGATCTGACTACTGTAACCTCTGCTCCGGGTTCAAGCGATTCTCTGCTCAGGCT 1075
DB 370 CGATCTGGCTCAGTCAAGCTCTGCTCCAGGTTCAAGTATTTCTCTGCTCAGGCT 311
QY 1076 CTGCA-----CATACAGCGCCGCCACACATCTAGCTAAATTTTGTATTAG 1127
DB 310 CCGAGTACTAGACTACAGGACCGCCAGGCTGCTAAATTTTGTATTAG 251
QY 1128 TAAGACTGGGTTTCATCATCTGGCCAGGTTGGTTTCGAACTCTGAGCTGAGCTGAGC 1187
DB 250 TAGACAGGGGTTTCAACATCTGCTCAGGTTGGTTTGAACCTGAGCTGAGCTGAGC 191
QY 1188 TGTTCACCTTGCTCCCAAGTCTGGATTAAGGATGAGCTGAGCTGAGCTGAGC 1247
DB 190 CAGTGGCTTGCTCCCAAGTCTGGATTAAGGATGAGCTGAGCTGAGCTGAGC 171
QY 1248 GATGATCCCTTTCTAAGGCAACAGCTCTAAGTCTGAGGATGAGCTGAGCTGAGC 1306
DB 190 GAGATACATTTTGTAAATCTAGACTGAGTCTGAGCTGAGCTGAGCTGAGC 72

RESULT 6
LOCUS A0418551
DEFINITION RP11-11-203K4.TJ RP11-11 Homo sapiens cDNA clone
A0418551
VERSION A0418551
KEYWORDS GSS,
SOURCE human,
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
J.D.
TITLE Use of BAC End Sequences from library RP11-11 for Sequence Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Other GSSs: RP11-11-203K4.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: huetigr.org
Clones are derived from the human BAC library RP11-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/submit) or from
Research Genet cs (info@resgen.com) BAC end search page:

http://www.tigr.org/Ldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends
Location/Qualifiers
1. .544
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/db_xref="taxon:9606"
/clone_lib="RP11-11-203K4"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC111 Human Male BAC Library"

BASE COUNT 207 a 86 c 165 g 85 t
ORIGIN

Query Match 6.8%; Score 218.6; DB 17; Length 544;
Best Local Similarity 70.5%; Pred. No. 3.3e-15;
Matches 306; Conservative 0; Mismatches 125; Indels 3; Gaps 1;

QY 353 CCATTTTAAAGATGAAGAAAGAGCGCGGCACAAATGGCTTAATCCAGCACT 412
DB 81 CCATTAAGAAATAAAGGAAGAGCGCGGAGGAGTAGTGGCTCATGCCCTGTAAAT*GCAGCACT 140
QY 413 TTGGAGGCTCAGCGGAGGAGTGGCTTGAGCTCCAGAGTTTTCAGACCAAGCTGGATAAC 472
DB 141 TTGGAGGCTCAGCGGAGGAGTGGCTTGAGCTCCAGAGTTTTCAGACCAAGCTGGATAAC 200
QY 473 ATGCCAAACCCCTGTCTCTACAAAAAATACAAAAATTAGATGGGTGGGTGATCA 532
DB 201 ATGTTGAACCCCTGTCTCTATAAAA---ATACAAAAATTAGCAGCGCTGGTGGGCA 257
QY 533 CCTGTGTCCTCAGTACTTGGAGGCTTAAGTGGAGGATCGCTTGAGCCAGGAGTCA 592
DB 258 CCTGTATCCAGCTTCTCAGGAGCTGAGCGAGGAGGATCATTCACTGGGAGCA 317
QY 593 AGTCTACACTGAGCTATGATTGGATCCTCCTCAGCTCCAGCTGGGTAGACAGAGCAAGACC 652
DB 318 AGTTGAGTGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 377
QY 653 CTGTCTCAAAAAAGAAATGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGATGAGG 712
DB 378 CAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 437
QY 713 GGATGAGGAGGAGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 772
DB 438 AAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 497
QY 773 AAAAACAAGATGAA 786
DB 498 AAGAGCAGCAAAA 511

RESULT 7
LOCUS BQ775487
DEFINITION BQ775487 620 bp mRNA linear EST 26-JUL-2002
UT-H-FH0-bc1-1-24-0-01.3' NCI-CCAP_FH0 Homo sapiens cDNA clone
UT-H-FH0-bc1-1-24-0-01.3', mRNA sequence.
ACCESSION BQ775487
VERSION BQ775487.1 GI:21983963
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 620)
TITLE NCI-CCAP http://www.ncbi.nlm.nih.gov/nciccap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: ccap@tmail.nih.gov

Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 17-306, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA-Yes

FEATURES
Source Location/Qualifiers
1..620
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-H-FHO-bc1-1-24-0-01"
/clone_lib="NCI CGAP FHO"
/tissue_type="Human Chondrosarcoma Cell Line"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Bone; Vector: p773-Pac (Plasmid) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP FHO is a cDNA library containing the following tissue(s): Human Grade I Chondrosarcoma Cell Line. The library was constructed according to Bonaldi, Benson and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGAATCGGC. The cell line was provided by Dr. James Martin from University of Iowa
TAG LIB=UI-H-FHO
TAG TISSUE=Human Chondrosarcoma Cell Line CSE - Grade I Chondrosarcoma
TAG_SEQ=AGAATCGGC"

BASE COUNT 118 a 154 c 159 g 185 t 4 others
ORIGIN
Query Match 6.7%; Score 217; DB 14; Length 620;
Best Local Similarity 85.6%; Pred. No. 4.4e-15;
Matches 256; Conservative 0; Mismatches 15; Indels 8; Gaps 1;
QY 954 TTCCTTTTATTTTTCAGACGAGGCTTCCTTGTGATCACTGAGTGGAGTGCATGG 1013
DB 7 TTTTTCCTTGTGTTGAGATGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 66
QY 1014 CATGATCTGACTGCTGTAACCTCGCTCGGAGGATCAAGCACTGCTGCTGCTGCTG 1073
DB 67 CATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 126
QY 1074 CTC-----CTGAGATAACAGGGCGGGCGGACCACTGCTGCTGCTGCTGCTG 1125
DB 127 CTCGATGATGCTGAGATTACAGGCGGCGGACCACTGCTGCTGCTGCTGCTGCTG 185
QY 1126 AGTAAGACGTGGTTCATCATGTTGGCCAGGTTGTTTGGAACTGCTGCTGCTGCTG 1185
DB 187 AGTAGAGTGGGGTTTTCATCATGTTGACACAGGCTTCTCAAACTGCTGCTGCTGCTG 246
QY 1186 GTGGCCACCTTGGGCTCCCAAGTGTGGGATTACAGGATGAGGATGCTGCTGCTGCTG 1244
DB 247 TCTGCTCACTTGGCTCCCAAGTGTGGGATTACAGGATGAGGATGCTGCTGCTGCTG 305

RESULT 8
BM803650
LOCUS BM803650 990 bp mRNA linear EST 05-MAR-2002
DEFINITION AGENCOURT_6439541 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5520297
ACCESSION 5', mRNA sequence.
VERSION BM803650
SOURCE BM803650.1 GI:19120473

KEYWORDS EST.
SOURCE human
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 990)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cyapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM12184 row: b column: 10
High quality sequence stop: 632.

FEATURES
Source Location/Qualifiers
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/clone="IMAGE:5520297"
/clone_lib="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb.
BASE COUNT 170 a 277 c 268 g 275 t
ORIGIN

Query Match 6.7%; Score 216.4; DB 14; Length 990;
Best Local Similarity 80.7%; Pred. No. 3.5e-15;
Matches 248; Conservative 0; Mismatches 56; Indels 8; Gaps 1;
QY 942 GAGATCATCCCTTCTTTTATTTTCTTGACACGAGCTTGTGCTGCTGCTGCTGCT 1001
DB 15 GAGCGCGCGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 74
QY 1002 GGAGTCGATGGCTATCATCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1061
DB 75 GGAGTCGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 134
QY 1062 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1113
DB 135 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 194
QY 1114 TTTTGTATTTTATGTAAGACTGGTTTCATCATGTTGGCCAGGTTGGTTTCGAACCTCT 1173
DB 195 TTTTGTGTTTATGTAAGACTGGTTTCATCATGTTGGCCAGGTTGGTTTCGAACCTCT 254
QY 1174 GAGTCGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1233
DB 255 GAGTCGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 314
QY 1234 CTGCGGCCAGCTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1265
DB 315 CCGCGCCAGCCAGGCTTAATTAATTTTAAAG 346

RESULT 9
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LOCUS AQ475181 714 bp DNA linear GSS 23-APR-1999
DEFINITION CITBI-E1-2589H9.TF CITBI-E1 Homo sapiens genomic clone 2589H9, DNA sequence.
ACCESSION AQ475181
VERSION AQ475181.1 GI:4657300
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 719)
 Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M., and
 Venter, J.C.
 Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
 Map Building
 Unpublished (1997)
 Other_GSSs: CITBI-E1-2589B9.TR
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are available from Research Genetics (tigr_resgen.com). BAC
 end search page:
 http://www.tigr.org/tdb/human/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES

Location/Qualifiers
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 /cell_type="sperm"
 /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
 Caltech Human BAC Library D"

BASE COUNT 228 a 162 c 180 g 149 t
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 Best Local Similarity 75.7%; Pred. No. 6.1e-15;
 Matches 283; Conservative 0; Mismatches 83; Indels 8; Gaps 1;

QY 893 TCGCTCTCTGGGCTTGGGCTTTAGAACCTCATCTCTGGCTTTCGAGATCCATCC 952
 DB 433 TCCATCTCAGAGCCCTCCGAGCACTGGTTATCTCTATAAATGATCCATCTTT 372
 QY 953 CTCTCTTTTATTTCTGACACGAGTCTTGGCTCTGCTGACTAGAGTACAGTGCAGTG 1012
 DB 111 TTTTCTTTTATTTTGGACACAGATCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 312
 QY 1013 ATATGATCTGACCTGACTGATACCTCTGCTCTGGGCTTTCGAGATCCATCCATCC 1072
 DB 311 GATATGCTGGGCTCACTGCAACCTCCGCTCCGCTTTCGAGATCCATCCATCCATCC 252
 QY 1073 CT 1124
 DB 251 CT 192
 QY 1125 TAGTAAGACTGGTTTCATGATGTTGCCAGGTGGTTTCCGAAATCTGAGACTGAGGTG 1184
 DB 191 TAGTAAGACTGGTTTTCATGATGTTGCCAGGTGGTTTCCGAAATCTGAGACTGAGGTG 132
 QY 1185 AGTGTGCCACCTTGGCT 1244
 DB 131 ATCT 72
 QY 1245 TCGATCCATCCCT 1258
 DB 71 CTGATCCATCTCT 58

RESULT 10
 BM991096/c
 LOCUS
 DEFINITION
 IMAGE:5862692 3', mRNA sequence.
 ACCESSION
 BM991096

VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

BM991096.1 GI:19710485
 EST.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 423)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs.rem.nhl.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 The following repetitive elements were found in this cDNA
 sequence: 1-21, >AT-rich; Low_complexity 77-366, >ALU
 Seq primer: M13 FORWARD
 POLYA: Yes.

FEATURES

Location/Qualifiers
 1..423
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5862692"
 /clone_lib="NCI-CGAP_D10"
 /tissue_type="Lung Focal Fibrosis"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoRI; Site_2: Not I;
 NCI-CGAP_D10 is a cDNA library containing the following
 tissue(s): A pool of Lung Focal Fibrosis. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dr primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoRI
 adaptor, digested with Not I, and cloned directionally
 into pT73-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 ATACCGGTC.

TAG_L1B-01-H-D10
 TAG_TISSUE-lung with fibrosis
 TAG_SEQ-ATACCGGTC"

BASE COUNT 111 a 100 c 111 g 101 t
 ORIGIN

Query Match 6.6%; Score 214.4; DB 14; Length 423;
 Best Local Similarity 76.8%; Pred. No. 1.1e-14;
 Matches 278; Conservative 0; Mismatches 76; Indels 8; Gaps 1;

QY 911 GGCTTTAGAAAGCTCATCTCTGGCTTTCTGAGATCCATCCCTCTCTTTTATTTTCT 970
 DB 419 GAGGTTTACCATCTCTGATCTGAGCGCGGCGATACGGGCTCTTTTCTTTTCTT 360
 QY 971 TGACAGGAGCTTGTCTGTCTGCTCAGCTGGAGTGGAGTGGATGATCTCGACTACT 1030
 DB 359 TGACAGGAGTGTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 QY 1031 GTAACTCTGCTCCCGGGTTCAGCGATTCCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1082
 DB 299 GCAACCTCCACTCCCGGGTTCAGTGATTCCTCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 1083 TAACAGCGCGCGCCACCACCATCTGCTGAATTTTGTATTTTGTAGTAAGACTGGGTTC 1142
 DB 239 TTACAGCGCGCGCCACCACCATCTGCTGAATTTTGTATTTTGTAGTAAGACTGGGTTC 180
 QY 1143 ATCATCTGGCAGGTTGGTTTCGAACTCCTGACCTGAGGTGAGCTGCCACCTTGGCT 1202

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OM nucleic - nucleic search, using sw model

Run on: May 9, 2003, 12:19:31 ; Search time 174.597 Seconds
(without alignments)
5671.939 Million cell updates/sec

Title: US-09-846-456-1
Perfect score: 3231
Sequence: 1 acaggcatggtgcagggtg.....gccccacatcccaactt 3231

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTOUS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	297.6	9.2	43950	US-09-735-934A-3	Sequence 3, Appli
2	292.6	9.1	162450	US-09-345-882-1	Sequence 1, Appli
3	285.4	8.8	20674	US-09-641-638-651	Sequence 651, App
4	278.2	8.6	84495	US-09-797-906-3	Sequence 3, Appli
5	277.2	8.6	84495	US-09-797-906-3	Sequence 3, Appli
6	271.8	8.4	15297	US-09-817-180-3	Sequence 3, Appli
7	271.6	8.4	162450	US-09-345-882-1	Sequence 1, Appli
8	271.2	8.4	43950	US-09-735-934A-3	Sequence 3, Appli
9	269.4	8.3	28720	US-09-341-587-7	Sequence 7, Appli
10	268	8.3	38564	US-09-734-673-3	Sequence 3, Appli
11	267.6	8.3	81001	US-09-750-580-1	Sequence 1, Appli
12	267	8.3	45716	US-08-965-048-5	Sequence 5, Appli
13	267	8.3	45989	US-08-965-048-6	Sequence 6, Appli
14	261.6	8.1	18073	US-09-078-294-12	Sequence 12, Appli
15	257.8	8.0	246240	US-08-724-394A-20	Sequence 20, Appli
16	257.8	8.0	246240	US-08-724-394A-21	Sequence 21, Appli
17	257.8	8.0	246240	US-08-724-394A-22	Sequence 22, Appli
18	253.6	7.8	20674	US-09-641-638-651	Sequence 651, App
19	253	7.8	6719	US-09-740-235-36	Sequence 36, Appli
20	253	7.8	8021	US-09-740-235-2	Sequence 2, Appli
21	253	7.8	162450	US-08-724-394A-20	Sequence 20, Appli
22	253	7.8	246240	US-08-724-394A-21	Sequence 21, Appli
23	253	7.8	246240	US-08-724-394A-22	Sequence 22, Appli
24	252.2	7.8	35060	US-08-814-095-7	Sequence 7, Appli
25	251.4	7.8	7680	US-09-210-748A-3	Sequence 3, Appli
26	250.2	7.7	21234	US-09-810-671-3	Sequence 1, Appli
27	249.6	7.7	81001	US-09-750-580-1	Sequence 1, Appli

28	246.4	7.6	38564	4	US-09-734-673-3	Sequence 3, Appli
29	243.4	7.5	7210	2	US-08-257-963B-10	Sequence 10, Appl
30	243.4	7.5	7210	4	US-08-367-841A-10	Sequence 10, Appl
31	243.4	7.5	7210	5	PCT-US95-07201-12	Sequence 43, Appl
32	243.4	7.5	22481	4	US-08-367-841A-43	Sequence 43, Appl
33	243.4	7.5	22481	5	PCT-US95-07201-43	Sequence 43, Appl
34	243.4	7.5	22484	4	US-09-875-223-2	Sequence 2, Appli
35	243.4	7.5	176373	3	US-09-128-155-17	Sequence 17, Appl
36	242.4	7.5	72604	4	US-09-268-992-7	Sequence 7, Appli
37	242.4	7.5	72604	4	US-09-657-474-7	Sequence 7, Appli
38	242	7.5	12134	4	US-09-810-671-3	Sequence 3, Appli
39	240.2	7.4	14796	4	US-08-975-080-35	Sequence 35, Appl
40	240.2	7.4	14796	4	US-09-630-706-10	Sequence 10, Appl
41	240.2	7.4	14796	4	US-09-496-694B-3	Sequence 3, Appli
42	240	7.4	35060	3	US-08-814-095-7	Sequence 7, Appli
43	239	7.4	3507	1	US-08-832-883-67	Sequence 67, Appl
44	239	7.4	3507	2	US-08-832-877-67	Sequence 67, Appl
45	238.8	7.4	87350	3	US-08-781-891-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1
US-09-735-934A-3
; Sequence 3, Application US/09735934A
; Patent No. 6372468
; GENERAL INFORMATION:
; APPLICANT: LI, JIAYIN et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000851
; CURRENT APPLICATION NUMBER: US/09/735,934A
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 43950
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-735-934A-3

Query Match	9.2%	Score	297.6;	DB	4;	Length	43950;
Best Local Similarity	62.5%	Pred. No.	1.6e-63;				
Matches	554;	Conservative	0;	Mismatches	314;	Indels	18;
Gaps	5;						
QY	375	GGCCGGGCACAAATGGCTAATGCCATCCAGCACTTTGGGAGGCTTGAGCCAGAGGA	434				
Db	37664	GGCCAGGTGTGTCTCTCATGCTGTAATCCAGCACTTTGGGAGGCTTGAGCCAGAGGA	37723				
QY	435	TCGCTTGAGCTCCAGAGTTTGAGACCAGCTTGATACATGGCAAAACCCCTGCTCTACA	494				
Db	37724	ACACCTGAGCTCAGGAGTTTGGGAGCCAGCTGCTGATGTAATGCTGCTCTAC-	37782				
QY	495	AAAAAATACAAAAATAGATGGTGTGGGCATGCACCTGTGGTCCAGCTACTTGGG	554				
Db	37783	-TAAATAACAAAATAGCCAGCATGGTGGCGGTCCTGTGATCCAGCTATTTCGGG	37841				
QY	555	AGGCTAAGTGGGAGGATCCCTTGAGCCAGGAGTCAAGTCTACACTGAGCCATGATTG	614				
Db	37842	AGGCTAGGAGGAGGAAATCTTTGAACCCGGAGGAGGAGTGGCAGCAATCA	37901				
QY	615	GATCACTGCACTCCAGCTGGGTAGACAGAGCAAGACCTGTCTCAAAAAAAGAAATGA	674				
Db	37902	CGTACTGCACTCCAGCTGGG-CGACAGAGGAGACTCCGTCTCAAAAAAATAAACA	37960				
QY	675	A-----AGAGAAGAAAGAAAGAGAGGAGGAGGAGGAGGAGGGGG	728				
Db	37961	ATGAAGAAAGGTAGGCATACACCATCTGTCTGCCAGCTACCGCACTCAGCACCCACTC	38020				
QY	729	GAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG	788				

DB 48021 CTACCTAATCCCGAGGAAGCCTGAGAGGAGGCTGCTATCAACAAACCCGCTAATACAGAT 38080
QY 789 AGAGCGAGAAGACTTTACGPAATTCCTCATCATGTTGGTGTGAAGTTTACCTGCAAAA 848
DB 38081 GACAAATCAAGGCTCGAGAAATAGGTCTCTGACCTGAGATCGAGGCTATCTG 38140
QY 849 GCAATTATTAGCAAGGTTATTCTTGTAGTACGAGCAAGGAGTCTGCTTGGGCT 908
DB 48141 TCTAGACACTGCTCTTAACACGTTGTCATACATTTCTCTTCTGCTTCTTCTTCTTCT 38200
QY 909 TTGGGCTTTAGAAAGCTCATCTCTGGCTTTCTGAGATCATCTCTCTCTCTCTCTCTCT 968
DB 38201 TTAAGCTAGGACTCTTAAGATCTCCATTAAGTTTCTCTCTCTCTCTCTCTCTCTCT 38255
QY 969 CTTCACACGAGGCTCTGCTCTGTCACACGCTGAGTGGAGTGGAGTGGAGTGGAGTGG 3828
DB 38256 TTTCAGACGAGGCTCTGCTCTGTCACACGCTGAGTGGAGTGGAGTGGAGTGGAGTGG 38315
QY 1029 CTCTAACCTCTGCTCTCCGGGTTCAAGGATCTCTGCTCTGCTCTGCTCTGCTCTGCTCT 1088
DB 38316 CTGCAACCTCTGCTCTCCGGGTTCAAGGATCTCTGCTCTGCTCTGCTCTGCTCTGCTCT 38375
QY 1089 GCGGCGGCGCACCATCTGGCTAATTTTGTATTTTGTAAAGACATCGGTTTCATCATG 1148
DB 38376 G---GACCGGAGGCGTGTCTAATTTTGTATTTTGTAAAGACATCGGTTTCATCATG 38431
QY 1149 TTGCGCAGGTTGCTTTCTGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1208
DB 38432 TTGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 38491
QY 1209 GGTCTGGATTACAGGCTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1254
DB 38492 GTCTGAGATTGCGAGGCTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 38547

RESULT 2
US-09-345 #82 1
: Sequence 1, Application US/09345882
: Patent No. 6399373
: GENERAL INFORMATION:
: APPLICANT: Hoechst Celanese, Lydic
: TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOL-INDUCIBLE PROTEIN (RBP-7)
: FILE REFERENCE: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
: CURRENT APPLICATION NUMBER: US/09/345.882
: PRIOR FILING DATE: 1999-06-30
: PRIOR APPLICATION NUMBER: US 60/091,415
: PRIOR FILING DATE: 1998-06-30
: PRIOR APPLICATION NUMBER: US 60/111,909
: NUMBER OF SEQ ID NOS: 140
: SOFTWARE: Patent.pm
: SEQ ID NO 1
: LENGTH: 162450
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: allele
: LOCATION: 72794
: OTHER INFORMATION: 5-124-273 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 88073
: OTHER INFORMATION: 5-127-261 : polymorphic base A or C
: FEATURE:
: NAME/KEY: allele
: LOCATION: 90842
: OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 93714
: OTHER INFORMATION: 5-128-60 : polymorphic base deletion of G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 97122
: OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 97152
: OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 99098
: OTHER INFORMATION: 5-140-257 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 99117
: OTHER INFORMATION: 5-130-276 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 103806
: OTHER INFORMATION: 5-131-395 : polymorphic base A or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 106940
: OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108106
: OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108149
: OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108308
: OTHER INFORMATION: 5-135-357 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108471
: OTHER INFORMATION: 5-136-174 : polymorphic base C or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 134134
: OTHER INFORMATION: 5-140-120 : polymorphic base C or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 134362
: OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
: FEATURE:
: NAME/KEY: allele
: LOCATION: 134374
: OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
: FEATURE:
: NAME/KEY: allele
: LOCATION: 146328
: OTHER INFORMATION: 5-143-84 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 146345
: OTHER INFORMATION: 5-143-101 : polymorphic base A or C
: FEATURE:
: NAME/KEY: allele
: LOCATION: 150329
: OTHER INFORMATION: 5-145-24 : polymorphic base A or G
: FEATURE:
: NAME/KEY: allele
: LOCATION: 160031
: OTHER INFORMATION: 5-148-352 : polymorphic base G or T
: FEATURE:
: NAME/KEY: allele
: LOCATION: 72771..72817
: OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID36
: FEATURE:
: NAME/KEY: allele

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: LOCATION: 72771..72817
: OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID#1
: FEATURE:
: NAME/KEY: allele
: LOCATION: 88050..88096
: OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID#2
: FEATURE:
: NAME/KEY: allele
: LOCATION: 88050..88096
: OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID#2
: FEATURE:
: NAME/KEY: allele
: LOCATION: 90819..90865
: OTHER INFORMATION: complement polymorphic fragment 99-147-325 SEQ ID#9
: FEATURE:
: NAME/KEY: allele
: LOCATION: 90819..90865
: OTHER INFORMATION: complement polymorphic fragment 99-147-325 SEQ ID#9
: FEATURE:
: NAME/KEY: allele
: LOCATION: 93690..93736
: OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID#4
: FEATURE:
: NAME/KEY: allele
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: OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID#4
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: NAME/KEY: allele
: LOCATION: 97099..97145
: OTHER INFORMATION: polymorphic fragment 99-144-224 SEQ ID#5
: FEATURE:
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: OTHER INFORMATION: polymorphic fragment 99-144-224 SEQ ID#5
: FEATURE:
: NAME/KEY: allele
: LOCATION: 97130..97177
: OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID#3
: FEATURE:
: NAME/KEY: allele
: LOCATION: 97130..97177
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: FEATURE:
: NAME/KEY: allele
: LOCATION: 99075..99121
: OTHER INFORMATION: polymorphic fragment 5-130-267 SEQ ID#5
: FEATURE:
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: OTHER INFORMATION: polymorphic fragment 5-130-267 SEQ ID#5
: FEATURE:
: NAME/KEY: allele
: LOCATION: 99094..99140
: OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID#6
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: FEATURE:
: NAME/KEY: allele
: LOCATION: 103783..103828
: OTHER INFORMATION: polymorphic fragment 5-131-495 SEQ ID#4
: FEATURE:
: NAME/KEY: allele
: LOCATION: 103783..103828
: OTHER INFORMATION: polymorphic fragment 5-131-495 SEQ ID#4
: FEATURE:
: NAME/KEY: allele
: LOCATION: 106918..106966
: OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID#7
: FEATURE:
: NAME/KEY: allele
: LOCATION: 106918..106966
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: OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID#8
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108084..108130
: OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID#8
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108084..108130
: OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID#9
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108127..108177
: OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID#9
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108127..108177
: OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID#6
: FEATURE:

Query Match          9.1%; Score 292.6; DB 4; Length 162450;
Best Local Similarity 61.2%; Pred. No. 5.2e-62;
Matches 564; Conservative 0; Mismatches 339; Indels 18; Gaps 5;

QY 375 GCGGGGCACAAATGGCTTAATGCCGTGAATCCAGACACITTTGGAGGCTCGAGCCAGAGA 434
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Db 27416 GCGTGGCGGTAGTGGTCACGCCCTATAATCCAGCACTCTGGAGCGCCAGCAGAGA 27475
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 435 TCGCTTGAGCTCCAGAGITTTAGACAGCGCTGGATACATGGCCAAACCCCTCTCTACA 494
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 27476 TCA--TGAGGTCAAGAGNTTGGAGCCATCTGSCCAATATAGTGAACCCGCCCTCTACT 27533
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 495 AAAAAATACA----AAATATAGATGGGTGTGGTGGCATGGACCTGTGTCGCCAGCTAC 549
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 27534 AAAATATACACACAAAAATAGCTGGAGCTGGTGGCATGGACCTGTGTCGCCAGCTAC 27593
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 550 TTGGAGGCTAAGGTGGGAGGATCGCTTGAGCCAGGAGTCAAGTCTACACTGAGCCAT 609
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 27594 TCGGAGGCTGAGCGAGGACAAATCGCTTGAACCTGGAGGTGCGAGGTGCGACTGCA 27653
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QY 610 GATTGGATCATCTGACTTCAGCTCGAGCTGGGTAGACAGACAGACACCTCTCTCAAAA 669
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 27654 GATCTGCGACTTCAGCTTCAGCTCGAGCTGGGTAGACAGACAGACCTCTCTCAAAA 27713
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 670 AATGAAGACAAAGAAAGAGAGGAGGAGGAGATGAGGGGAGGAGGAGGGGGG 729
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 27714 AAAAAAGATATCTTGTAGTTCTTTTCTCTCAAGGCACTTTTATGTAGAAATAA 27773
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 730 AGGAAGGACAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 789
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 27774 GCTAAATATAGTAAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 27833
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QY 790 GAGGACAGAAAGATTTACGTAAATTTCTCATCATGTGTGTGTGTGTGTGTGTGTGTGT 849
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 27834 TAIGTTTATGTTCTTTCTAAGCACAGATATCTCATTTAATCTCATGAGCAGCTATG 27893
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QY 850 CCAATTATTCACCAAGGTTATTTCTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 909
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 27894 AGAATACCTTAATTTCTGCTTTTACAGATAGGGAATAATGGCCACAGAGAAATAG 27953
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 910 TGGCTTTAGAAAGCTCATCTCTGCGCTTTCTGAGATCCATCCCTCTCTTTTATTTTC 969
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 27954 AGCATAGAGTTGAATCTCAATTTTGACC--TCCAGAGTCTGTTTCTTTTCTTTT 28011
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 970 TGCAGAGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1029
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 28012 ATGACAGGAGCTTCAITCTGTCGCCAGGCTGGAGTGGAGTGGAGTGGAGTGGAGT 28071
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1030 TGTAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1081
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 28072 TACAACCTCAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 28131
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1082 ATAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
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NAME/KEY: allele
LOCATION: 5903 : polymorphic base A or G
OTHER INFORMATION: 10-346-23 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6019 : polymorphic base A or G
OTHER INFORMATION: 10-346-141 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6141 : polymorphic base G or C
OTHER INFORMATION: 10-346-263 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 6183 : polymorphic base C or T
OTHER INFORMATION: 10-346-305 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 6338 : polymorphic base A or G
OTHER INFORMATION: 10-347-74 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6375 : polymorphic base G or C
OTHER INFORMATION: 10-347-111 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 6429 : polymorphic base C or T
OTHER INFORMATION: 10-347-165 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 6467 : polymorphic base A or G
OTHER INFORMATION: 10-347-203 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6484 : polymorphic base A or G
OTHER INFORMATION: 10-347-220 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6534 : polymorphic base A or T
OTHER INFORMATION: 10-347-271 : polymorphic base A or T
NAME/KEY: allele
LOCATION: 6611 : polymorphic base A or G
OTHER INFORMATION: 10-347-348 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 7668 : polymorphic base A or G
OTHER INFORMATION: 10-348-391 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8608 : polymorphic base C or T
OTHER INFORMATION: 10-349-47 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 8658 : polymorphic base A or G
OTHER INFORMATION: 10-349-97 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8703 : polymorphic base G or C
OTHER INFORMATION: 10-349-142 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 8777 : polymorphic base G or T
OTHER INFORMATION: 10-349-216 : deletion of CIG
NAME/KEY: allele
LOCATION: 8785 : polymorphic base C or T
OTHER INFORMATION: 10-349-224 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 8926 : polymorphic base C or T
OTHER INFORMATION: 10-349-368 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12171 : polymorphic base C or T
OTHER INFORMATION: 10-350-72 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12429 : polymorphic base C or T
OTHER INFORMATION: 10-350-332 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 13341 : polymorphic base A or G
OTHER INFORMATION: 10-507-170 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 13492 : polymorphic base A or C
OTHER INFORMATION: 10-507-321 : polymorphic base A or C
NAME/KEY: allele
LOCATION: 13524 : polymorphic base C or T
OTHER INFORMATION: 10-507-353 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 13535 : polymorphic base C or T

Query Match

8.8% Score 285.4 DB 4 Length 20674

Best Local Similarity 62.7% Pred. No. 1.2e-60;
Matches 556; Conservative 0; Mismatches 301; Indels 30; Gaps 6;
QY 357 TTATAAGATCAAGAAACAGCCGGGCACAAATGCTAATGCTAATCCACGACCTTTGG 416
DB 16196 TTAAGAAATGAGGATGCGCGCGCGCGCTGCTACCGCTGATGCTCCAGCAGCTGG 16137
QY 417 GAGGTCAGGCTCAGAGGATGCTTGAGCTCCAGAGTTTGAGACCGCCTGGAIAACATGG 476
DB 16136 GAGGCCAAGATGGCGGATCAC--GAGGTCAGGAGATCGAGACCATCTCGCTGAACAGG 16079
QY 477 CAAACGCTTCTCTACAAAAAATACAAAAATAGATGGTGTGGTGGCATGCACCTG 536
DB 16078 TGAACGCGCTCTCTACTAAAAATA--CGAAAGATTAGCCAGTGTGGTGGCGGSCACCTG 16020
QY 537 TGGTCGAGTACTTGGGAGGCTTAAGTGGGAGGATCGCTTCAGCGAGGAGTCAAGTC 596
DB 16019 TAGTCCGAGTACTCGGAGGCTGAGCGAGGAGATGGCGTGAACCGGGGAGAGAGCT 15960
QY 597 TACACTGAGCCATGATTGGATCACTGCTCCAGCTGGGTAGACAGCAGACGCTGT 656
DB 15959 TCGAGCGAGTGAATCCCGCCACTGCTACCTCCAGCTGGG--CGACACACAGAGATCTGT 15901
QY 657 CTCAAAAAAGAAATGAAGAGA-----AAGAAAGAAAGAGAGAGAGA 702
DB 15900 CTCAAAAAAGAAATGAAGAGA-----AAGAAAGAAAGAGAGAGAGA 15841
QY 703 GGAGATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 762
DB 15840 GCACCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 15781
QY 763 GAAAAAGAAAAAACAGATGAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 822
DB 15780 TCTCTATTTAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAATTT 15721
QY 823 TGTGGTGTGCAAGCTTTGACCCCAAAACCAATTTATTGACCAAGGTTATCTTTGACTGA 882
DB 15720 ACAGAAATACAGCTCTGGTTATATGTGGGATAAGTCAATGATTTCCAGTGTCTAC 15661
QY 883 GGCAGGGGTCTCGCTCTCTCGGGCTTGGGCTTTAGAAAGGATCATCTCTGCGCTT---- 938
DB 15660 AGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 15601
QY 939 TCTGAGATCAAGCT 998
DB 15600 GCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 15541
QY 999 GCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1058
DB 15540 GCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 15491
QY 1059 TTTCT 1110
DB 15480 TTTCT 15421
QY 1111 AATTTTGTATTTTAGTAAAGACTGGGTTTTCATGATGTTGCCAGGTTGGTTTTCGAAT 1170
DB 15420 AATTTTGTATTTTAGTAAAGACTGGGTTTTCATGATGTTGCCAGGTTGGTTTTCGAAT 15361
QY 1171 CTTGACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1217
DB 15360 CTTGACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 15314

RESULT 4

US-09-797-906-3

: Sequence 3, Application US/09797906

: Patent No. 6329188

: GENERAL INFORMATION:

: APPLICANT: Zhanhe YAN, Karen A. KEICHUM, Valentina DIFRANCESCO, Ellen M. BEAS

: TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, ENCODING HUMAN PROTEASE PROTEINS, A

: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, A

: TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CL001151CIP
CURRENT FILLING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 84495
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(84495)
OTHER INFORMATION: n = A,T,C or G
US-09-797-906-3

Query Match 8.6%; Score 278.2; DB 4; Length 84495;
Best Local Similarity 61.5%; Pred. No. 1.4e-58;
Matches 553; Conservative 0; Mismatches 328; Indels 18; Gaps 6;
QY 360 AAGATGAAGAAACAGCGCGGCACAAATGCTTAATGGCTGCTGAATCTAGCACTTGGGAG 419
DB 34817 AAAAATTGACTTGGAGCGCGCGGCTGGCTCAGCGGCTGTAATTCACACGCTGGGAG 34876
QY 420 GTGAGGCGAGAGGATCGCTTGAGCTCCAGAGATTGATGATAGCTGATATATAGTAA 479
DB 44877 GCGAGGCGAGGTGGATCAC--GAGGTGAGCGGATCGAGCAATATCGATATACAGTGA 34934
QY 480 AATCGCTGCTCTACAAAAAATACAAAAATGAGATGAGTGTGGTGTGAGTGTGGT 549
DB 44945 AATCGCATCTCTACTAAAA--ATAAAAATAGCTGAGGTGTGATGTGTGTGTGTGT 34990
QY 540 TCCAGCTACTTGGGAGGCTAAGTGTGAGGATGCTTTGATAGCTTAAGATCAAGTGA 599
DB 44991 TCCAGCTACTCGGAGGCTGAGGCGAGGAGATGCTGGAACCGGAGAGTGGACCTGAC 35050
QY 600 ATGAGCGATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 659
DB 45051 AGCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 35109
QY 660 AAAAAAAGAAATGAAG 719
DB 45110 TAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 35159
QY 720 GAGGCGGAG 779
DB 45170 GCTAGATTAATATGTCTACAGGAATACAAAGAGAGAGAGAGAGAGAGAGAGAGAG 35229
QY 779 AAGATGAAACAGAGCGAG 848
DB 45230 ACCAGATACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 899
QY 839 GAGCGCAAAACCCAAATTTATGACCAAGGTTATTTTCTGATGATGATGATGATGAT 899
DB 45290 TAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 35449
QY 899 CTGCTGGGCTTGGGCTTTAGAAAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 958
DB 45350 ATAGTAATCAAGTACATAGAGCTTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 35409
QY 959 TTTTATTTTCTTACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1014
DB 45410 TTTTATTTTCTTACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 35469
QY 1019 TCTGACCTACTGTAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076
DB 45470 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 35529
QY 1077 -----CTGAGATACAGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 45530 AAGTAAGTGGGATACAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 35589
QY 1131 AGA--CTGAGTTTCATCATGTTGGCGAGTGTGTTTGAAGAGTCTGATGAGAGAGAG 1188
DB 45591 TTTTATTTTCTTACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 35649

DB 35590 AGAGCAAGGTTTCATCTAGCTTGGCGAGGCTGGTTTCCGATTCCTGACCTCAAGTGATGT 35649
QY 1189 GCCACCTTGGCTCCCAAGAGTCTGGGATTACAGCATGAGCACTCGCGCCAGCTCA 1247
DB 35650 GCTGTCTGGGCTCCCAAGAGTGCAGGATTACAGGTGTGAGCCACCGGCGCCGCCCA 35708
RESULT 5
US-09-797-906-3/c
Sequence 3, Application US/09797906
Patent No. 6429188
GENERAL INFORMATION:
APPLICANT: Ziaohue YAN, Karen A. KETCHUM, Valentina DIFFANCIO, Ellen M. BEA
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS,
FILE REFERENCE: CL001151CIP
CURRENT FILLING DATE: 2001-03-05
CURRENT APPLICATION NUMBER: US/09797,906
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 84495
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(84495)
OTHER INFORMATION: n = A,T,C or G
US-09-797-906-3

Query Match 8.6%; Score 277.2; DB 4; Length 84495;
Best Local Similarity 61.1%; Pred. No. 2.5e-58;
Matches 556; Conservative 0; Mismatches 338; Indels 16; Gaps 6;
QY 345 TCTTCTCTCATTTTAAAGATGAAGAACAGCGCGGCACAAATGGCTAATGCTGTATC 404
DB 35736 TCATATATCTTTTAAATTAACAAATGGCTGGCGCGCTGCTCACACCTGTAATC 35677
QY 405 CCAGCACTTGGGAGGATGAGCGCCAGAGATCGCTTGAGCTCCAGATTTTCCAGACAGCC 464
DB 35676 CTGCACTTGGGAGGCGGAGAGCGACATCTTGGCTAGGTCAGGAATTCGAAACAGCC 35617
QY 465 TGCAATAATGAGTAAATCTGCTCTACAAAAAATACAAAAATAGTGGCTGTGT 524
DB 35616 TGCCCACTAGTGAACCT 35557
QY 525 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 584
DB 35556 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 35497
QY 585 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 644
DB 35496 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 35438
QY 645 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 704
DB 35437 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 35378
QY 705 AGATGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 764
DB 35377 AGATGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 35318
QY 765 AAAAAAAG 824
DB 35317 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 35258
QY 825 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 884
DB 35257 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 35199
QY 885 CAGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 944
DB 35199 CAGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 944

NAME/KEY: allele	LOCATION: 160031	OTHER INFORMATION: polymorphic base G or T	FEATURE:	LOCATION: 160031	OTHER INFORMATION: polymorphic base G or T	FEATURE:
NAME/KEY: allele	LOCATION: 72771..72817	OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30	FEATURE:	LOCATION: 72771..72817	OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30	FEATURE:
NAME/KEY: allele	LOCATION: 72771..72817	OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID31	FEATURE:	LOCATION: 72771..72817	OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID31	FEATURE:
NAME/KEY: allele	LOCATION: 88050..88096	OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID33	FEATURE:	LOCATION: 88050..88096	OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID33	FEATURE:
NAME/KEY: allele	LOCATION: 88050..88096	OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52	FEATURE:	LOCATION: 88050..88096	OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52	FEATURE:
NAME/KEY: allele	LOCATION: 90819..90865	OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49	FEATURE:	LOCATION: 90819..90865	OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49	FEATURE:
NAME/KEY: allele	LOCATION: 90819..90865	OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID50	FEATURE:	LOCATION: 90819..90865	OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID50	FEATURE:
NAME/KEY: allele	LOCATION: 93690..93736	OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32	FEATURE:	LOCATION: 93690..93736	OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32	FEATURE:
NAME/KEY: allele	LOCATION: 93690..93736	OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID55	FEATURE:	LOCATION: 93690..93736	OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID55	FEATURE:
NAME/KEY: allele	LOCATION: 97099..97145	OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71	FEATURE:	LOCATION: 97099..97145	OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71	FEATURE:
NAME/KEY: allele	LOCATION: 97099..97145	OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33	FEATURE:	LOCATION: 97099..97145	OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33	FEATURE:
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NAME/KEY: allele	LOCATION: 99075..99121	OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34	FEATURE:	LOCATION: 99075..99121	OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34	FEATURE:
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NAME/KEY: allele	LOCATION: 99094..99140	OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56	FEATURE:	LOCATION: 99094..99140	OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56	FEATURE:
NAME/KEY: allele	LOCATION: 103783..103828	OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36	FEATURE:	LOCATION: 103783..103828	OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36	FEATURE:
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? NAME/KEY: primer_bind
? LOCATION: 12029..12050
? OTHER INFORMATION: 17-42.pu
? NAME/KEY: primer_bind
? LOCATION: 12581..12603
? OTHER INFORMATION: 17-42.rp complement
? NAME/KEY: primer_bind
? LOCATION: 14992..15012
? OTHER INFORMATION: 17-41.pu
? NAME/KEY: primer_bind
? LOCATION: 15460..15482
? OTHER INFORMATION: 17-41.rp complement
? NAME/KEY: primer_bind
? LOCATION: 42070..42090
? OTHER INFORMATION: 20-841.pu
? NAME/KEY: primer_bind
? LOCATION: 42572..42591
? OTHER INFORMATION: 20-841.rp complement
? NAME/KEY: primer_bind
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? OTHER INFORMATION: 20-842.pu
? NAME/KEY: primer_bind
? LOCATION: 45863..45883
? OTHER INFORMATION: 20-842.rp complement
? NAME/KEY: primer_bind
? LOCATION: 76644..76664
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? OTHER INFORMATION: 20-853.rp complement
? NAME/KEY: primer_bind
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? OTHER INFORMATION: 20-828-311.mis
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? OTHER INFORMATION: 20-828-311.mis complement
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? NAME/KEY: primer_bind
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? OTHER INFORMATION: 20-841-149.mis complement
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? LOCATION: 45443..45461
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? NAME/KEY: primer_bind
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? NAME/KEY: primer_bind
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? OTHER INFORMATION: 20-853-415.mis complement
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? LOCATION: 12335..12359
? OTHER INFORMATION: 17-42-319.probe
? NAME/KEY: misc_binding
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? OTHER INFORMATION: 17-41-250.probe
? NAME/KEY: misc_binding
? LOCATION: 42206..42230
? OTHER INFORMATION: 20-841-149.probe
? NAME/KEY: misc_binding
? LOCATION: 45430..45454
? OTHER INFORMATION: 20-842-115.probe
? NAME/KEY: misc_binding
? LOCATION: 77046..77070
? OTHER INFORMATION: 20-853-415.probe
? US-09-750-580-1
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Query Match      8 38: Score 267.6; DB 4; Length 81001;
Best Local Similarity 62.68; Pred. No. 5.8e-56;
Matches 581; Conservative 0; Mismatches 309; Indels 38; Gaps 9;
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QY 358 TTAAGATGAAGAAACAGCGCGGCACCAATGGCTAATCGCTGTATATCCAGCAGCTTTGGG 417
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DB 53994 TTTAAGAGGGCAAGCTTGGCGGCACATGCTGCTCAGCGCTGTATATCCAGCAGCTTTGGG 53935

QY 418 AGGCTGAGGCAGAGGATCGCTTGAGCTCCAGAGTTTGAGACCGCCTGGATACATGGC 477
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DB 53934 AGGCGGAGCGCAGTCAATCACCTGAGATGAGAAGTTTCGAGACCGCCTGGCCACATGGT 53875

QY 478 AAAACCCCTGCTCTACAAAAAATACAAAAATAGATGGTGGTGGTGGCGATGCACCTGT 537
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DB 53874 GAAACCCCTGCTCTAC--TAAAAATACAAAAATAGCTGGGGTGGT--GCICAGCCCTGT 53818

QY 538 GGTCCAGCTACTTGGGAGGCTAAGTGGGAGGATCGCTTGAGCCCGAGGAGTCAAGTCT 597
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DB 53817 AATCCAGCTACTCGGAGGCTGAGCGCAAGAGATTTGCTGAACCTAGGAGCGGAGGTT 53758

QY 598 ACACGTGAGCCCATGATGGATCA--CTGCACCTCCAGCCTGGGTAGACAGCAAGACCTG 655
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 53757 CCAGTGAGCCCAAGATCGTCCCATTTTGCACTCCAGCCTGAGCAACAGAGGGAATTCCG 53698

QY 656 TCTCAAAAAAAGA--AATGAAGAGAAAGAAAGAGAGGAGGAGGAGATGAGGGG 714
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DB 53697 TCTCAAAAAAAGAAGGAGGAGCTTATTATATGGCATCTCTCCAA--CTTAAGACA 53638

QY 715 AGGAGGAGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 774
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 53637 TGGATGGTATTCCAAAGCACCAGGAAACCACTGTTTTTACCTTGGAAATAGGCTCTTA 53578

QY 775 AAACAAGATGAACAACAGAGCGACAGAAAGACTTTACGTAATATGCTCATCATGTGCTT 834
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DB 53577 AAGAGATTACA--TAATATCATATATCAAGGACATATGAATAACAAACACCAAAATCTTAA 53518

QY 835 GTTGAACGCAAAATCAATTA----TTGACCAAGGTTATTCTTTGACTGAGGCAA 887
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DB 53517 GCAGAAATCAGAAACAAATTCAGGAGAACTCACAGTGAAGAGCTTTGGACAGAGAA 53458

QY 888 GGGGTGCGCTCTCTCTGGGCTTGGGCTTTAGAAAGCTCATCTCTGGGCTTCTGAGATC 947
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DB 53457 TCAGGAAGCAGAGTTCTAAITCCAGCTTTCTCAGGGAATTTGATGACTCTAGGCAAC 53398

QY 948 -- ----- CATCCCTTCTCTTTTATTCTTGACACGAGTCTTGTCTGCTCACTC 996
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DB 53397 TCTATTATTGAGGCTCAGTTCTCTTTTGTGACAGGAGTCTTGCTCTGTGCTTCTGCTCC 53338

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QY 1057 GATTCCTGCTTACGCT- -----CCTGAGATACAGGCGCGCGCCACCACTCTGG 1108
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QY 1109 CTAATTTT ---GTAATTTTAGTAAGACACTGGGTTTTCATCATGTGTCGCGAGTGGTTT 1164
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DB 53217 CTAATTTTGTATTTT--TTTAGTAGAGAGGAGGTTTCCACCATGTTAGCCAGGATGGTCT 53158
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COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/98/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: G17957-006100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MULTIPLE TYPE: cDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note "HCA-B.CON.1G"
US-98-724,394A-20

Query Match	8.0%	Score	257.8	DB	2	Length	246240
Best local Similarity	61.4%	Prod.	No.	2.7e+53			
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GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2003, 11:21:45 ; Search time 461.057 Seconds
(without alignments)
8708.643 Million cell updates/sec

Title: US-09-846-456-1

Perfect score: 3231

Sequence: 1 acaggcgatggtgcaggtg.....gccccacatccaccactt 3231

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 783854 seqs, 621352466 residues

Total number of hits satisfying chosen parameters: 1557708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2893	89.5	2893	9	US-09-846-827-23
4	2893	89.5	2893	10	US-09-846-456-1
5	2891.4	89.5	2893	9	US-09-846-827-147
6	2891.4	89.5	2893	9	US-09-846-827-149
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9	2891.4	89.5	2893	9	US-09-846-827-142
10	2891.4	89.5	2893	9	US-09-846-827-143
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12	2891.4	89.5	2893	9	US-09-846-827-145
13	2891.4	89.5	2893	9	US-09-846-827-146
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18	2891.4	89.5	2893	9	US-09-846-827-154
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ALIGNMENTS

RESULT 1

US-09-984-827-3

; Sequence 3, Application US/09984827

; Publication No. US20030056234A1

; GENERAL INFORMATION:

; APPLICANT: DENEFFLE, PATRICE

; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE

; APPLICANT: ARNOULD-REGUIGNY, ISABELLE

; APPLICANT: DUVERGER, NICOLAS

; APPLICANT: CAMBIEN, FRANCOIS

; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES

; FILE REFERENCE: 03806.0522-00000

; CURRENT APPLICATION NUMBER: US/09/984,827

; CURRENT FILING DATE: 2002-04-01

; PRIOR FILING DATE: 2000-12-11

; PRIOR APPLICATION NUMBER: FR 00/14037

; PRIOR FILING DATE: 2000-10-31

; NUMBER OF SEQ ID NOS: 161

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 3231

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-984-827-3

Query Match 100.0%; Score 3231; DB 9; Length 3231;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 AAAAAAAGAAATGATTTTGGTGTCCACTTCAATAGGTAGGAGAGAGAGAGAGG 180

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1153

REF ID: A646456

03-09-843-410-1 : Sequence 1. Application US/09846456

Sequence 1, Application US,
Patent No. US20020146792A1

FILE NO. 032002014
GENERAL INFORMATION:

APPLICANT: ROSIER, Marie

APPLICANT: Prades, Catherine

APPLICANT: Lemoine, Cendrine

; APPLICANT: Naudin, Laurent

APPLICANT: Denefle, Patrice

; APPLICANT: Duverger, Nicolas

; APPLICANT: Brewer, Bryan

; APPLICANT: Remaley, Alan

```

: APPLICANT: Pojo, Silvia
: TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifi
:
: DATE OF INVENTION: Activity and Therapeutic Uses
:
: FILE REFERENCE: 3806.0505
:
: CURRENT APPLICATION NUMBER: US/09/846,456
:
: CURRENT FILING DATE: 2001-05-02
:
: PRIOR APPLICATION NUMBER: US 60/201,280
:
: PRIOR FILING DATE: 2000-05-02
:
: NUMBER OF SEQ ID NOS: 20
:
: SOFTWARE: PatentIn version 3.0
:
: SEQ ID NO 1
:
: LENGTH: 3231
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: US-09-846-456-1

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Query Match	100.0%	Score 3231	DB 10	Length 3231
Best Local Similarity	100.0%	Pred. No. 0		
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US 09 984 827 23
Sequence 23, Application US/09984827
Publication No. US20030056234A1
GENERAL INFORMATION:
APPLICANT: DENEFELE, PATRICE
APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-REUIGNÉ, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN AKM1 GENE, THEIR USES, AND
FILE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
FILE REFERENCE: 03806.0522-00000
CURRENT APPLICATION NUMBER: US/09/984.827
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254.108
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 23
LENGTH: 2893
TYPE: DNA
ORGANISM: Homo sapiens
US-09-984-827-23

Query Match 89.5% Score 2893 DB 9 Length 2893
Best Local Similarity 100.0% Pred. No. 0
Matches 2893 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 1 ACAGGGCATGGTGGCAGGTGGCTGTAATCTCAATTAATCGAGAGTGGAGGTGAATGA 60
DB 1 ACAGGGCATGGTGGCAGGTGGCTGTAATCTCAATTAATCGAGAGTGGAGGTGAATGA 60
QY 61 GCCCAGATCCGACCATTTGGTGGTGGAGTTCACATAGTAGGAGAGAGAGAGAGAG 120
DB 61 GCCCAGATCCGACCATTTGGTGGTGGAGTTCACATAGTAGGAGAGAGAGAGAGAG 120
QY 121 AAAAAAAGAGATGATTTGGTGGTGGAGTTCACATAGTAGGAGAGAGAGAGAGAGAG 180
DB 121 AAAAAAAGAGATGATTTGGTGGTGGAGTTCACATAGTAGGAGAGAGAGAGAGAGAG 180
QY 181 AGATGAGGGTTCAGGAGATCTAATTAATCTCTAAATCATCTAGGAGAGAGAGAGAG 240
DB 181 AGATGAGGGTTCAGGAGATCTAATTAATCTCTAAATCATCTAGGAGAGAGAGAGAG 240
QY 241 TTTAATAACACTCTGCTTTTATAACATCATCTGCTGAGGAGTTCAGAGTTCAGAGT 300
DB 241 TTTAATAACACTCTGCTTTTATAACATCATCTGCTGAGGAGTTCAGAGTTCAGAGT 300
QY 301 AAGTTCAGTTCAGAAACCCCTTTCAGGAAGACAGAAATATACATCTCTCTCAATTA 360
DB 301 AAGTTCAGTTCAGAAACCCCTTTCAGGAAGACAGAAATATACATCTCTCTCAATTA 360
QY 361 AAGTTCAGTTCAGAAACCCCTTTCAGGAAGACAGAAATATACATCTCTCTCAATTA 360

QY 361 AAGATGAAGAAACAGGCGGGCACAAATGGCTAATGCTGTATATCCAGCACTTTGGAGG 420
DB 361 AAGATGAAGAAACAGGCGGGCACAAATGGCTAATGCTGTATATCCAGCACTTTGGAGG 420
QY 421 CTGAGGCGAAGGATCGCTTGAGCTCCAGAGTTTGAGACCGAGCTGGATTAACATGCAAA 480
DB 421 CTGAGGCGAAGGATCGCTTGAGCTCCAGAGTTTGAGACCGAGCTGGATTAACATGCAAA 480
QY 481 ACCTGTCTCTACAAAAAATACAAAAATAGATGGGTGTGGTGGCATGCACTTGTGT 540
DB 481 ACCTGTCTCTACAAAAAATACAAAAATAGATGGGTGTGGTGGCATGCACTTGTGT 540
QY 541 CCGAGCTAATTGGAGGCTAAGTGGGAGGATCGCTTGAGCCAGGAGTCAAGTCTACA 600
DB 541 CCGAGCTAATTGGAGGCTAAGTGGGAGGATCGCTTGAGCCAGGAGTCAAGTCTACA 600
QY 601 CTGAGTCATGATTGGATCACTGCACTCCAGCTGGGTAGACAGAGCAACACCTCTCTCA 660
DB 601 CTGAGTCATGATTGGATCACTGCACTCCAGCTGGGTAGACAGAGCAACACCTCTCTCA 660
QY 661 AAAAAAGAAATGAACAGAAAGAAAGAGAGAGAGAGAGATGAGGGAGGAGG 720
DB 661 AAAAAAGAAATGAACAGAAAGAAAGAGAGAGAGAGAGATGAGGGAGGAGG 720
QY 721 GAGGGGGAG 780
DB 721 GAGGGGGAG 780
QY 781 GATCAACAG 840
DB 781 GATCAACAG 840
QY 841 CCCCCAACCCAAATTTATTGACCAAGGTTATTCTTTGACTGAGGCAAGGGGTCCGCTCT 900
DB 841 CCCCCAACCCAAATTTATTGACCAAGGTTATTCTTTGACTGAGGCAAGGGGTCCGCTCT 900
QY 901 CCGTGGGCTTGGGCTTTAGAAAGCTCATCTCTGGGCTTTCTGAGATCCATCCCTTCTTT 960
DB 901 CCGTGGGCTTGGGCTTTAGAAAGCTCATCTCTGGGCTTTCTGAGATCCATCCCTTCTTT 960
QY 961 TTATTTTCTTGACACGAGCTCTGTCTCTCACTCAGGCTGGAGTGGAGTGGATGATC 1020
DB 961 TTATTTTCTTGACACGAGCTCTGTCTCTCACTCAGGCTGGAGTGGAGTGGATGATC 1020
QY 1021 TCGACTCAGTGTAACTCTGCTCCCGGTTCAAGCGATCTCTGCTCCAGCTCCGCTCA 1080
DB 1021 TCGACTCAGTGTAACTCTGCTCCCGGTTCAAGCGATCTCTGCTCCAGCTCCGCTCA 1080
QY 1081 GATAACAGGCGCGCGCCACACATCTGGCTAATTTTGTATTTTATAGTAAGAGTGGGTT 1140
DB 1081 GATAACAGGCGCGCGCCACACATCTGGCTAATTTTGTATTTTATAGTAAGAGTGGGTT 1140
QY 1141 TCATCATCTGTCAGGAGTGGTTCGAACTCTGAGCTGAGGTGAGCTGCCACCTTGGC 1200
DB 1141 TCATCATCTGTCAGGAGTGGTTCGAACTCTGAGCTGAGGTGAGCTGCCACCTTGGC 1200
QY 1201 CTCCTCAAGTCTGGGATTAACAGCATGAGCAGCTGCGCCAGCTCAGATCCATCCCTTT 1260
DB 1201 CTCCTCAAGTCTGGGATTAACAGCATGAGCAGCTGCGCCAGCTCAGATCCATCCCTTT 1260
QY 1261 CTAGGCGCAACAGTCCATGGTGCAGAGGGGCTCCACCCAGCTTATAGTACCTGG 1320
DB 1261 CTAGGCGCAACAGTCCATGGTGCAGAGGGGCTCCACCCAGCTTATAGTACCTGG 1320
QY 1321 GACTCCAGAAATCTCTGCTGGGCTCCACATGAGCTTCCAGGGGCTGCTGAGGCTC 1380
DB 1321 GACTCCAGAAATCTCTGCTGGGCTCCACATGAGCTTCCAGGGGCTGCTGAGGCTC 1380
QY 1381 TCTATCGGCTCTCTGCTGAGTGTGTAGAACCACTGATGTAGTACCTGGGCTTGAGGC 1440
DB 1381 TCTATCGGCTCTCTGCTGAGTGTGTAGAACCACTGATGTAGTACCTGGGCTTGAGGC 1440
QY 1441 GTGCCCCTGGAGATCTCTGTTGACTGTAGCTGAGGGGGCTTGTGCACTGAAATGTGCA 1500

1441 GTGGCTGGAGATCTGTGACTGTAGCATGGAGGGGCTGTGCAGCTGAATGCTGCA 1500
1501 TGCAGGTGGTGGAGTTCTGGAATATGATGGAGCTGGAGTGGGAAGAGAAAGTAGGCTG 1560
1501 TGCAGGTGGTGGAGTTCTGGAATATGATGGAGCTGGAGTGGGAAGAGAAAGTAGGCTG 1560
1561 GGGGAGCTCTCTCATGTCACCTCATCTGGCCAAACTCAAGTCAAACTGTGAAGAGCT 1620
1561 GGGGAGCTCTCTCATGTCACCTCATCTGGCCAAACTCAAGTCAAACTGTGAAGAGCT 1620
1621 AAATGTGAATCTGCCCTTCAAGGTGGCTTACAAGGTATCTTTGTCAAGTAGGAGAGCTT 1680
1621 AAATGTGAATCTGCCCTTCAAGGTGGCTTACAAGGTATCTTTGTCAAGTAGGAGAGCTT 1680
1681 GTGGCTCCAGCTGCACTTCAGGGGCTGCTTGGGCTCTCTTACGGGCTCTGCTGAGT 1740
1681 GTGGCTCCAGCTGCACTTCAGGGGCTGCTTGGGCTCTCTTACGGGCTCTGCTGAGT 1740
1741 CTCTATGAATCCTTCAGGCGAGATTCAATATTAGACTCTTCAGCTTTCAGCTGAGCTT 1800
1741 CTCTATGAATCCTTCAGGCGAGATTCAATATTAGACTCTTCAGCTTTCAGCTGAGCTT 1800
1801 TGGCCAGAAATAGGTGACATTTAGTTTGTGGCTTGTAGTATGATGATTAATAATTTAGACA 1860
1801 TGGCCAGAAATAGGTGACATTTAGTTTGTGGCTTGTAGTATGATGATTAATAATTTAGACA 1860
1861 TGGTGTAGGCTGCATCTTACCTTACCTTGGCTTTTGTTCCTCTGAGTATTTTGGGT 1920
1861 TGGTGTAGGCTGCATCTTACCTTACCTTGGCTTTTGTTCCTCTGAGTATTTTGGGT 1920
1921 AGTTTGTCTGCTTACAGCCAAAGCAACAGAGAAAGTGGAGTCTGGAATGGTATAT 1980
1921 AGTTTGTCTGCTTACAGCCAAAGCAACAGAGAAAGTGGAGTCTGGAATGGTATAT 1980
1981 AATTTTACAGACTGCAATCTCTGGCTGCTTACAGAAATGATACAAATAAATAACAA 2040
1981 AATTTTACAGACTGCAATCTCTGGCTGCTTACAGAAATGATACAAATAAATAACAA 2040
2041 GTCTGTGTTTATACAGAGAGGCTGATCAATAATGAATGAATGAATGAATGAATGAAT 2100
2041 GTCTGTGTTTATACAGAGAGGCTGATCAATAATGAATGAATGAATGAATGAATGAAT 2100
2101 CATATGTTCTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 2160
2101 CATATGTTCTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 2160
2161 TCTTCTCTCAATTTATCAGAGAGAGTATACAGAGAGTATACAGAGAGTATACAGAGAG 2220
2161 TCTTCTCTCAATTTATCAGAGAGAGTATACAGAGAGTATACAGAGAGTATACAGAGAG 2220
2221 CTGGGAGCTCAGGCTGGGATCTCCAGGCTATACAGAGAGTATACAGAGAGTATACAGAG 2280
2221 CTGGGAGCTCAGGCTGGGATCTCCAGGCTATACAGAGAGTATACAGAGAGTATACAGAG 2280
2281 CAGGTTTGGGGGAAACAAAGAGAGGCTATACAGAGAGTATACAGAGAGTATACAGAGAG 2340
2281 CAGGTTTGGGGGAAACAAAGAGAGGCTATACAGAGAGTATACAGAGAGTATACAGAGAG 2340
2341 CACCCAGCTAGGCTTTGAAGGAGAAACAAAGAGAGTATACAGAGAGTATACAGAGAGTAT 2400
2341 CACCCAGCTAGGCTTTGAAGGAGAAACAAAGAGAGTATACAGAGAGTATACAGAGAGTAT 2400
2401 GGGAGATTGAGGCTTCT 2460
2401 GGGAGATTGAGGCTTCT 2460
2461 AAAGGAAAAAAATTTGGGAAAGCAGGATTTAGAGAGAGTATACAGAGAGTATACAGAGAG 2520
2461 AAAGGAAAAAAATTTGGGAAAGCAGGATTTAGAGAGAGTATACAGAGAGTATACAGAGAG 2520
2521 GGTCTCGGAGCTGAGCTAGAGAGTCTGGGAGAGTATACAGAGAGTATACAGAGAGTATACAG 2580

Db 2521 GGCTGCCGGAAAGCTGGACTAGAGAGTCTGCGGCGAGCCCGAGCCCGAGCGCTTCCCGC 2580
QY 2581 GGCTCTTAGCG 2640
Db 2581 GGCTCTTAGCG 2640
QY 2641 CGTGTCTACCTTCCACCGCCACCGCCACCGCCACCGCCACCGCCACCGCCACCGCCACCG 2700
Db 2641 CGTGTCTACCTTCCACCGCCACCGCCACCGCCACCGCCACCGCCACCGCCACCGCCACCG 2700
QY 2701 TCGTGGCGGCTGAAAGCTGCGCGCGTTTAAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2760
Db 2701 TCGTGGCGGCTGAAAGCTGCGCGCGTTTAAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2760
QY 2761 TGACTCACTGAAGTCACTAATAACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2820
Db 2761 TGACTCACTGAAGTCACTAATAACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2820
QY 2821 GCTTTGACCGATAGTAACTCTGCGCTGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2880
Db 2821 GCTTTGACCGATAGTAACTCTGCGCTGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2880
QY 2881 CGGCAAAACCC 2893
Db 2881 CGGCAAAACCC 2893

RESULT 4

US-09-846-456-3
; Sequence 3, Application US/09846456
; Patent No. US20020146792A1
; GENERAL INFORMATION:
; APPLICANT: Rosier, Marie
; APPLICANT: Prades, Catherine
; APPLICANT: Lemoine, Cendrine
; APPLICANT: Naudin, Laurent
; APPLICANT: Denelle, Patrice
; APPLICANT: Duverger, Nicolas
; APPLICANT: Brewer, Bryan
; APPLICANT: Romaley, Alan
; APPLICANT: Polo, Silvia
; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifi
; TITLE OF INVENTION: Activity and Therapeutic Uses
; FILE REFERENCE: 1806.0505
; CURRENT APPLICATION NUMBER: US/09/846,456
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,280
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 2893
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-846-456-3

Query Match: 89.5%; Score 2893; DB 10; Length 2893;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2893; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGGGCATGCTGGCAGGTGCGCTGTAATCTCAGTTACTCGGAGGTGGAGGTGCAATGA 60
Db 1 ACAGGGCATGCTGGCAGGTGCGCTGTAATCTCAGTTACTCGGAGGTGGAGGTGCAATGA 60
QY 61 GCCCAGATCCACCATTTGCACCTCCAGCTGGGCAACAAAGAGTGAACCTCCATCTCAATT 120
Db 61 GCCCAGATCCACCATTTGCACCTCCAGCTGGGCAACAAAGAGTGAACCTCCATCTCAATT 120
QY 121 AAAAAAAGAAATGATTTTGGTGTGCTGACTTCAATAGTAGGAGAGAGAGAGAGAGG 180
Db 121 AAAAAAAGAAATGATTTTGGTGTGCTGACTTCAATAGTAGGAGAGAGAGAGAGAGG 180
QY 181 AGATGAGGCTGAGGAGAGATCTAAATTACTCTCTAAATATGCTAGGAAAGATAACACT 240

QY	2401	GGGAGATTCAGGCTTAGAGCTCTCTCTCCGCCAATCCGCTCCGCTCCGGCTGAGAGAAATTAAC	2460
DB	2401		2460
QY	2401	GGGAGATTCAGGCTTAGAGCTCTCTCTCCGCCAATCCGCTCCGCTCCGGCTGAGAGAAATTAAC	2460
DB	2401		2460
QY	2461	AAGGAAAGAAAATTTGGCGAAGCAGGATTTAGAGAGAGCAAAATTCGACATCGTCACTT	2520
DB	2461		2520
QY	2521	GGCTGCCGGGAACGTGCATCTAGAGAGCTCTGTGTGTACGCTCGGAGAGCTAGCTCTTCCGCG	2580
DB	2521		2580
QY	2581	GGCTCTTAGCCCGCGGGCTGTGGGTGGGGAAGAGAGATAGAGATCTGGATTAAGATATA	2640
DB	2581		2640
QY	2641	CCTGTCTTACCTCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCC	2700
DB	2641		2700
QY	2701	TCCGTGGCGGCTGAACGTCGCCCGTTTAAGGGGTGGGGTCCGGTTCCATCTGCTTTCTCC	2760
DB	2701		2760
QY	2761	TGAGTGCATCAACTACATAAAGCAGAGCCGTGATTAAGCGGCGGCGGAGAGCAAGTACAGACAG	2820
DB	2761		2820
QY	2821	GCCTTGACCATAGTAACCTCTCCGCTCTGGTGTGGTGTGATGCGCAATCTATAAAGAACTAGTCC	2880
DB	2821		2880
QY	2881	CGGCAAAAACCCC	2893
DB	2881		2893

RESULTS

US-09-984-827-137

? Sequence 137, Application US/09984827
? Publication No. US20030056234A1
? GENERAL INFORMATION:
? APPLICANT: DENEFLÉ, PATRICE
? APPLICANT: ROSIER-MONTUS, MARIE-FRANÇOISE
? APPLICANT: ARNOULD-REGUIGNE, ISABELLE
? APPLICANT: DUVERGER, NICOLAS
? APPLICANT: CAMBIEN, FRANÇOIS
? TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN APOA1 GENE, THEIR USES, AND
? TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
? FILE REFERENCE: 03806.0522-000000
? CURRENT APPLICATION NUMBER: US/09/984.827
? CURRENT FILING DATE: 2002-04-01
? PRIOR APPLICATION NUMBER: 60/254.108
? PRIOR FILING DATE: 2000-12-11
? PRIOR APPLICATION NUMBER: FR 00/14047
? PRIOR FILING DATE: 2000-10-31
? NUMBER OF SEQ ID NOS: 161
? SOFTWARE: PatentIn ver. 2.1
? SEQ ID NO: 137
? LENGTH: 2893
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-984-827-137

Query Match	89.5%	Score 2891.4	DR 9	Length 2893
Best Local Similarity	100.0%	Pred. No. C		
Matches 2892	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0

QY 1 ACAGGCATGGTGGCAGGTGCCTGTAAATTCAGTTACTTCGGACGTTGCAGTTTGTAAATGA 60
|||||
|||

DB 1 ACAGGCATGGTGGCAGGTGCCTGTAAATTCAGTTACTTCGGACGTTGCAGTTTGTAAATGA 60
|||||
|||

Qy	61	GC	CAGATCGC	ACCAATGTG	CACCTCC	AGCCTGG	CGCACAAAGAGT	GAACTCC	ATCAATT	120
Db	61	GC	CCAGATCGC	ACCATTTGC	ACCTCC	AGCCTGG	CGCACAAAGAGT	GAACTCC	ATCAATT	120
Qy	121	AAAA	AAAAAGAAAT	GTATTGTG	TGGTTC	AGACTTCA	AAATAGT	AGGAGAAAGAGAGAGG	180	
Db	121	AAAA	AAAAAAGAAAT	GTATTGTG	TGGTTC	AGACTTCA	AAATAGT	AGGAGAAAGAGAGAGG	180	
Qy	181	AGAT	GGAGGGT	CAGGAGATCT	AAATTACT	TCTCTAAA	ATCATGCT	TAGGAAAGAT	AACACT	240
Db	181	AGAT	GGAGGGT	CAGGAGATCT	AAATTACT	TCTCTAAA	ATCATGCT	TAGGAAAGAT	AACACT	240
Qy	241	TTTA	ATAAATCA	TCTCTGTCTTT	TATACATCT	CTTGCC	AAAGAGCT	CAAGAGTTTCAACA	300	
Db	241	TTTA	ATAAATCA	TCTCTGTCTTT	TATACATCT	CTTGCC	AAAGAGCT	CAAGAGTTTCAACA	300	
Qy	301	AAAT	TTCACTTTC	AGAAAGCCCTT	TGAGG	AGACAGAAT	TACATCT	TCTCTCCATTTTA	360	
Db	301	AAAT	TTCACTTTC	AGAAAGCCCTT	TGAGG	AGACAGAAT	TACATCT	TCTCTCCATTTTA	360	
Qy	361	AAGAT	GAAGAAAC	CAGCCGGG	CACATGCT	TAATGCCT	TGTAAT	CCCAGCACTT	TGGGAGG	420
Db	361	AAGAT	GAAGAAAC	CAGCCGGG	CACATGCT	TAATGCCT	TGTAAT	CCCAGCACTT	TGGGAGG	420
Qy	421	CTG	AGCCAGAG	AGATGCTT	TGAGCTCC	AGAGTTTG	AGACAC	AGCCTGG	ATAACAT	480
Db	421	CTG	AGCCAGAG	AGATGCTT	TGAGCTCC	AGAGTTTG	AGACAC	AGCCTGG	ATAACAT	480
Qy	481	ACCT	CTCTCTAC	AAAAAAAAT	TACAAAAAT	TAGATGG	TGGTGG	TGGCCAT	GCACAT	540
Db	481	ACCT	CTCTCTAC	AAAAAAAAT	TACAAAAAT	TAGATGG	TGGTGG	TGGCCAT	GCACAT	540
Qy	541	CCC	AGCTACT	TGGCAGGCT	AAAGCTGG	AGCATCGCT	TGAGCC	CAGGGAGT	CAATCT	600
Db	541	CCC	AGCTACT	TGGCAGGCT	AAAGCTGG	AGCATCGCT	TGAGCC	CAGGGAGT	CAATCT	600
Qy	601	CTG	AGCCATG	ATTGGATCT	GCATCC	AGCCTGGG	TAGAC	AGCAAGACCC	TGCTCA	660
Db	601	CTG	AGCCATG	ATTGGATCT	GCATCC	AGCCTGGG	TAGAC	AGCAAGACCC	TGCTCA	660
Qy	661	AAAA	AAAAAATAAT	TAAGAGAAAC	AAAGAAAG	AGGAGAGAT	TAGGGAGGAGG	720		
Db	661	AAAA	AAAAAATAAT	TAAGAGAAAC	AAAGAAAG	AGGAGAGAT	TAGGGAGGAGG	720		
Qy	721	GAGG	GGGGGAGG	AGGAGG	AAAGAAAG	AAAGAAAG	AAGATG	AAAAAAGAAAAA	AAACAA	780
Db	721	GAGG	GGGGGAGG	AGGAGG	AAAGAAAG	AAAGAAAG	AAGATG	AAAAAAGAAAAA	AAACAA	780
Qy	781	GAT	GAACATAG	AGGCAC	AAAGACTTT	TACGTAA	ATTGCT	CATCAT	TGCTTGTCA	840
Db	781	GAT	GAACATAG	AGGCAC	AAAGACTTT	TACGTAA	ATTGCT	CATCAT	TGCTTGTCA	840
Qy	841	CCCC	AAAAATCA	ATTATT	TGACCAAG	GTATTCTT	TGACT	TAGGCAAG	GGGGTCCGGTCT	900
Db	841	CCCC	AAAAATCA	ATTATT	TGACCAAG	GTATTCTT	TGACT	TAGGCAAG	GGGGTCCGGTCT	900
Qy	901	CTG	GGGCTTGG	GGCTTTAG	AAAGCTCA	CTCTGG	CGCTTCT	CGAGAT	CCCTTCTCTT	960
Db	901	CTG	GGGCTTGG	GGCTTTAG	AAAGCTCA	CTCTGG	CGCTTCT	CGAGAT	CCCTTCTCTT	960
Qy	961	TTATT	TTCTTG	ACATGG	AGCTTGTCT	TGCTCACT	CAGCGT	CGAGTGG	GTATGATC	1020
Db	961	TTATT	TTCTTG	ACATGG	AGCTTGTCT	TGCTCACT	CAGCGT	CGAGTGG	GTATGATC	1020
Qy	1021	TCG	ACTACATG	TAACTCT	CGCTCC	CGGGTTC	AAGGAT	TTCTCT	CGCCTCAG	1080
Db	1021	TCG	ACTACATG	TAACTCT	CGCTCC	CGGGTTC	AAGGAT	TTCTCT	CGCCTCAG	1080
Qy	1081	GATA	ACAGGCGCC	CGCCAC	CAATCT	TGGCTAA	TTTTTT	TAGTAA	AGACTGGGTT	1140
Db	1081	GATA	ACAGGCGCC	CGCCAC	CAATCT	TGGCTAA	TTTTTT	TAGTAA	AGACTGGGTT	1140
Qy	1141	TCAT	CTATGTTGG	CGCAGG	TGGTTT	TCGA	ACTCT	CGACT	CGAGT	1200
Db	1141	TCAT	CTATGTTGG	CGCAGG	TGGTTT	TCGA	ACTCT	CGACT	CGAGT	1200

[illegible]

Db	2221	CCTGGGAGCTCAGGCTGGGAATCTCCAAAGGCAGTAGGTGCGCTATCAAAAATCAAAATC	2280
Qy	2281	CAGCTTTGTGGGGGAAACAAAGACAGCCCATTAACCAAGAGACTGTCCGCTTCCCT	2340
Db	2281	CAGCTTTGTGGGGGAAACAAAGACAGCCCATTAACCAAGAGACTGTCCGCTTCCCT	2340
Qy	2341	CACCCAGCTAGGCTTTGAAAGGAAACAAAGACAGACAAATGATTGGCTCTCTGA	2400
Db	2341	CACCCAGCTAGGCTTTGAAAGGAAACAAAGACAGACAAATGATTGGCTCTCTGA	2400
Qy	2401	GGGAGATTCAAGCTAGAGCTCTCTCCGCCCAATCCCTCCGGGTGAGAACTAAC	2460
Db	2401	GGGAGATTCAAGCTAGAGCTCTCTCCGCCCAATCCCTCCGGGTGAGAACTAAC	2460
Qy	2461	AAGGAAAAAAATTCGCGAAGCAGGATTTAGAGGAAGCAAAATTCACGTGGCTT	2520
Db	2461	AAGGAAAAAAATTCGCGAAGCAGGATTTAGAGGAAGCAAAATTCACGTGGCTT	2520
Qy	2521	GGCTGCCGGGAAGCTGGACTAGAGACTCTGGCGCAGCCCGAGCCAGCGCTTCCGC	2580
Db	2521	GGCTGCCGGGAAGCTGGACTAGAGACTCTGGCGCAGCCCGAGCCAGCGCTTCCGC	2580
Qy	2581	CGCTCTTAGCCCGCGGGCCGGCGGGAAGGAGCGACAGCCGGGACCTTAAGACA	2640
Db	2581	CGCTCTTAGCCCGCGGGCCCGCGGGAAGGAGCGACAGCCGGGACCTTAAGACA	2640
Qy	2641	CTCTGTAGCTGTCCACCCGCCACCCACCCACCCACCTCCGCCCACTCCCTAGATGTG	2700
Db	2641	CTCTGTAGCTGTCCACCCGCCACCCACCCACCCACCTCCGCCCACTCCCTAGATGTG	2700
Qy	2701	TCGTGGCGGTGAACGTGCCCGTTTAAGGGCGGGCCCGGTGCACAGTGTCTTCG	2760
Db	2701	TCGTGGCGGTGAACGTGCCCGTTTAAGGGCGGGCCCGGTGCACAGTGTCTTCG	2760
Qy	2761	TGAGTGACTGAATACATAACAGAGCGCCGGAAGGGCGGGAGGAGGAGACAG	2820
Db	2761	TGAGTGACTGAATACATAACAGAGCGCCGGAAGGGCGGGAGGAGGAGACAG	2820
Qy	2821	GCTTTGACCGATAGTAACCTCTCGCTCGGTGCAGCCGGAATCTATAAGGGAACCTCC	2880
Db	2821	GCTTTGACCGATAGTAACCTCTCGCTCGGTGCAGCCGGAATCTATAAGGGAACCTCC	2880
Qy	2881	CGGCAAAAGCCC	2893
Db	2881	CGGCAAAAGCCC	2893

RESULT 6

US-09-984-827-139

: Sequence 139, Application US/09984827

: Publication No. US20030056234A1

: GENERAL INFORMATION:

: APPLICANT: DENEFELE, PATRICE

: APPLICANT: KOSTER-MONTUS, MARIE-FRANCOISE

: APPLICANT: ARNOULD-REGUIGNE, ISABELLE

: APPLICANT: DUVERGER, NICOLAS

: APPLICANT: CAMHIEN, FRANCOIS

: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,

: TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR

: FILE REFERENCE: 03806.0522-00000

: CURRENT APPLICATION NUMBER: US/09/984,827

: CURRENT FILING DATE: 2002-04-01

: PRIOR APPLICATION NUMBER: 60/254,108

: PRIOR FILING DATE: 2000-12-11

: PRIOR APPLICATION NUMBER: FR 00/14037

: PRIOR FILING DATE: 2000-10-31

: NUMBER OF SEQ ID NOS: 161

: SOFTWARE: PatentIn Ver. 2.1

: SEQ ID NO 139

: LENGTH: 2893

: TYPE: DNA

: ORGANISM: Homo sapiens

US-09-984-827-139

Query Match 89.5%; Score 2891.4; DB 9; Length 2893;		
Best local Similarity 100.0%; Pred. No. 0;		
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY 1	ACAGGCGATGGTGGCAGTCCCTGTAATCTCACTTACTCGGAGGTGGAGGTTCGAATCA	60
DB 1		
QY 1	ACAGGCGATGGTGGCAGTCCCTGTAATCTCACTTACTCGGAGGTGGAGGTTCGAATCA	60
DB 1		
QY 61	GCCAGATCCACCAATTCGACTCCAGCTCGGCAATCAAAAGTCAAACTGATCTCAAT	120
DB 61		
QY 61	GCCAGATCCACCAATTCGACTCCAGCTCGGCAATCAAAAGTCAAACTGATCTCAAT	120
DB 61		
QY 121	AAAAAAGAGATGATTTTGGTGGTGGTTCGAAATAGTACAGCAAAAGAGAGAGAG	180
DB 121		
QY 121	AAAAAAGAGATGATTTTGGTGGTGGTTCGAAATAGTACAGCAAAAGAGAGAGAG	180
DB 121		
QY 181	AGATGAGGCTCAGGAGATCTAATTAATCTCTCAAAATCATGTAAGCAAAATACACCT	240
DB 181		
QY 181	AGATGAGGCTCAGGAGATCTAATTAATCTCTCAAAATCATGTAAGCAAAATACACCT	240
DB 181		
QY 241	TTTAATAACACTCTCTGCTTTTATAACATCATCTCTGCAAGAGCTCAAAAGTTCAACA	300
DB 241		
QY 241	TTTAATAACACTCTCTGCTTTTATAACATCATCTCTGCAAGAGCTCAAAAGTTCAACA	300
DB 241		
QY 301	AAGTCACTTTCAGAAACCCCTTTGAGAGAGACAAATATACATCTCTCTCCATTTTA	360
DB 301		
QY 301	AAGTCACTTTCAGAAACCCCTTTGAGAGAGACAAATATACATCTCTCTCCATTTTA	360
DB 301		
QY 361	AAGATGAAGAAACAGCGCGGACAAATGCTTAATGCTTAATGCTTAATGCTTAATGCT	420
DB 361		
QY 361	AAGATGAAGAAACAGCGCGGACAAATGCTTAATGCTTAATGCTTAATGCTTAATGCT	420
DB 361		
QY 421	CTGAGCCAGAGATGCTTCTAGCTCCAGAGTTTGACAGCAGCTCGATTAAGATGCAAA	480
DB 421		
QY 421	CTGAGCCAGAGATGCTTCTAGCTCCAGAGTTTGACAGCAGCTCGATTAAGATGCAAA	480
DB 421		
QY 481	ACCTGCTCTTACAAAAAATACAAAAATTAGATGCTGCTGGCAATGCACTGCT	540
DB 481		
QY 481	ACCTGCTCTTACAAAAAATACAAAAATTAGATGCTGCTGGCAATGCACTGCT	540
DB 481		
QY 541	CCAGCTACTTGGAGGCTAAGGTGGAGGATGCTTGGAGGAGGAGTCAAGCTTACA	600
DB 541		
QY 541	CCAGCTACTTGGAGGCTAAGGTGGAGGATGCTTGGAGGAGGAGTCAAGCTTACA	600
DB 541		
QY 601	CTGAGCCATGATGGATCCTGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAG	660
DB 601		
QY 601	CTGAGCCATGATGGATCCTGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAG	660
DB 601		
QY 661	AAAAAAGAAATGAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	720
DB 661		
QY 661	AAAAAAGAAATGAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	720
DB 661		
QY 721	GAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	780
DB 721		
QY 721	GAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	780
DB 721		
QY 781	GATCAAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	840
DB 781		
QY 781	GATCAAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	840
DB 781		
QY 841	CCCCAAACCAATTTATTGACCAAGGTTATTTTTCATGATGATGATGATGATGATG	900
DB 841		
QY 841	CCCCAAACCAATTTATTGACCAAGGTTATTTTTCATGATGATGATGATGATGATG	900
DB 841		
QY 901	CTGAGGCTTGGGCTTTAGAGGCTATCTGAGGCTTCTGAGGCTTCTGAGGCTTCTG	960
DB 901		
QY 901	CTGAGGCTTGGGCTTTAGAGGCTATCTGAGGCTTCTGAGGCTTCTGAGGCTTCTG	960
DB 901		
QY 961	TTATTTCCTGACACGGAGCTTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1020
DB 961		
QY 961	TTATTTCCTGACACGGAGCTTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1020
DB 961		

QY 901 CTTGGGCTTGGGCTTTAGAAAGCTCATCTCTGGGCTTCTCAGATCCATCCCTTCTTT 960
DB 901 CTTGGGCTTGGGCTTTAGAAAGCTCATCTCTGGGCTTCTCAGATCCATCCCTTCTTT 960
QY 961 TATTTTCTTGACAGGAGCTTCTCTGTCTGACAGCTGAGTGGAGTGGAGTGC 1020
DB 961 TATTTTCTTGACAGGAGCTTCTCTGTCTGACAGCTGAGTGGAGTGGAGTGC 1020
QY 1021 TCGACTACTGTAACTCTGCCCTCCCGGTTCAAGGATTCCTCTGCTCAGGCTCTGA 1080
DB 1021 TCGACTACTGTAACTCTGCCCTCCCGGTTCAAGGATTCCTCTGCTCAGGCTCTGA 1080
QY 1081 GATAACAGGCGCGCCGACACACATCTGGCTAATTTTGTATTTTGTAGTAAGAGTGG 1140
DB 1081 GATAACAGGCGCGCCGACACACATCTGGCTAATTTTGTATTTTGTAGTAAGAGTGG 1140
QY 1141 TCATCATGTTGGCAGGTTGGTTTCCAACTCCGAGTGGAGTGGAGTGGAGTGG 1200
DB 1141 TCATCATGTTGGCAGGTTGGTTTCCAACTCCGAGTGGAGTGGAGTGGAGTGG 1200
QY 1201 CTCCTCAAGTCTGGGATACAGGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1260
DB 1201 CTCCTCAAGTCTGGGATACAGGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1260
QY 1261 CTAAAGGCAACAGCTCCATGGTGCAGAGGCGCATGCGACAGAGTATGAGTACCTGG 1320
DB 1261 CTAAAGGCAACAGCTCCATGGTGCAGAGGCGCATGCGACAGAGTATGAGTACCTGG 1320
QY 1321 GATCTCCAGAACTTCTTGGCTTGGTGGCTCCACATGACTCCAGGCGCTTGGGCTTC 1380
DB 1321 GATCTCCAGAACTTCTTGGCTTGGTGGCTCCACATGACTCCAGGCGCTTGGGCTTC 1380
QY 1381 TTCTATGCTGCTGCTGAGTGTGTATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1440
DB 1381 TTCTATGCTGCTGCTGAGTGTGTATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1440
QY 1441 GTGGCTGGAGTCTGTTGACTGTAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 1500
DB 1441 GTGGCTGGAGTCTGTTGACTGTAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 1500
QY 1501 TGCAGTGTGGGAGTCTTGGAAATATGATGAGGCTGAGGCTGAGGCTGAGGCTGAG 1560
DB 1501 TGCAGTGTGGGAGTCTTGGAAATATGATGAGGCTGAGGCTGAGGCTGAGGCTGAG 1560
QY 1561 GGGGAGTCTCTCATGCGGCTTCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1620
DB 1561 GGGGAGTCTCTCATGCGGCTTCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1620
QY 1621 AAATGTGAATCTGCGCTTCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1680
DB 1621 AAATGTGAATCTGCGCTTCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1680
QY 1681 GTGGCTTCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1740
DB 1681 GTGGCTTCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1740
QY 1741 CTCTATGATCTCTCAGGCGAGTTCATATTTAGATCTTACAGTGTGAGTGTGAGTGT 1800
DB 1741 CTCTATGATCTCTCAGGCGAGTTCATATTTAGATCTTACAGTGTGAGTGTGAGTGT 1800
QY 1801 TGCCAGAAATAGGTGACATTTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860
DB 1801 TGCCAGAAATAGGTGACATTTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860
QY 1861 TGTGTGTAGGCTGATCTCTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1920
DB 1861 TGTGTGTAGGCTGATCTCTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1920
QY 1921 AGTGTGTCTCTCTACAGGCAAGGCAAGAGAGTGTGAGGCTGAGTGTGAGTGTGAGT 1980
DB 1921 AGTGTGTCTCTCTACAGGCAAGGCAAGAGAGTGTGAGGCTGAGTGTGAGTGTGAGT 1980

QY 1981 AATTTTACAGCACTGCAATTTCTCTGGCTGCACTTCCAAATGTATACAAATTAATCAA 2040
DB 1981 AATTTTACAGCACTGCAATTTCTCTGGCTGCACTTCCAAATGTATACAAATTAATCAA 2040
QY 2041 GTCTCTGTCTTTATCACAGGAGGCTGATCAATATATGAAATTAAGAGGGGCTGGTC 2100
DB 2041 GTCTCTGTCTTTATCACAGGAGGCTGATCAATATATGAAATTAAGAGGGGCTGGTC 2100
QY 2101 CATATTGTCTGTCTTTTGTCTTTGTCTTTGTCTTTGTCTTTGTCTTTGTCTTTGT 2160
DB 2101 CATATTGTCTGTCTTTTGTCTTTGTCTTTGTCTTTGTCTTTGTCTTTGTCTTTGT 2160
QY 2161 TCTCTCTCTCAATTTATGACAGAGGAGTAAAGATGTCTCTCTGGGCTCTCTGAGGGA 2220
DB 2161 TCTCTCTCTCAATTTATGACAGAGGAGTAAAGATGTCTCTCTGGGCTCTCTGAGGGA 2220
QY 2221 CTTGGGAGCTCAGGCTGGGATCTTCCAAAGGAGTGTCTCTCTATCAAAATCAAGTCT 2280
DB 2221 CTTGGGAGCTCAGGCTGGGATCTTCCAAAGGAGTGTCTCTCTATCAAAATCAAGTCT 2280
QY 2281 CAGTGTGTGGGGGAAACAAAGAGGCTTACCCAGAGGAGTGTCTCTCTCTCTCTCT 2340
DB 2281 CAGTGTGTGGGGGAAACAAAGAGGCTTACCCAGAGGAGTGTCTCTCTCTCTCTCT 2340
QY 2341 CACCCAGGCTAGGCTTGTGAAGGAAACAAAGAGGAGTGTCTCTCTCTCTCTCTCT 2400
DB 2341 CACCCAGGCTAGGCTTGTGAAGGAAACAAAGAGGAGTGTCTCTCTCTCTCTCTCT 2400
QY 2401 CGGAGTTACGCTAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2460
DB 2401 CGGAGTTACGCTAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2460
QY 2461 AAGGAAACAAATTTGGGAAAGAGGATTTAGAGGAGGAGTGTCTCTCTCTCTCTCTCT 2520
DB 2461 AAGGAAACAAATTTGGGAAAGAGGATTTAGAGGAGGAGTGTCTCTCTCTCTCTCTCT 2520
QY 2521 GCTCTCGGAGGAGTGGAGTCTGAGAGTCTGCGGCGAGGCGGAGGCGGAGGCGG 2580
DB 2521 GCTCTCGGAGGAGTGGAGTCTGAGAGTCTGCGGCGAGGCGGAGGCGGAGGCGG 2580
QY 2581 GCTCTTACGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 2640
DB 2581 GCTCTTACGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 2640
QY 2641 CTTCTGTACCTTCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCAC 2700
DB 2641 CTTCTGTACCTTCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCAC 2700
QY 2701 TCTGTGGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 2760
DB 2701 TCTGTGGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 2760
QY 2761 TGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2820
DB 2761 TGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2820
QY 2821 GCTTTGAGGCTGAGTGAAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2880
DB 2821 GCTTTGAGGCTGAGTGAAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2880
QY 2881 CGGCAAAACCC 2893
DB 2881 CGGCAAAACCC 2893

RESULT 8
US-09-984-827-141
; Sequence 141, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFE, PATRICE
; APPLICANT: ROSTIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE

```

1  APPLICANT: DUVERGER, NICOLAS
2  APPLICANT: CAMBIEN, FRANCOIS
3  TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
4  TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
5  FILE REFERENCE: 03806.0522-00000
6  CURRENT APPLICATION NUMBER: US/09/984,827
7  CURRENT FILING DATE: 2002-04-01
8  PRIOR APPLICATION NUMBER: 60/254,108
9  PRIOR FILING DATE: 2000-12-11
10 PRIOR APPLICATION NUMBER: FR 00/14037
11 PRIOR FILING DATE: 2000-10-31
12 NUMBER OF SEQ ID NOS: 161
13 SOFTWARE: PatentIn Ver. 2.1
14 SEQ ID NO 141
15 LENGTH: 2893
16 TYPE: DNA
17 ORGANISM: Homo sapiens
18 US-09-984-827-141

```

[illegible][illegible]

QY 2821 GCTTTGACCATAGTAACCTCTGGCTCGTGCACCGCAATCTATAAAGGAACCTAGTCC 2880
|||||
DB 2821 GCTTTGACCATAGTAACCTCTGGCTCGTGCACCGCAATCTATAAAGGAACCTAGTCC 2880
QY 2881 CGGCAAAACCCC 2893
|||||
DB 2881 CGGCAAAACCCC 2893

RESULT 10

US-09-984-827-143
: Sequence 143, Application US/09984827
: Publication No. US20030056234A1
: GENERAL INFORMATION:
: APPLICANT: DNEEFLE, PATRICE
: APPLICANT: FOSTER-MONTUS, MARIE-FRANCOISE
: APPLICANT: ARNOULD-REGUIONE, ISABELLE
: APPLICANT: DUVERGER, NICOLAS
: APPLICANT: CAMBIEN, FRANCOIS
: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABLAL GENE, THEIR USES, AND
: TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
: FILE REFERENCE: 03806.0522-00000
: CURRENT APPLICATION NUMBER: US/09/984,827
: PRIOR FILING DATE: 2002-04-01
: PRIOR APPLICATION NUMBER: 60/254,108
: PRIOR FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: FR 00/14037
: PRIOR FILING DATE: 2000-10-31
: NUMBER OF SEQ ID NOS: 161
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 143
: LENGTH: 2893
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-984-827-143

Query Match 89.5% Score 2891.4 DB 9: Length 2893:
Rest Local Similarity 100.0% Pred. No. 0:
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0:

QY 1 ACAGGCGATGGTGGCAGGTGGCTGTAAATCTCACTACTCGGAGGTGGAGCTGGCAATGA 60
|||||
DB 1 ACAGGCGATGGTGGCAGGTGGCTGTAAATCTCACTACTCGGAGGTGGAGCTGGCAATGA 60
QY 61 GCGCAGATCGCCATTGCACTCCAGCTGGGCAACAAAGGTGAACTCACTCAAT 120
|||||
DB 61 GCGCAGATCGCCATTGCACTCCAGCTGGGCAACAAAGGTGAACTCACTCAAT 120
QY 121 AAAAAAAGAAATGATTTTGGTGGTGGTAAATAGTAAAGTAAAGTAAAGTAAAGTAAAG 180
|||||
DB 121 AAAAAAAGAAATGATTTTGGTGGTGGTAAATAGTAAAGTAAAGTAAAGTAAAGTAAAG 180
QY 181 AGATGAGGCTCAGGAGATCTAATTAATCTCAATATGCTAGGAGTAAAGTAAAGTAAAGT 240
|||||
DB 181 AGATGAGGCTCAGGAGATCTAATTAATCTCAATATGCTAGGAGTAAAGTAAAGTAAAGT 240
QY 241 TTAATAACACTCTGCTTTTATACATCTATCTGCAAGTAAAGTAAAGTAAAGTAAAGTAA 400
|||||
DB 241 TTAATAACACTCTGCTTTTATACATCTATCTGCAAGTAAAGTAAAGTAAAGTAAAGTAA 400
QY 301 AAGTTCACCTTTTCAAGAAACCCCTTTGAGGAGACAGAAATATATCTTCTCTCCATTTTA 360
|||||
DB 301 AAGTTCACCTTTTCAAGAAACCCCTTTGAGGAGACAGAAATATATCTTCTCTCCATTTTA 360
QY 361 AAGATGAAGAACAGCGCGGCAATGCTAATGCTGTATATCCAGCACTTTGGAGG 420
|||||
DB 361 AAGATGAAGAACAGCGCGGCAATGCTAATGCTGTATATCCAGCACTTTGGAGG 420
QY 421 CTGAGGCCAGAGATCGCTTGAGCTCCAGCTTTTACAGATCACTGGATATGAATGCAAAA 480
|||||
DB 421 CTGAGGCCAGAGATCGCTTGAGCTCCAGCTTTTACAGATCACTGGATATGAATGCAAAA 480

QY 481 ACCCTGCTCTACAAAAAATACAAAAATTTAGATGGTGTGGTGGCATGCACCTGTGGT 540
|||||
DB 481 ACCCTGCTCTACAAAAAATACAAAAATTTAGATGGTGTGGTGGCATGCACCTGTGGT 540
QY 541 CCCAGCTACTTGGGAGGCTAAGGTGGGAGGATCGCTTTAGCCCGAGGAGTCAAGTCTACA 600
|||||
DB 541 CCCAGCTACTTGGGAGGCTAAGGTGGGAGGATCGCTTTAGCCCGAGGAGTCAAGTCTACA 600
QY 601 CTGAGCCATGATTGGATCTACTGCACTCCAGCTGGGTAGACAGAGCAAGCCCTGTCTCA 660
|||||
DB 601 CTGAGCCATGATTGGATCTACTGCACTCCAGCTGGGTAGACAGAGCAAGCCCTGTCTCA 660
QY 661 AAAAAAGAAAATGAAGAGAAAGAAAGAGGAGGAGGAGGAGAGATGAGGCGAGGAGG 720
|||||
DB 661 AAAAAAGAAAATGAAGAGAAAGAAAGAGGAGGAGGAGGAGAGATGAGGCGAGGAGG 720
QY 721 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
|||||
DB 721 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 781 GATGAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
|||||
DB 781 GATGAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 841 CCCCAAAACCCAAATTTATTGACCAAGGTTATTCTTCTGACTGAGGCAAGGGGTCGCTCT 900
|||||
DB 841 CCCCAAAACCCAAATTTATTGACCAAGGTTATTCTTCTGACTGAGGCAAGGGGTCGCTCT 900
QY 901 CCGTGGCCCTGGGCTTTTAGAAGGCTCATCTCTGGCCCTTTCTGAGATCCATCCCTTTCTTT 960
|||||
DB 901 CCGTGGCCCTGGGCTTTTAGAAGGCTCATCTCTGGCCCTTTCTGAGATCCATCCCTTTCTTT 960
QY 961 TTATTTTCTTGACACGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
|||||
DB 961 TTATTTTCTTGACACGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 TCGACTCACTGTAACTCTGCTCCCGGTTTCAAGCGATTCTCTGCTGCTGCTGCTGCTGCTGA 1080
|||||
DB 1021 TCGACTCACTGTAACTCTGCTCCCGGTTTCAAGCGATTCTCTGCTGCTGCTGCTGCTGCTGA 1080
QY 1081 GATAACAGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
|||||
DB 1081 GATAACAGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 TCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
|||||
DB 1141 TCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY 1201 CTCCCAAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
|||||
DB 1201 CTCCCAAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
QY 1261 CTAAAGGCAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
|||||
DB 1261 CTAAAGGCAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
QY 1321 GACTCCAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
|||||
DB 1321 GACTCCAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1381 TTCTATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
|||||
DB 1381 TTCTATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
QY 1441 GTGGCTGCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
|||||
DB 1441 GTGGCTGCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1501 TGCAGGCTGGGAGTCTGCAATATGATGAGCTGAGGCTGGGAGGAGGAGGAGGAGGAGGAGG 1560
|||||
DB 1501 TGCAGGCTGGGAGTCTGCAATATGATGAGCTGAGGCTGGGAGGAGGAGGAGGAGGAGGAGG 1560
QY 1561 GGGAGGCTCTCTCATGCTGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620

Db	1561	 GGCAGCTCTCTCATGCCACCTCATTTCTGGCCAAACTCAGGTCMAACTGTGAAGAGTCT	1620
Qy	1521	 AAATGTGAATCTGCCCTTCCAAGGTGGCTACAAGGTATCTTTGTCAAGGTAGGAGACCTT	1680
Db	1521	 AAATGTGAATCTGCCCTTCCAAGGTGGCTACAAGGTATCTTTGTCAAGGTAGGAGACCTT	1680
Qy	1581	 GTGGCTCCACAGTGCACCTTCCAGGGCGCTGCTTUGGCTCTCTCTACGAGTCTGTCTCTGAGT	1740
Db	1681	 GTGGCTCCACAGTGCACCTTCCAGGGCGCTGCTTUGGCTCTCTCTACGAGTCTGTCTCTGAGT	1740
Qy	1741	 CTCTATGAATCTCTCAGGCGAGATTCATATTCAGACTCTTCACAGTTTCAGCTGAGTTT	1800
Db	1741	 CTCTATGAATCTCTCAGGCGAGATTCATATTCAGACTCTTCACAGTTTCAGCTGAGTTT	1800
Qy	1801	 TGGCCAGAATAAGGTGACATTTAGTTTGTCTGCTTGATGGAAGACTTAAATATTAGACA	1860
Db	1801	 TGGCCAGAATAAGGTGACATTTAGTTTGTCTGCTTGATGGAAGACTTAAATATTAGACA	1860
Qy	1861	 TGGTGTGTAGGCTCGATTCTTACTCTTGCTTTTCTTGCTCCCTTCACCTTGTGTGGGT	1920
Db	1861	 TGGTGTGTAGGCTCGATTCTTACTCTTGCTTTTCTTGCTCCCTTCACCTTGTGTGGGT	1920
Qy	1921	 AGTTTGTCTCCCTACAGCCAAAGCGAAGTATGGAGTGTGGAATGGCTACAT	1980
Db	1921	 AGTTTGTCTCCCTACAGCCAAAGCGAAGTATGGAGTGTGGAATGGCTACAT	1980
Qy	1981	 AAATTTACAGACTGCAATCTCTGCTGCAATTCACAAATGATACAAATCAAAATACAA	2040
Db	1981	 AAATTTACAGACTGCAATCTCTGCTGCAATTCACAAATGATACAAATCAAAATACAA	2040
Qy	2041	 GTCTCTGTGTTTTATCACAGGAGGCTGATCAATATATGSAATTAAGAGGCGCTGGTC	2100
Db	2041	 GTCTCTGTGTTTTATCACAGGAGGCTGATCAATATATGSAATTAAGAGGCGCTGGTC	2100
Qy	2101	 CATATTGTCGTGTTTTGTTGTTGTTGTTTGTGTTTGTGTTTCTTTTCTTTTCTTTT	2160
Db	2101	 CATATTGTCGTGTTTTGTTGTTGTTGTTTGTGTTTGTGTTTCTTTTCTTTTCTTTT	2160
Qy	2161	 TCCTTCCTCTCAATTTATGAAGAGAAGCAGTAAAGATGTTCTCTCGGCTCTCTGAGGGA	2220
Db	2161	 TCCTTCCTCTCAATTTATGAAGAGAAGCAGTAAAGATGTTCTCTCGGCTCTCTGAGGGA	2220
Qy	2221	 CTCTGGGAGCTCAGCTGGGAATCTCTCAAGGCAGTAGTGTGCTATCAAAATCAAGTCT	2280
Db	2221	 CTCTGGGAGCTCAGCTGGGAATCTCTCAAGGCAGTAGTGTGCTATCAAAATCAAGTCT	2280
Qy	2281	 CAGCTTTGTGGGGGAAAAACAAAGCAGGCCATTACCCAGAGAGCTGTCCGCTCTCCCT	2340
Db	2281	 CAGCTTTGTGGGGGAAAAACAAAGCAGGCCATTACCCAGAGAGCTGTCCGCTCTCCCT	2340
Qy	2341	 CACCCAGCTAGGCTTTGAAAGGAACAAGAGACAATAAAATGATTGGCTCTCTCTG	2400
Db	2341	 CACCCAGCTAGGCTTTGAAAGGAACAAGAGACAATAAAATGATTGGCTCTCTCTG	2400
Qy	2401	 GGGAGATTGAGCTTAGAGTCTCTCTCCCGCAATCCCTGCTCTGCTGCTGAGCAAACTAAC	2460
Db	2401	 GGGAGATTGAGCTTAGAGTCTCTCTCCCGCAATCCCTGCTCTGCTGCTGAGCAAACTAAC	2460
Qy	2461	 AAAGGAAAAAATTCGGGAAAGCAGGATTTAGAGGAAGCAAAATTCACCTGCTGGCTT	2520
Db	2461	 AAAGGAAAAAATTCGGGAAAGCAGGATTTAGAGGAAGCAAAATTCACCTGCTGGCTT	2520
Qy	2521	 GGCTGCGGGAGACTGAGTATAGAGTCTGCGGGCGACGCCGAGCTCCAGTCTGCTGCGG	2580
Db	2521	 GGCTGCGGGAGACTGAGTATAGAGTCTGCGGGCGACGCCGAGCTCCAGTCTGCTGCGG	2580
Qy	2581	 GGCTTTTAGGCCGGCCGGCCGGGGGGAAGGGCAATCCAGAGCGGGCAATCTAAGACA	2640
Db	2581	 GGCTTTTAGGCCGGCCGGCCGGGGGGAAGGGCAATCCAGAGCGGGCAATCTAAGACA	2640
Qy	2641	 CTGCTGTACCTCCACCCCAACCCCAACCTACCTACCTTCCCTCCCAACTCTCTATATG	2700

Db	2641	CCTGCTGTACCTTCGACCCCGCACCCNCCCAACCACTCCCGCCCACTCCCTAGATGTG	27100
QY	2701	TCGTGGCGGCTGAAGCTGCGCCGTTTAAAGGGCGGGCCCGGCTCCACGTGCTTCTGCG	2760
Db	2701	TCGTGGCGGCTGAAGCTGCGCCGTTTAAAGGGCGGGCCCGGCTCCACGTGCTTCTGCG	2760
QY	2761	TGAGTGACTCAACTACATAAACAGAGCGCCGGGAAGGGCGGGAGGAGGAGACACAG	2820
Db	2761	TGAGTGACTCAACTACATAAACAGAGCGCCGGGAAGGGCGGGAGGAGGAGACACAG	2820
QY	2821	GCTTTGACCGAATAGTAACCTCTCGCTCGGTGCAGCCGAATCTTATAAAGGAACCTAGTCC	2880
Db	2821	GCTTTGACCGAATAGTAACCTCTCGCTCGGTGCAGCCGAATCTTATAAAGGAACCTAGTCC	2880
QY	2881	CGGCAAAAGCCC	2893
Db	2881	CGGCAAAAGCCC	2893

RESULT 11

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RES001 11
US-09-984-827-144
: Sequence 144, Application US/09984827
: Publication No. US2003056234A1
: GENERAL INFORMATION:
: APPLICANT: DENEFFE, PATRICE
: APPLICANT: KOSTER-MONTUS, MARIE-FRANCOISE
: APPLICANT: ARNOULD-REGUIGNE, ISABELLE
: APPLICANT: DOVERGER, NICOLAS
: APPLICANT: CAMBIEN, FRANCOIS
: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ARCAI GENE, THEIR USES,
: TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
: FILE REFERENCE: 03806.0522-00000
: CURRENT APPLICATION NUMBER: US/09/984,827
: CURRENT FILING DATE: 2002-04-01
: PRIOR APPLICATION NUMBER: 60/254,108
: PRIOR FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: FR 00/14037
: PRIOR FILING DATE: 2000-10-31
: NUMBER OF SEQ ID NOS: 161
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 144
: LENGTH: 2893
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-984-827-144

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Query Match	89.5%	Score 2891.4	DB 9	Length 2893
Best Local Similarity	100.0%	Pred. No. 0		
Matches 2892	Conservative	Mismatches 1	Indels 0	Gaps 0

Qy	1	ACAGGCGATGGTGGCAGGTGCCTGTGTAATCTCAGTTACTCGGAGGTGGAGGTTCCAATGA	60
Db	1	ACAGGCGATGGTGGCAGGTGCCTGTGTAATCTCAGTTACTCGGAGGTGGAGGTTCCAATGA	60
Qy	61	GCCGAGATCGACCAATTGCACCTCCAGCCTGGGCAACAAAAGGTGAAACTCCATCTCAATT	120
Db	61	GCCGAGATCGGACCAATTGCACCTCCAGCCTGGGCAACAAAAGGTGAAACTCCATCTCAATT	120
Qy	121	AAAAAAAAGCAATCATTTTGGTGGTCGACTTCAAAATAGTAGGAGAGAGGAGGAGGAGG	180
Db	121	AAAAAAAAGCAATGATTTTGGTGGTCGACTTCAAAATAGTAGGAGAGAGGAGGAGGAGG	180
Qy	181	AGATGGAGGTCAGGAGATCTAAATTACTCTCTAAATCATGCTAGGAAGATACACCT	240
Db	181	AGATGGAGGTCAGGAGATCTAAATTACTCTCTAAATCATGCTAGGAAGATACACCT	240
Qy	241	TTTAATAACACTCTCTGCTTTTATAACATCATTTCTGCCAAGGAGCTCAAAAGTTTCAACA	300
Db	241	TTTAATAACACTCTCTGCTTTTATAACATCATTTCTGCCAAGGAGCTCAAAAGTTTCAACA	300
Qy	301	AGGTTCACTTTCAGAAACCCCTTTCAGAGACAGACATATACATCTTCTCTCCATTITA	360
Db	301	AGGTTCACTTTCAGAAACCCCTTTCAGAGACAGACATATACATCTTCTCTCCATTITA	360

[illegible][illegible]

1b 2521 GGTGCGGGAAGCTGGACTAGAGAGTCTGCGCGCGAGCCCGGAGCCGAGCTTCCGCG 2580
QY 2581 GGTCTTAGCGCGGCGCGCGGCGGGAAGGCGAGCGAGCGCGGAGCCCTAAGACA 2640
Db 2581 GGTCTTAGCGCGGCGCGCGGCGGGAAGGCGAGCGAGCGCGGAGCCCTAAGACA 2640
QY 2641 CCGTGTGTAGCTTCCACCCCGGAGCGCGGAGCGAGCGAGCGAGCGAGCGAGCGAG 2700
Db 2641 CCGTGTGTAGCTTCCACCCCGGAGCGCGGAGCGAGCGAGCGAGCGAGCGAGCGAG 2700
QY 2701 TCGTGGCGGCTGAAGCTCGCGGCTTGAAGGCGCGGAGCGAGCGAGCGAGCGAGCGAG 2760
Db 2701 TCGTGGCGGCTGAAGCTCGCGGCTTGAAGGCGCGGAGCGAGCGAGCGAGCGAGCGAG 2760
QY 2761 TGAGTCACTGAAGCTACATAACAGAGCGCGGGAAGGCGCGGAGCGAGCGAGCGAGCGAG 2820
Db 2761 TGAGTCACTGAAGCTACATAACAGAGCGCGGGAAGGCGCGGAGCGAGCGAGCGAGCGAG 2820
QY 2821 GCTTTGACCGTAGTAGTAACTCTCGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2880
Db 2821 GCTTTGACCGTAGTAGTAACTCTCGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2880
QY 2881 CGGCAAAACCCC 2893
Db 2881 CGGCAAAACCCC 2893

RESULTS 12
US-09-984-827-145
Sequence 145, Application US/05984827
Publication No. US20030056234A1
GENERAL INFORMATION:
APPLICANT: DENEULE, PATRICE
APPLICANT: KOSTER-MONTUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ANKRA GENE, THEIR USES, AND
TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
FILE REFERENCE: 03806.0522-00000
CURRENT APPLICATION NUMBER: US/09/984.827
PRIOR FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: FR 00/14037
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 145
LENGTH: 2893
TYPE: DNA
ORGANISM: Homo sapiens
US-09-984-827-145

Query Match 89.5%, Score 2891.4, DB 9, Length 2893;
Best Local Similarity 100.0%, Pred. No. 6;
Matches 2892: Conservative 0; Mismatches 1; Indels 0; Gaps 3;
QY 1 ACAGGCGATGGTGGCAGGTGCGCTGTAACTCACTTATCGGAGGTGGAGTTGCAATGA 60
Db 1 ACAGGCGATGGTGGCAGGTGCGCTGTAACTCACTTATCGGAGGTGGAGTTGCAATGA 60
QY 61 GCCCAGATCGCACCATTGACCTCCAGCGCTGGGCAAGGAGTGAACATCAATCAAT 120
Db 61 GCCCAGATCGCACCATTGACCTCCAGCGCTGGGCAAGGAGTGAACATCAATCAAT 120
QY 121 AAAAAAAGAAATGATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
Db 121 AAAAAAAGAAATGATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
QY 181 AGATGAGGTGAGGAGATCTAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db 181 AGATGAGGTGAGGAGATCTAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240

Db 181 AGATGAGGTGAGGAGATCTAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 TTTAATAACACT 300
Db 241 TTTAATAACACT 300
QY 301 AAGTTCACTTTICAGAAACACCCCTTTGAGGAAGACAGAAATATACATCTCTCTCTCTCTCT 360
Db 301 AAGTTCACTTTICAGAAACACCCCTTTGAGGAAGACAGAAATATACATCTCTCTCTCTCTCT 360
QY 361 AAGTGAAGAACAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
Db 361 AAGTGAAGAACAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 421 CTGAGGCGCAGAGGATCGCTTGAGCTCCAGAGTTTGAGACACCGAGCTGGATCAACATGSCAAA 480
Db 421 CTGAGGCGCAGAGGATCGCTTGAGCTCCAGAGTTTGAGACACCGAGCTGGATCAACATGSCAAA 480
QY 481 ACCCTGTCTCTACAAAAAATAACAAAAATAGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 540
Db 481 ACCCTGTCTCTACAAAAAATAACAAAAATAGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 540
QY 541 CCCAGCTACTTTGGGAGGCTAAGGTGGGAGGATCGCTTGAGCCACGAGGAGTCAAGTCTACA 600
Db 541 CCCAGCTACTTTGGGAGGCTAAGGTGGGAGGATCGCTTGAGCCACGAGGAGTCAAGTCTACA 600
QY 601 CTGAGGCGATGATGGATCACTCCAGCTCCAGCTGGGTAGACAGAGCAAGACCCCTGCTCA 660
Db 601 CTGAGGCGATGATGGATCACTCCAGCTCCAGCTGGGTAGACAGAGCAAGACCCCTGCTCA 660
QY 661 AAAAAAACAATGAAGACAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 AAAAAAACAATGAAGACAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 GAGGCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 721 GAGGCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 781 GATGAACAGAGGCGAGAAAGACTTTACGTAATTTGCTCATCATCTGCTGCTGCTGCTGCTGCT 840
Db 781 GATGAACAGAGGCGAGAAAGACTTTACGTAATTTGCTCATCATCTGCTGCTGCTGCTGCTGCT 840
QY 841 CCCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 900
Db 841 CCCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 900
QY 901 CCGTGGCGCTGGGCTTTAGAAAGCTCATCTCGGCTTTCTGAGATCCATCCCTTTCTTT 960
Db 901 CCGTGGCGCTGGGCTTTAGAAAGCTCATCTCGGCTTTCTGAGATCCATCCCTTTCTTT 960
QY 961 TIATTTTCTTTCACAGGAGTCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 961 TIATTTTCTTTCACAGGAGTCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 TCGACTCACTGTAACCTCGCTCCCGGTTTCAAGCGATCTCTCTGCTGCTGCTGCTGCTGCTG 1080
Db 1021 TCGACTCACTGTAACCTCGCTCCCGGTTTCAAGCGATCTCTCTGCTGCTGCTGCTGCTGCTG 1080
QY 1081 CATTAACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGTT 1140
Db 1081 CATTAACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGTT 1140
QY 1141 TCATCATGTTGGCAGGTTGGTTCGAACTCTGCACTCTGAGGTGAGGTGAGGTGAGGTGAGGTG 1200
Db 1141 TCATCATGTTGGCAGGTTGGTTCGAACTCTGCACTCTGAGGTGAGGTGAGGTGAGGTGAGGTG 1200
QY 1201 CCCCCAAGTCTGGGATTACAGGCGATGAGCCACTCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTT 1260
Db 1201 CCCCCAAGTCTGGGATTACAGGCGATGAGCCACTCGGCGGCGGCGGCGGCGGCGGCGGCTTT 1260
QY 1261 CTAAGGCGCAACAGTCCATGCTGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1320
Db 1261 CTAAGGCGCAACAGTCCATGCTGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1320

QY	1421	GACTCCAGAAATTCCTTGCTGTGCTGCCCTCCACATGCACTTCCAGGGGCGCTGCTTGGGGCTC	1380
Db	1421	GACTCCAGAAATTCCTTGCTGTGCTGCCCTCCACATGCACTTCCAGGGGCGCTTGGGGCTC	1380
QY	1481	TTCTATGCGCTGTGCTGTGCTGTTCATACCAACCATCATGTGTGAGTACCTTGGGCTTGAGGC	1440
Db	1481	TTCTATGCGCTGTGCTGTGCTGTTCATACCAACCATCATGTGTGAGTACCTTGGGCTTGAGGC	1440
QY	1441	GTGGGCTGGAGATCCCTGTGTGACTGTAGCAAGAGGGGCGTCTGCAGCTGAATGTCTCCCA	1500
Db	1441	GTGGGCTGGAGATCCCTGTGTGACTGTAGCAAGAGGGGCGTCTGCAGCTGAATGTCTCCCA	1500
QY	1501	TCCAGGTGGTGGGAGTCTTGGAATATGATGTGAGCTGTGAGGTGTGAGGTGTGAGGTGTG	1560
Db	1501	TCCAGGTGGTGGGAGTCTTGGAATATGATGTGAGCTGTGAGGTGTGAGGTGTGAGGTGTG	1560
QY	1561	GGGCAAGCTCTCTCATGCGCACCTTCATCTTGGGCGAAAGCTCAGGTCAAACTCTTGAGAGTCT	1620
Db	1561	GGGCAAGCTCTCTCATGCGCACCTTCATCTTGGGCGAAAGCTCAGGTCAAACTCTTGAGAGTCT	1620
QY	1621	AAATGTGAATCTGCCCTTCAAGGTGCGCTACAAGGTATCTTGTGTCAGGTGTGAGGTGTG	1680
Db	1621	AAATGTGAATCTGCCCTTCAAGGTGCGCTACAAGGTATCTTGTGTCAGGTGTGAGGTGTG	1680
QY	1681	GTGGGCTCCACGTGCACTTCCAGGCGCTGCTTGGGCGCTCTTCTACGGGCTCTGTCCTGAGT	1740
Db	1681	GTGGGCTCCACGTGCACTTCCAGGCGCTGCTTGGGCGCTCTTCTACGGGCTCTGTCCTGAGT	1740
QY	1741	CTTCTATGAATCCTTCAGGGCAGATTCATATTACAGTCTTTCACAGTCTTACAGTCTGAGTCT	1800
Db	1741	CTTCTATGAATCCTTCAGGGCAGATTCATATTACAGTCTTTCACAGTCTTACAGTCTGAGTCT	1800
QY	1801	TGGCAGAAATAGGTGTGACATTTAGTTCTTGCGCTGTGATGTGATGATTAATAATATAACA	1860
Db	1801	TGGCAGAAATAGGTGTGACATTTAGTTCTTGCGCTGTGATGTGATGATTAATAATATAACA	1860
QY	1861	TGGTGTGTAGGCTGCACTTCTGCTACTCTGCTCTTTTCTTGGGCGCTGAGTGTGAGTCT	1920
Db	1861	TGGTGTGTAGGCTGCACTTCTGCTACTCTGCTCTTTTCTTGGGCGCTGAGTGTGAGTCT	1920
QY	1921	AGTTTTCCTCCCTACAGGCAAGGCAACAAGAAATGTGAGGCTGTGAGTGTGATATAT	1980
Db	1921	AGTTTTCCTCCCTACAGGCAAGGCAACAAGAAATGTGAGGCTGTGAGTGTGATATAT	1980
QY	1981	AATTTTACAGGAGTGAATCTCTGCTTGCATCTGCATCTGCATCTGCATCTGCATCTGCAT	2040
Db	1981	AATTTTACAGGAGTGAATCTCTGCTTGCATCTGCATCTGCATCTGCATCTGCATCTGCAT	2040
QY	2041	GTCCTGTGTTTTATCAGGAGGAGGCTGATCAATATAAGAAATATAAAATGAGGCTGCTG	2100
Db	2041	GTCCTGTGTTTTATCAGGAGGAGGCTGATCAATATAAGAAATATAAAATGAGGCTGCTG	2100
QY	2101	CATATGCTCTGTGTTTTTGTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTG	2160
Db	2101	CATATGCTCTGTGTTTTTGTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTG	2160
QY	2161	TCCTTCTCTCAATTTATCAAGAGAGGAGCTAAGATGTTCCTGTGGGTGCTCTGAGGAGA	2220
Db	2161	TCCTTCTCTCAATTTATCAAGAGAGGAGCTAAGATGTTCCTGTGGGTGCTCTGAGGAGA	2220
QY	2221	CCTTGGGAGCTCAGGCTGGGAATCTCCAGAGTGTAGTGTGTGCTTATCAAAATCAAAATC	2280
Db	2221	CCTTGGGAGCTCAGGCTGGGAATCTCCAGAGTGTAGTGTGTGCTTATCAAAATCAAAATC	2280
QY	2281	CAGGTTTGTGGGGGGAACAAAGCAGGCAATTAACACAGAGGAGCTGTGGGCTCTCCGCT	2340
Db	2281	CAGGTTTGTGGGGGGAACAAAGCAGGCAATTAACACAGAGGAGCTGTGGGCTCTCCGCT	2340
QY	2341	CACCCCAAGCTAGGCTTTTGAAGGGAACAAAGACAGACAAATGATTTGGGCTCTCTG	2400
Db	2341	CACCCCAAGCTAGGCTTTTGAAGGGAACAAAGACAGACAAATGATTTGGGCTCTCTG	2400

Qy	2401	GGAGATTGAGCTAGAGCTCTCTCTCCCCCAATCCCTCCGCTCGAGAACTAAC	2460
Db	2401	GGAGATTGAGCTAGAGCTCTCTCCCCCAATCCCTCCGCTCGAGAACTAAC	2460
Qy	2461	AAAGGAAAAAAAATTCGGAAGCAGGATTTAGAGGAAGCAAAATTCACCTGGTGGCCCTT	2520
Db	2461	AAAGGAAAAAAAATTCGGAAGCAGGATTTAGAGGAAGCAAAATTCACCTGGTGGCCCTT	2520
Qy	2521	GGTTCGGGGAACTGGTGACTAGAGAGTCTGGGGCGAGCCCGAGCCACGGCTTCCGCG	2580
Db	2521	GGTTCGGGGAACTGGTGACTAGAGAGTCTGGGGCGAGCCCGAGCCACGGCTTCCGCG	2580
Qy	2581	GGCTCTTAGCGCTGGGGGGCTGGGGCGGGGAAGGGAGCGAGACCGCGGACCTTAAGACA	2640
Db	2581	GGCTCTTAGCGCGGGGGCGGGGGGAAGGGAGCGAGACCGCGGACCTTAAGACA	2640
Qy	2641	CTTGCTGTACGCTCCACCCCAACGACCCACCCACCTCCGCCAACTCCCTAJATGTG	2700
Db	2641	CTTGCTGTACGCTCCACCCCAACGACCCACCCACCTCCGCCAACTCCCTAJATGTG	2700
Qy	2701	TCGTGGCGCGCTGAACGTGGCCGTTTAAAGGGGGGGCCCGGCTCCACGTGCTCTGC	2760
Db	2701	TCGTGGCGGCTGAACGTGGCCGTTTAAAGGGGGGGCCCGGCTCCACGTGCTCTGC	2760
Qy	2761	TGAGTGACTGAACATACATAAAGAGAGCGCGGAAGGGGGGGGAGGAGGAGACACAG	2820
Db	2761	TGAGTGACTGAACATACATAAAGAGAGCGCGGAAGGGGGGGGAGGAGGAGACACAG	2820
Qy	2821	GCTTTCACCGATAGTAACCTCTGCCTCGGTGCAGCGCAATCTATAAAGGAACCTAGTCC	2880
Db	2821	GCTTTCACCGATAGTAACCTCTGCCTCGGTGCAGCGCAATCTATAAAGGAACCTAGTCC	2880
Qy	2881	CGGCAAAAACCCC	2893
Db	2881	CGGCAAAAACCCC	2893

RESULT 13

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US-09-984-827-146
: Sequence 146, Application US/09984827
: Publication No. US20030056234A1
: GENERAL INFORMATION:
: APPLICANT: DENEFFLE, PATRICE
: APPLICANT: AGNIEK-MONIEUX, MARIE-FRANCOISE
: APPLICANT: ROSIOLD-REUIGNE, ISABELLE
: APPLICANT: DUVERGER, NICOLAS
: APPLICANT: CAMBLEN, FRANCOIS
: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,
: TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
: FILE REFERENCE: 03806.0522-00000
: CURRENT APPLICATION NUMBER: US/09/984,827
: CURRENT FILING DATE: 2002-04-01
: PRIORITY APPLICATION NUMBER: 60/254,108
: PRIORITY FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: FR 00/14037
: PRIOR FILING DATE: 2000-10-31
: NUMBER OF SEQ ID NOS: 161
: SOFTWARE: PatentIn ver. 2.1
: SEQ ID NO 146
: LENGTH: 2893
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-984-827-146

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Query Match	89.5%	Score 2891.4;	DB 9;	Length 2893;
Best local Similarity	100.0%	Pred. No. 0;		
Matches 2892;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1	ACAGGCGATGTTGGCAGGTGCCGTGTAATCTCAGTTACTCGGAGGTGGAGTTCGAATCA	60
Db	1	ACAGGCGATGTTGGCAGGTGCCGTGTAATCTCAGTTACTCGGAGGTGGAGTTCGAATCA	60
Qy	61	GCCACGATTGCACATTGCACCTCCAGCTGGGCAACAAAGGTGAAACTCCATCTCAATT	120

Db	61	GC	CAGATCGCCATTTGGACTCCAGCTCGGCCACAAAAGCTGAAC	TCCATCTCAATT	120
Qy	121	AAAA	AAAAAAGATGATTTTGGTGTGGACTTCAATAGTAGGAGAGAAGAGAGAGG	180	
Lb	121	AAAA	AAAAAAGATGATTTTGGTGTGGACTTCAATAGTAGGAGAGAAGAGAGAGG	180	
Qy	181	AGATG	GAGGCTGAGGAGATCTAATTACTCTTAATAATCATCTAGGAAATATATACCT	240	
Lb	181	AGATG	GGGGTGCAGGAGATCTAATTACTCTTAATAATCATCTAGGAAATATATACCT	240	
Qy	241	TTTAAT	AACACTCTCTGCTTTTATAACATCATCTGCCCAAGAGCTCAAAAGTTCACAA	300	
Lb	241	TTTAAT	AACACTCTCTGCTTTTATAACATCATCTGCCCAAGAGCTCAAAAGTTCACAA	300	
Qy	301	AAGTT	CACTTTTCAGAAAAACCCCTTTTGAGAAACACAAATATACATCTCTCTCTCATTTA	360	
Lb	301	AAGTT	CACTTTTCAGAAAAACCCCTTTTGAGAAACACAAATATACATCTCTCTCTCATTTA	360	
Qy	361	AAGATG	AGAAACAGCGCGGACAAATGGCTAATGCTCTTAATCCAGACTTTTGGGAGG	420	
Lb	361	AAGATG	AGAAACAGCGCGGACAAATGGCTAATGCTCTTAATCCAGACTTTTGGGAGG	420	
Qy	421	CTGAGG	CCAGGATCGCTTGAGCTCCAGAGTTTGAGATCGCTTGGTGGCAATGACCTGTGCT	480	
Lb	421	CTGAGG	CCAGGATCGCTTGAGCTCCAGAGTTTGAGATCGCTTGGTGGCAATGACCTGTGCT	480	
Qy	481	ACCTG	TCTCTACAAAAAANAATACAAAAATATAGATGGGTGGTGGGCAATGACCTGTGCT	540	
Lb	481	ACCTG	TCTCTACAAAAAANAATACAAAAATATAGATGGGTGGTGGGCAATGACCTGTGCT	540	
Qy	541	CCCAG	CTACTTGGAGGCTAAGGTGGAGGATCGCTTCAGCCACAGGAGTCAAGTCTTACA	600	
Lb	541	CCCAG	CTACTTGGAGGCTAAGGTGGAGGATCGCTTCAGCCACAGGAGTCAAGTCTTACA	600	
Qy	601	CTGAG	CCATGTTGGATCTGCATCTCAGCTTGGTAGACACAGACAAATCTGTCTCTCA	660	
Lb	601	CTGAG	CCATGTTGGATCTGCATCTCAGCTTGGTAGACACAGACAAATCTGTCTCTCA	660	
Qy	661	AAAAA	AGAAATGAACAGAAAAAGAAAGAGGAGAGAGAGAGAGTGAAGGAGGAGG	720	
Lb	661	AAAAA	AGAAATGAACAGAAAAAGAAAGAGGAGAGAGAGAGAGTGAAGGAGGAGG	720	
Qy	721	GAGGG	GGGAGGAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG	780	
Lb	721	GAGGG	GGGAGGAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG	780	
Qy	781	GATCAA	CAGAGGCGAGAAAGACTTTATCTAATCTCTATCTATCTGTCTGTCTCAAGTCTGA	840	
Lb	781	GATCAA	CAGAGGCGAGAAAGACTTTATCTAATCTCTATCTATCTGTCTGTCTCAAGTCTGA	840	
Qy	841	CCCCA	ACCCCAATTTATTCACCAAGTATATCTCTGACAGGAGGAGGAGGAGGAGGAGG	900	
Lb	841	CCCCA	ACCCCAATTTATTCACCAAGTATATCTCTGACAGGAGGAGGAGGAGGAGGAGG	900	
Qy	901	CCTGG	CTTGGGCTTTAGAAAGCTCATCTCTGGCTTCTCAGATCCATCCCTTCTTT	960	
Lb	901	CCTGG	CTTGGGCTTTAGAAAGCTCATCTCTGGGCTTCTCAGATCCATCCCTTCTTT	960	
Qy	961	TTATTT	TCTTTGACCGAGCTTGGCTCTGTCTCACTCAGGCTGCGAGTGGCATGATC	1020	
Lb	961	TTATTT	TCTTTGACCGAGCTTGGCTCTGTCTGTCTCACTCAGGCTGCGAGTGGCATGATC	1020	
Qy	1021	TCGAC	TCACTGTAACTCTGCCCTCCGGGTTCAAGGATCTCTCTGCCCTCAGCTCTCTGA	1080	
Lb	1021	TCGAC	TCACTGTAACTCTGCCCTCCGGGTTCAAGGATCTCTCTGCCCTCAGCTCTCTGA	1080	
Qy	1081	GATAAC	GGGCGCGCCACCACTCTGGCTAATTTTGTATTTTAGTAAGACTGGGTT	1140	
Lb	1081	GATAAC	GGGCGCGCCACCACTCTGGCTAATTTTGTATTTTAGTAAGACTGGGTT	1140	
Qy	1141	TCATCA	TGTTGGCAGGTTGGTTTCGAACTCTCTGACTGAGGTGAGCTGCCACCTTGGC	1200	

! PRIOR FILING DATE: 2000-10-31
! NUMBER OF SEQ ID NOS: 161
! SOFTWARE: PatentIn Ver. 2.1
! SEQ ID NO 149
! LENGTH: 2893
! TYPE: DNA
! ORGANISM: Homo sapiens
US-09-984-827-149

Query Match 89.5% Score 2891.4; DB 9; length: 2893.
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 1 ACAGGCGATGGTGGCAGGTGCTGTAACTCAGTTACTGGCAGGTGCGAGTGTGCAATGA 60
DB 1 ACAGGCGATGGTGGCAGGTGCTGTAACTCAGTTACTGGCAGGTGCGAGTGTGCAATGA 60
QY 61 GGTCCAGATCGCCACCATTCACATCCAGGCTGGCCAAACAAAGGTCGAAATTCATGCAAT 120
DB 61 GGTCCAGATCGCCACCATTCACATCCAGGCTGGCCAAACAAAGGTCGAAATTCATGCAAT 120
QY 121 AAAAAAAGAAATGATTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
DB 121 AAAAAAAGAAATGATTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
QY 181 AGATGGAGGTGAGGAGATCAATTAATCTCTAAATCATGCTAGGAAATATACATCACT 240
DB 181 AGATGGAGGTGAGGAGATCAATTAATCTCTAAATCATGCTAGGAAATATACATCACT 240
QY 241 TTATAAGACTCTCTGTTTATTAACATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 TTATAAGACTCTCTGTTTATTAACATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 AAGTTCACCTTCAGAAAGCCCTTTGAGAGAGACAGATATACATCTCTCTCTCTCTCTCT 360
DB 301 AAGTTCACCTTCAGAAAGCCCTTTGAGAGAGACAGATATACATCTCTCTCTCTCTCTCT 360
QY 361 AAGATGAGAAACAGCGCGGCGACAAATGGCTAATGCCGTAA1GCCAGCACTTTGGGAGG 420
DB 361 AAGATGAGAAACAGCGCGGCGACAAATGGCTAATGCCGTAA1GCCAGCACTTTGGGAGG 420
QY 421 CTGAGGCGAGAGGATCGCTTGAGCTCCAGAGTTTGAGAGCTAGCTTGAATATATATATAT 480
DB 421 CTGAGGCGAGAGGATCGCTTGAGCTCCAGAGTTTGAGAGCTAGCTTGAATATATATATAT 480
QY 481 AGCTGTCTCTACAAAAAATACAAAAATAGATAGGCTGAGTGGTGGTGGTGGTGGTGGTGG 540
DB 481 AGCTGTCTCTACAAAAAATACAAAAATAGATAGGCTGAGTGGTGGTGGTGGTGGTGGTGG 540
QY 541 CCAGCTACTTGGGAGGTAAAGTGGGAGGATGGTGGGAGGATGGTGGGAGGATGGTGGGAG 600
DB 541 CCAGCTACTTGGGAGGTAAAGTGGGAGGATGGTGGGAGGATGGTGGGAGGATGGTGGGAG 600
QY 601 CTGAGGCGATGTTGGATCACTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAG 660
DB 601 CTGAGGCGATGTTGGATCACTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAG 660
QY 661 AAAAAAGAAATGAAAGAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 AAAAAAGAAATGAAAGAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 GAGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
DB 721 GAGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
QY 781 GATGAACAGAGGCGAAGAGCTTTACGTAAATTCCTCATCATCTGGTTGTCAGCTTTGA 840
DB 781 GATGAACAGAGGCGAAGAGCTTTACGTAAATTCCTCATCATCTGGTTGTCAGCTTTGA 840
QY 841 CCCCCAAACCCAAATTTATGACCAAGGTTATCTTGTGAGGCTAGGAGGAGGAGGAGGAGG 900
DB 841 CCCCCAAACCCAAATTTATGACCAAGGTTATCTTGTGAGGCTAGGAGGAGGAGGAGGAGG 900

QY 901 CCTGGGCGTTGGCGTTTAGAAAAGCTCATCTCTGGCCTTTCTGAGATCCATCCCTTTCTTT 960
DB 901 CCTGGGCGTTGGCGTTTAGAAAAGCTCATCTCTGGCCTTTCTGAGATCCATCCCTTTCTTT 960
QY 961 TTATTTTCTTGACACGGAGCTCTGCTGCTCACTCAGGCTGAGTGCAGTGCAGTGCATGATC 1020
DB 961 TTATTTTCTTGACACGGAGCTCTGCTGCTCACTCAGGCTGAGTGCAGTGCAGTGCATGATC 1020
QY 1021 TCGACTCACTGTAACCTCTCCCTCCGCGGTTCAGGAGTTCCTCCTCCCTCAGCTCCCTCA 1080
DB 1021 TCGACTCACTGTAACCTCTCCCTCCGCGGTTCAGGAGTTCCTCCTCCCTCAGCTCCCTCA 1080
QY 1081 GATAACAGGCGTCCGTCACACATCTGCTGCTAAATTTTGTATTTTGTAGTAAGAGCTGGTT 1140
DB 1081 GATAACAGGCGTCCGTCACACATCTGCTGCTAAATTTTGTATTTTGTAGTAAGAGCTGGTT 1140
QY 1141 TCATCATGTTTGGGCGAGGTTGTTTTCGAACCTCTGAGCTGAGTGCAGTGCAGCTTCGCG 1200
DB 1141 TCATCATGTTTGGGCGAGGTTGTTTTCGAACCTCTGAGCTGAGTGCAGTGCAGCTTCGCG 1200
QY 1201 CTCCCAAGTGTGTTGGATFACAGGCGATGAGCCACTGCGGCCAGCTCAGATCCATCCCTTT 1260
DB 1201 CTCCCAAGTGTGTTGGATFACAGGCGATGAGCCACTGCGGCCAGCTCAGATCCATCCCTTT 1260
QY 1261 CTAGGGCAAAACAGTCCATGCTGCAAGGGGCCATGCCACCCAGAGTTATGAGTACCTGGS 1320
DB 1261 CTAGGGCAAAACAGTCCATGCTGCAAGGGGCCATGCCACCCAGAGTTATGAGTACCTGGS 1320
QY 1321 GACTCCAGAAATTCCTGCTGAGTGTGATAGAACCCACTGATGTGAGTACCTGGGCTTTGAGCC 1380
DB 1321 GACTCCAGAAATTCCTGCTGAGTGTGATAGAACCCACTGATGTGAGTACCTGGGCTTTGAGCC 1380
QY 1381 TTCTATCCGTTCTGCTGAGTGTGATAGAACCCACTGATGTGAGTACCTGGGCTTTGAGCC 1440
DB 1381 TTCTATCCGTTCTGCTGAGTGTGATAGAACCCACTGATGTGAGTACCTGGGCTTTGAGCC 1440
QY 1441 GTGGCTTGGAGATCTCTGCTGAGTGTGATAGAACCCACTGATGTGAGTACCTGGGCTTTGAGCC 1500
DB 1441 GTGGCTTGGAGATCTCTGCTGAGTGTGATAGAACCCACTGATGTGAGTACCTGGGCTTTGAGCC 1500
QY 1501 TGCAGTGGTGGGAGTTCCTGGAATATGATGAGCTGGAGTGGGAGAGAAATAGGCTTG 1560
DB 1501 TGCAGTGGTGGGAGTTCCTGGAATATGATGAGCTGGAGTGGGAGAGAAATAGGCTTG 1560
QY 1561 GGGCAGCTCTGATGAGCTCCCTCATCTGCGCAAACTCAGTCAAACTGTCAGAGTCT 1620
DB 1561 GGGCAGCTCTGATGAGCTCCCTCATCTGCGCAAACTCAGTCAAACTGTCAGAGTCT 1620
QY 1621 AAATGTGAAATCTGCGCTTCAAGGTGGCTACAAAGGTATCTTTGTCAGGTAGGAGACCTT 1680
DB 1621 AAATGTGAAATCTGCGCTTCAAGGTGGCTACAAAGGTATCTTTGTCAGGTAGGAGACCTT 1680
QY 1681 GTGGCTTCCAGCTCCAGGCGCTCTTGGGCGCTCTTACGGGCTCTGTCTGAGT 1740
DB 1681 GTGGCTTCCAGCTCCAGGCGCTCTTGGGCGCTCTTACGGGCTCTGTCTGAGT 1740
QY 1741 CTCTATCAATCTCTCAGGCGAGATTCATATTTAGACTCTTCACTGTTGAGCTGAGCTTT 1800
DB 1741 CTCTATCAATCTCTCAGGCGAGATTCATATTTAGACTCTTCACTGTTGAGCTGAGCTTT 1800
QY 1801 TGCCCAAGATTAAGTGCATATTTAGTGTGTTGGCTTGATGGATGACTTAATATTTAGACA 1860
DB 1801 TGCCCAAGATTAAGTGCATATTTAGTGTGTTGGCTTGATGGATGACTTAATATTTAGACA 1860
QY 1861 TGTGTGTAGGCTGCTTCT 1920
DB 1861 TGTGTGTAGGCTGCTTCT 1920
QY 1921 AGTTTGTCTCCCTACAGGCAAG 1980
DB 1921 AGTTTGTCTCCCTACAGGCAAG 1980
QY 1981 AATTTTACAGAGCTGGAATTTCTCTGGCTGCACTTCACAAATGTATACAAATAAATAACAA 2040

Dd 237 CTAACCTCGGCTTGGCGAGCTTGGGATAGGTTGGCTTCCA CAGCTTTCAGGCTG 174
QY 167 ACCTGGGCGTGTGGCTGAGGGAACAGGCACTGTGGGCTCAGCTTTCAGCTTTCAGCTG 224
Dd 177 TGGGAAGTCCTTCTAGTGGCGGCGACACCAAGCTGGGCGGCTTCTCTCTCTCTCTCT 114
QY 227 GGAAGAACCTCAGCTTTCAGGAAGACAGAAACAGTAAGCTTGGCTTCTCTCTCTCTCT 245
Dd 317 ACTGACCAAGCACTGACCAACCCCGGGAACITACGCTGCTGCTGCTGCTGCTGCTGCT 54
QY 287 GTCTCTCAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 424
Dd 57 TTAGCTTGATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 20

RESULT 5

US-09-173-914-3/c
Sequence 3, Application US/09173914
Patent No. 6171857
GENERAL INFORMATION:
APPLICANT: Hendrickson, Eric
TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and
TITLE OF INVENTION: Methods of Regulating DNA Dependent Protein Kinase Activity
FILE REFERENCE: B0877/7017/HK
CURRENT APPLICATION NUMBER: US/09/173,914
CURRENT FILING DATE: 1998-10-16
EARLIER APPLICATION NUMBER: 60/064,557
EARLIER FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2473
TYPE: DNA
ORGANISM: Mesocricetus Auratus
US-09-173-914-3

Query Match 8.5%; Score 30.4; DB 4; Length 2473

Best Local Similarity 57.3%; Pred. No. 5.6;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 250 AGACAAACAGTAAGCTGGTGTTCAGCAGCGGCGGCTTCTCTCTCTCTCTCTCTCTCT 409
Dd 1629 AGAGCAATCTCACATTTGGCTTTCACCTCAGTGGGCGATTCAGTAATTCAAAATCTGC 1570
QY 410 TTTGACATGGGATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 145
Dd 1509 TGTCAATTGGGGTAGACGCTCTCTGGGGATGTAGG 1514

RESULT 7

US-08-988-321B-37/c
Sequence 37, Application US/08988321B
Patent No. 6174868
GENERAL INFORMATION:
APPLICANT: Kevin P. Anderson et al.
TITLE OF INVENTION: Compositions And Methods For Treatment Of Hepatitis C V
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
STATE: NJ
COUNTRY: USA
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.1 FOR WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,321B
FILING DATE: December 10, 1997
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/650,093
FILING DATE: May 17, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/452,841
FILING DATE: May 30, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/397,220
FILING DATE: March 9, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/945,289
FILING DATE: September 10, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0245
TELECOMMUNICATION INFORMATION:
TELEPHONE: (856) 810-1515
TELEFAX: (856) 810-1454
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 686
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: No
US-08-988-321B-37

Query Match 8.4%; Score 30; DB 4; Length 686;

Best Local Similarity 46.3%; Pred. No. 3.9;
Matches 99; Conservative 0; Mismatches 115; Indels 0; Gaps 0;
QY 111 CCAGGGCGTCCCTGCTGTCTCAGCTCTGGCGGCTTCAGGGCTCCCGAGCCACACGC 170
Dd 558 CCTCGGGCGAGCGGCTTGGGATAGCGCTGTGCTCCACGGGTTCCGACCGCTCGG 499
QY 171 TGGCGGTGCTGAGGGAACATGTCCTGCGCTCAGCTCAGCTTCTCTGTGTGGAA 230
Dd 498 AAGTCTCTGATGCTGCGGACACCACTGGGCGCCCTGCGCGGACACAGTAACATC 439
QY 231 GAACCTCAGCTTCAGAAAGACAAACAGTAAGCTTGGGTTTTTTCAGCAGCGGGGGTTC 290
Dd 438 CACCAACGATCTGACCAACCGCCGGGAACCTTGACCTCTCTGTGGCGCGGTTGGTGTAC 379
QY 291 TCTCAITTTTCTTCTGCTTTCAGTTAGTTGGGAT 324
Dd 378 GTTGTGTTTTTCTTACGCTTAGGATCTGTCT 345

RESULT 8

US-08-397-220B-25/c
Sequence 25, Application US/08397220B
Patent No. 6284458
GENERAL INFORMATION:
APPLICANT: Anderson et al.
TITLE OF INVENTION: Compositions And Methods For Treatment Of Hepatitis C Virus-Associated Diseases
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,220B
FILING DATE: 09-Mar-1995

Mon May 12 08:12:12 2003

us-09-846-456-2.ini

Page 5

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: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: PCI/JP93/01293
:   FILING DATE: 10-Sep-93
:   APPLICATION NUMBER: JP 5-87195
:   FILING DATE: 14-Apr-93
:   APPLICATION NUMBER: 07/945,289
:   FILING DATE: 10-Sep-92
: ATTORNEY/AGENT INFORMATION:
:   NAME: Jane Massey Licata
:   REGISTRATION NUMBER: 32,257
:   REFERENCE/DOCKET NUMBER: ISPH-0031
: TELECOMMUNICATION INFORMATION:
:   TELEPHONE: (609) 779-8488
:   TELEFAX: (609) 779-2400
: INFORMATION FOR SEQ ID NO: 25:
:   LENGTH: 686
:   TYPE: nucleic acid
:   STRANDEDNESS: Single
:   TOPOLOGY: Linear
:   ANTI-SENSE: NO
:   SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-397-2208-25

Query Match      8.4%   Score 30; DB 4; Length 686;
Best Local Similarity 46.3%   Pred. No. 3.9;
Matches 99; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 111 CCACGGGCGTCTGCTCAGCTCTGCGCGTGGCTTCACGGGTCGCGAGGCAACGC 170
DB 558 CCGCGGCGCGGAGCCCTGGGATAGGCTGCGCTTCACGGGTCGCGAGGCAACGC 499
QY 171 TGGCGGTCGCTGGCTGAGGGAACATGCGATGTGGCTTCAGCTGAGTCTGCTGGGAA 240
DB 458 AAGTCTTCGTCATCGCGGCACACCCAACTGGGCGGCTGGCGGTAACAGTAAACTC 439
QY 231 GAACCTCACTTCAGAGAGAGACAAACAGTAAGCTTGGGTTTTCAGCAGCGGGGGTTC 290
DB 448 CACCAATGATCGACCGCGCGGAACCTGAGCTGCTGCGGGAACCTGAGTCTGCTGGGAA 379
QY 291 TCTCAITTTTCTTTGCTTTGAGTTTGGTGGGAT 324
DB 378 GTTGGTTTTCCTTTCAGTTCAGTTCGCT 345

RESULT 9
US-08-650-093C-25/C
: Sequence 25; Application US/08650093C
: Patent No. 6391542
: GENERAL INFORMATION:
:   APPLICANT: Kevin P. Anderson et al.
:   TITLE OF INVENTION: Compositions And Methods For Treatment Of
:   Hepatitis C Virus-Associated Diseases
:   NUMBER OF SEQUENCES: 118
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: LICATA & TYRRELL P.C.
:     STREET: 66 E. Main Street
:     CITY: Marlton
:     STATE: NJ
:     COUNTRY: USA
:     ZIP: 08053
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
:   COMPUTER: IBM Compatible
:   OPERATING SYSTEM: Windows 95
:   SOFTWARE: WORDPERFECT 6.1 for Windows
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/08/650-093C
:   FILING DATE: 17-May-1996
:   CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: 08/452,841
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: FILING DATE: May 30, 1995
: APPLICATION NUMBER: 08/397,220
: FILING DATE: March 9, 1995
: APPLICATION NUMBER: 07/945,289
: FILING DATE: September 10, 1992
: ATTORNEY/AGENT INFORMATION:
:   NAME: Jane Massey Licata
:   REGISTRATION NUMBER: 32,257
:   REFERENCE/DOCKET NUMBER: ISPH-
: TELECOMMUNICATION INFORMATION:
:   TELEPHONE: (609) 779-2400
:   TELEFAX: (609) 779-8488
: INFORMATION FOR SEQ ID NO: 25:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 686
:     TYPE: Nucleic Acid
:     STRANDEDNESS: Single
:     TOPOLOGY: Linear
:     ANTI-SENSE: NO
:     SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-650-093C-25

Query Match      8.4%   Score 30; DB 4; Length 686;
Best Local Similarity 46.3%   Pred. No. 3.9;
Matches 99; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 111 CCACGGGTCGCTGCTCAGCTCTGCGCGTGGCTTCACGGGTCGCGAGGCAACGC 170
DB 558 CCGCGGCGCGGAGCCCTGGGATAGGCTGCGCTTCACGGGTCGCGAGGCAACGC 499
QY 171 TGGCGGTCGCTGGCTGAGGGAACATGCGATGTGGCTTCAGCTGAGTCTGCTGGGAA 230
DB 498 AAGTCTTCGTCATCGCGGCACACCCAACTGGGCGGCTGGCGGTAACAGTAAACTC 439
QY 231 GAACCTCACTTCAGAGAGAGACAAACAGTAAGCTTGGGTTTTCAGCAGCGGGGGTTC 290
DB 438 CACCAACGATCGACCGCGCGGAACCTGAGCTGCTGCGGGAACCTGAGTCTGCTGGGAA 379
QY 291 TCTCAITTTTCTTTGCTTTGAGTTTGGTGGGAT 324
DB 378 GTTGGTTTTCCTTTCAGTTCAGTTCGCT 345

RESULT 10
US-08-866-650-2
: Sequence 2; Application US/0866650
: Patent No. 5919321
: GENERAL INFORMATION:
:   APPLICANT: Greenstein, Daniel S
:   APPLICANT: Takahara, Kazuhiko
:   APPLICANT: Hoffman, Guy G
:   TITLE OF INVENTION: Mammalian Tolloid-Like Protein
:   NUMBER OF SEQUENCES: 13
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: Quarles & Brady
:     STREET: 1 South Pinckney Street
:     CITY: Madison
:     STATE: WI
:     COUNTRY: US
:     ZIP: 53703
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/08/866,650
:   FILING DATE:
:   CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
:   NAME: Berison, Bennett J
:   REGISTRATION NUMBER: 47094
:   REFERENCE/DOCKET NUMBER: 96C296.93839
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Db 4360 CCGCTCCCGCCAGTCCTCGCTGGCTGGTGGTGGCTGGACACA:TTCC:ACGAAGTGA 4301

QY 255 AACAGTAAGCTGGGTTTICA 276

Db 4300 GCGACAAATCTGGCTTTTITA 4279

RESULT 15

US-08-751-189-1
: Sequence : Application US/08751189
: Patent No. 5919656

: GENERAL INFORMATION:

: APPLICANT: Harrington, Lea A.
: APPLICANT: Robinson, Murray O.
: TITLE OF INVENTION: No. 5919656el Genes Encoding Telomerase Protein
: TITLE OF INVENTION: 1
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Amgen, Inc.
: STREET: 1840 De Havilland Drive
: CITY: Thousand Oaks
: STATE: California
: COUNTRY: USA
: ZIP: 91320-1789

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/751.189
: FILING DATE: 15-NOV-1996
: CLASSIFICATION: 435

: ATTORNEY/AGENT INFORMATION:

: NAME: Oleski, Nancy A.
: REGISTRATION NUMBER: 34,688
: REFERENCE/DOCKET NUMBER: A-433

: INFORMATION FOR SEQ ID NO: 1:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 7881 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: MOLECULE TYPE: cDNA

US-08-751-189-1

Query Match: 8.48; Score 30; Db 2; Length 7881;
Best Local Similarity 48.88; Pred. No. 14;
Matches R1: Conservative 0; Mismatches 85; Gaps 0;

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QY 66 TGATGGCTGTTTCCCTCCCTGCTTTTATCTTCACTTAATGACAGCAGACGAGGAGGCTGCTG 125

Db 5166 TGGTTTGTTCCTCCTCCGATGATACACTTCTTTATAGTGTCTTGAAGGCTGTGTGA 5225

QY 126 CTGTCAGCTCTGCCGCTGCTTCCAGGGCTCCGAGGACACAGCT 171

Db 5226 GCTCTGGGACCTCAGCATGGTTGCGGGTCTCCAGACTTAGGCT 527

Search completed: May 9, 2003, 16:36:08
Job time : 31.3027 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2003, 12:47:56 : Search time 599.179 seconds
(without alignments)
9649.520 Million cell updates/sec

Title: US-09-846-456-2
Perfect score: 357
Sequence: 1 tggagggtctagctgagag.....gagggaagaaagagatattg 357

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308152

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	73.8	20.7	292	14 Z44377	Z44377 BSC126C81 n
5	71.2	19.9	535	12 BG384217	BG384217 BG384217 MA
6	42.4	11.9	982	17 CNS02D01	A0135588 Tetraodon

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8	39.4	11.0	562	14	BQ609447
9	38.2	10.7	503	10	AV818336
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14	36.8	10.3	689	14	BQ609447
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16	36.4	10.2	579	10	AV892280
17	36	10.1	322	9	AU056364
18	36	10.1	393	9	AU162694
19	36	10.1	571	10	AV862022
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21	35.8	10.0	344	13	BM149133
22	35.8	10.0	785	17	AF010859
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ALIGNMENTS

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LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL698654 547 bp mRNA linear EST 21-MAR-2002
DKFZp686N12109.t1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686N12109 5', mRNA sequence.

AL698654
AL698654.1 GI:19619134
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human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 547)
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann
S.
EST (Duesterhoeft, et al.)
Unpublished (1999)
Contact: Duesterhoeft A
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Otago (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKFZp686N12109) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source

Location/Qualifiers
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/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pRipEx2; Site_1: SfiI; Site_2: SfiI; cDNA-collection"

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Matches 184; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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QY 277 GCAGCGGGGGTTCTCTCATTTTCTTGGCTTGGCTTGGCTTGGCTTGGCT 421
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RESULT 2
AUI35588
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VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Human
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 736)
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamanoto, J., Wakamatsu, A., Nakamura, Y., Naito, T., Sugano, S. and
Isogai, T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan.
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'-3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1002437"
/clone_lib="PLACE1"
/tissue_type="placenta"
/note="Vector: pME18SFL3"

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RESULT 3
BB657864
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

house mouse
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 619)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda,
M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki,
D., Shibata, K., Shinagawa, A., Shiraki, T., Sobabe, Y., Suzuki, H.,
Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyama, T.,
Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh,
M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Waghi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, K., Ozawa, K., Tanaka, T., Matsura,
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara,
Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa,
K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and

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VERSION	AI192682.1 GI:7830786		
KEYWORDS	GSS: genome survey sequence.		
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ORGANISM	Tetraodon nigroviridis		
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
	Actinopterygii; Neopterygii; Teleostei; Euflestei; Neoteleostei;		
	Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontidae;		
	Tetraodontidae; Tetraodon.		
REFERENCE	1 (bases 1 to 982)		
AUTHORS	Ruest-Crollius,H., Jaillon,O., Bastiva,C., Bouneau,L., Fisher,C.,		
	Bernot,A., Fizames,C., Wincker,P., Broillet,P., Quetier,F.,		
	Saurin,W. and Weissenbach,J.		
TITLE	human gene number estimate provided by genome wide analysis using		
JOURNAL	Tetraodon nigroviridis DNA sequence		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 982)		
	Ruest-Crollius,H., Jaillon,O., Bastiva,C., Fizames,C., Fisher,C.,		
	Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and		
	Weissenbach,J.		
TITLE	Characterization and repeat analysis of the compact genome of the		
JOURNAL	Freshwater pufferfish Tetraodon nigroviridis		
REFERENCE	Unpublished		
AUTHORS	3 (bases 1 to 982)		
TITLE	Genoscope.		
JOURNAL	Direct Submission		
COMMENT	Submitted (12-APR-2000)		
	This sequence is a single read and was generated as part of a large		
	scale clone-end sequencing project of the Tetraodon nigroviridis		
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VERSION    AV864011
KEYWORDS   AV864011.1 GI:16851535
SOURCE     EST.
ORGANISM   Ciona intestinalis.
            Ciona intestinalis
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            Phlebobranchia; Clonidae; Ciona.
REFERENCE  1 (bases 1 to 571)
            Satoh,N., Satoh,Y., Kohara,Y. and Shin-i,T.
            Expressed genes in Ciona intestinalis
            Unpublished (2000)
            JOURNAL
            COMMENT
            Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES   Location/Qualifiers
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Matches 85; Conservative 0; Mismatches 81; Gaps 0;
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DB 156 AAAATGCCAAGCTGTGCGCAGCTAGAGAGAAATGGAATGCGAGCTAATCTGAGAA 97
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QY 218 TGCCTGCTGTGGAAGAACCTTCTTCTGAGAGAGAAATAAATAGTAAAT 264
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 Job time : 605.179 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2003, 10:53:45 : Search time 92.5319 seconds
(without alignment)
8660.418 Million cell updates/sec

Title: US-09-846-456-2

Perfect score: 357

Sequence: 1 tggaggtctcagctgaggg.....gagggataaactgagtg 357

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370425

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

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2	351.2	98.4	183999	22	Human ABC1 genomic
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4	159.4	44.6	10442	22	Nucleotide sequence
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8	159.4	44.6	10474	22	Nucleotide sequence
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10	159	44.5	159	24	AA037269	Human ABC1 gene ex
11	145.8	40.8	446	22	AA04035	Partial human ABC1
12	145.8	40.8	7086	22	ABA09200	Human ABC1 homolo
13	145.8	40.8	7086	22	AAK52667	Human polynucleoti
14	145.8	40.8	7260	22	AA021326	Human ATP binding
15	145.8	40.8	7260	22	AA170315	Human polynucleoti
16	145.8	40.8	7281	22	AAK51683	Human polynucleoti
17	145.8	40.8	9741	22	AA061120	Human ABC1 DNA seq
18	145.8	40.8	9741	22	AA037273	Human ABC1 full-le
19	145.8	40.8	9854	22	AA061121	Human ABC1 DNA seq
20	144.2	40.4	736	22	AAH07432	Human cDNA clone (
21	144.2	40.4	1556	22	AAH18606	Human cDNA sequenc
22	135.8	38.0	7857	21	AAK69388	Human ABC1 choles
23	135.8	38.0	7860	22	AAF93826	Human ABC1 choles
24	135.8	38.0	7860	22	AAF92835	Human ABC1 choles
25	135.8	38.0	7861	21	AAK69387	Human ABC1 choles
26	135.8	38.0	7864	21	AAK69120	Human ABC1 choles
27	135.8	38.0	7864	21	AAK69385	Human ABC1 choles
28	135.8	38.0	7864	21	AAK69386	Human ABC1 choles
29	135.8	38.0	7864	21	AAK69389	Human ABC1 choles
30	99	27.7	99	24	AA037271	Human ABC1 gene in
31	99	27.7	99	24	AA037272	Nucleotide sequenc
32	42.6	11.9	23024	22	AAF25499	ABC1 polymorphism
33	36.4	10.2	38	22	AAF93082	Human novel protei
34	36	10.1	7661	22	AA016545	Human genomic DNA
35	36	10.1	7661	22	AA162954	Human polynucleoti
36	36	10.1	7661	22	AA163983	Human novel protei
37	36	10.1	11696	22	AA016546	Human novel protei
38	36	10.1	11696	22	AA016547	Human immune/haema
39	36	10.1	11696	22	AAK72951	Human immune/haema
40	36	10.1	11696	22	AAK72952	Human genomic DNA
41	36	10.1	11696	22	AA162955	Human genomic DNA
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ALIGNMENTS

RESULT 1

AA037266
ID AAD37266 standard: DNA; 357 BP.

XX AAD37266;

XX 21-AUG-2002 (first entry)

XX Human ABC1 transcription regulatory DNA #2.

XX Human: ATP-binding cassette 1; ABC1 gene regulation; atherosclerosis;
XX cholesterol metabolism; hypercholesterolaemia; antisense therapy; ds.

XX Homo sapiens.

XX WO200183746-A2.

XX 08-NOV-2001.

XX 02-MAY-2001: 2001WO-EP05488.

XX 02-MAY-2000: 2000US-201280P.

XX (AVET) AVENTIS PHARMA SA.

XX Rosier-Montus M, Prades C, Lemoine C, Naudin L, Deneffe P;

XX Brewer B, Duverger N, Remaley A, Santamarina-Fojo S;

XX WPI; 2002-154404/20.

XX Isolated nucleic acid useful for modifying the ATP-binding cassette 1
XX (ABC1) and screening for candidate modulatory compounds or substances

CC screen for compounds that regulate the expression of genes associated
CC with cholesterol transport. The genes and proteins are also useful for
CC are also useful as diagnostic indicators of cardiovascular disease and
CC other disorders associated with hypercholesterolemia.

XX Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match 44.6%; Score 159.4; DB 22; Length 10442;
Best Local Similarity 81.8%; Pred. No. 1.2e-38;
Matches 184; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 97 CAGTTAATGACACGACGCGGCGTCCCTGCTGTCAGCTGCGGCGGCTTCAGGGCT 156
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DB 195 CAGTTAATGACACGACGCGGCGTCCCTGCTGTCAGCTGCGGCGGCTTCAGGGCT 254
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QY 277 GAGCGGGGGGCTCTCTCATTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 321
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DB 375 GTGGCGTGGCGCTCTCTCATTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419

RESULT 5
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ID AAF24702 standard; DNA: 10442 BP.
AC AAF24702;
DT 20-APR-2001 (first entry)
DE Nucleotide sequence of a human ABC1 polypeptide.
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.
CS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 291..7076
FT /tag= a
FT /product= "ABC1 polypeptide"

PN W0200078971.A2.
PC 28-DEC-2000.
PF 16-JUN-2000; 2000WO-US16591.
PR 18-JUN-1999; 990S-0140264.
PR 14-SEP-1999; 990S-0153872.
PR 19-NOV-1999; 990S-0166573.
XX (CVT) CV THERAPEUTICS INC.
PA (UNIV) UNIV WASHINGTON.
P1 Lawe RW, Wade D, Oram JF, Garvin M;
XX WPI; 2001 137811/14.
DR P PSDB; AAB31465.
XX Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PI polynucleotides and polypeptides, useful for treatment of heart
PI and other disorders associated with hypercholesterolemia and
PI atherosclerosis.

PS Claim 3; Page 117-123; 21pp; English.

XX The present sequence encodes a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
CC membranes and utilises ATP hydrolysis to transport a wide variety of
CC substrates across the plasma membrane. ABC1 is a pivotal protein in
CC the apolipoprotein-mediated mobilisation of intracellular cholesterol
CC stores. ABC1 is defective in Tangier disease, a genetic disorder
CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
CC useful for developing pharmaceutical agents for the treatment of heart
CC disease and other disorders associated with hypercholesterolemia and
CC atherosclerosis. The genes are useful for developing screening assays to
CC screen for compounds that regulate the expression of genes associated
CC with cholesterol transport. The genes and proteins are also useful for
CC other disorders associated with hypercholesterolemia.

XX Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match 44.6%; Score 159.4; DB 22; Length 10442;
Best Local Similarity 81.8%; Pred. No. 1.2e-38;
Matches 184; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 97 CAGTTAATGACACGACGCGGCGTCCCTGCTGTCAGCTGCGGCGGCTTCAGGGCT 156
|||||
DB 195 CAGTTAATGACACGACGCGGCGTCCCTGCTGTCAGCTGCGGCGGCTTCAGGGCT 254
QY 157 CCGAGGCCACACGCTGGCGTGGCTGAGGGAACATGATGCTTCAGCTTCAGG 216
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DB 255 CCGAGGCCACACGCTGGCGTGGCTGAGGGAACATGATGCTTCAGCTTCAGG 314
QY 217 TTGCTGCTGTCGAGAGACCTCAGCTTCAGAGAGAACATGATGCTTCAGCTTCAGG 276
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DB 315 TTGCTGCTGTCGAGAGACCTCAGCTTCAGAGAGAACATGATGCTTCAGCTTCAGG 374
QY 277 GAGCGGGGGGCTCTCTCATTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 321
|||||
DB 375 GTGGCGTGGCGCTCTCTCATTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419

RESULT 6
AAF24685
ID AAF24685 standard; DNA: 10474 BP.
AC AAF24685;
DT 20-APR-2001 (first entry)
DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.
CS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 323..7108
FT /tag= a
FT /product= "detective ABC1 polypeptide"

PN W0200078972.A2.
PC 28-DEC-2000.
PF 16-JUN-2000; 2000WO-US16765.
PR 18-JUN-1999; 990S-0140264.
PR 14-SEP-1999; 990S-0153872.
PR 19-NOV-1999; 990S-0166573.
XX

PA	(CVTH-) CV THERAPEUTICS INC.
XX	Lawn RM, Wade D, Garvin M;
Pt	WP1; 2001-137812/14.
XX	
XX	Adenosine triphosphate (ATP) binding cassette (ABC) polypeptide,
Pt	useful for the development of agents for the treatment of heart disease
Pt	and other disorders associated with hypercholesterolemia and
Pt	atherosclerosis -
XX	
XX	Disclosure; Page 148-154; 215pp; English.
XX	
CC	The present sequence encodes a human adenosine triphosphate (ATP)
CC	binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC	a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC	ATP hydrolysis to transport a wide variety of substrates across the
CC	plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC	mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC	Tangier disease, a genetic disorder characterised by abnormal
CC	HDL cholesterol metabolism. The ABC1 gene is localised to chromosome
CC	9q22-q31. The ABC1 genes and proteins are useful for developing
CC	pharmaceutical agents for the treatment of heart disease and other
CC	disorders associated with hypercholesterolemia and atherosclerosis. The
CC	genes are useful for developing screening assays to screen for compounds
CC	that regulate the expression of genes associated with cholesterol
CC	transport. The genes and proteins are also useful for as diagnostic
CC	as diagnostic indicators of cardiovascular disease and other disorders
CC	associated with hypercholesterolemia.
XX	
SQ	Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;
	Query Match 44.6%; Score 159.4; DB 22; Length 10474;
	Best Local Similarity 81.8%; Pred. No. 1.2e-38;
	Matches 184; Conservative 0; Mismatches 41; Indels 9; Gaps 0
QY	97 CASITTAATGACAGCGGGGGTCCCTGTGTGTCAGCTCTGGCGGCTGCCTTCACAGGGCT 155
DB	
DB	227 CAATTAA TGACAGCAGCGGGGGTCCCTGTGTGAGTCTGGCGGCTGCCTTCACAGGGCT 295
QY	151 CCNAGACACAGCGCTGGCGTGCTGGCTGAGGAACAAGCATCTGAGCTGAGCTGAGG 216
DB	
DB	287 ACCGAGCACAGCTGGCGGTGCTGGCTCAGGGAACAGCTCTGCTGCTGAGCTGAGG 346
QY	217 TTGCTGCTGTGGAAGAAGCTCACTTTCSAAGAAGAACAGTAAGCTTTCGCTTTCA 275
DB	
DB	347 TTGCTGCTGTGGAAGAAGCTCACTTTCSAAGAAGAACAGTAAGCTTTCGCTTTCA 409
QY	277 GCAGCGGCGGGTCTCTCATTTTTCCTTTCGCTTCGCTTCGCTTCGCTTCGCTTCG 421
DB	
DB	407 GTGGCTGCGGCTCTATTATCTTCTGATTCGCTTCGCTTCGCTTCGCTTCGCTTCG 451
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ID	AAF24686 standard; DNA; 10474 BP.
XX	AAF24686;
XX	
XX	20 APR 2001 (first entry)
DE	
XX	Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
DE	
KW	Human: adenosine triphosphate binding cassette protein 1; ABC1;
KW	apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW	chromosome 9q22-q31; heart disease; hypercholesterolemia;
KW	atherosclerosis; cholesterol transport; ss.
XX	
OS	Homo sapiens.
XX	
XX	Key Location/Qualifiers
FH	323..7108
FT	CDS
FT	/tag= a
FT	

FT	/product= "defective ABC1 polypeptide"
PX	WO200078972-A2.
PN	
PP	28-DEC-2000.
PD	
PI	
PP	16-JUN-2000; 2000WO-US16765.
XX	
XX	18-JUN-1999; 99US-0140264.
PR	14-SEP-1999; 99US-0153872.
PR	19-NOV-1999; 99US-G166573.
XX	
XX	(CVTH-) CV THERAPEUTICS INC.
PA	
XX	Lawn RM, Wade D, Garvin M;
PT	WPI; 2001-137812/14.
DR	
XX	Adenosine triphosphate (ATP) binding cassette (ABC) polypeptide useful for the development of agents for the treatment of and other disorders associated with hypercholesterolemia and atherosclerosis -
PT	
PT	
XX	Disclosure; Page 170-176; 215pp; English.
XX	
CC	The present sequence encodes a human adenosine triphospho-
CC	binding cassette protein (ABC) 1 polypeptide, and is i-
CC	a Tangier disease patient. ABC1 resides in cell membra-
CC	ATP hydrolysis to transport a wide variety of substrat-
CC	plasma membrane. ABC1 is a pivotal protein in the apoli-
CC	mobilisation of intracellular cholesterol stores. ABC1
CC	Tangier disease, a genetic disorder characterised by a
CC	HDL-cholesterol metabolism. The ABC1 gene is localise-
CC	9q22-q31. The ABC1 genes and proteins are useful for
CC	pharmaceutical agents for the treatment of heart diseas-
CC	disorders associated with hypercholesterolemia and ath-
CC	genes are useful for developing screening assays to sele-
CC	that regulate the expression of genes associated with
CC	transport. The genes and proteins are also useful for
CC	as diagnostic indicators of cardiovascular disease and
CC	associated with hypercholesterolemia.
XX	
XX	Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 o
SQ	
Query Match 44.6%; Score 159.4; DB 22; Lemn	
Best Local Similarity 81.8% Pred. No. 1.2e-38;	
Matches 184; Conservative 0; Mismatches 41; Indels	
QY	97 CACTTAATGCTAGTACGGCGGTCCCTGCTGTTCAGCTGTGCCCTGGC
Dd	227 CAGTTAATGCTAGCACGGCGGTCCCTGCTGTTCAGCTGTGCCCTGGC
QY	157 CCCGACCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCATGTGGCG
Dd	287 CCCGACCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCTTGTGGCG
QY	217 TTGCTGCTGTGAAGAAGCTCACTTTTCAGAAAGAACAAACAGTAGCT
Dd	347 TTGCTGCTGTGAAGAAGCTCACTTTTCAGAAAGAACAAACATGTCAAGC
QY	277 GCAGCGGGGGGTCTCTCATTTTCTTTCGTTTGAAGTTGGG 321
Dd	407 GTGGCTGGCTCTTAATTATCTTCTCATCTCTGTTTCGG 451
RESULT 8	
AAF24707	
1D AAF24707 standard; DNA; 10474 BP.	
XX	
XX	AAF24707;
XX	
DT	20-APR-2001 (first entry)
XX	

[illegible]

DB	345	TTGCTGCTGCTGGAGAACCTCACCATTTCAGAGAGACAGAACATGTCAGCTCTTACTCGAA	404
QY	277	GCAGCGGGGGTTCTCTCATTTTCTTTTGCTGTTTTCAGTTGGG	321
DB	405	GTGGCGCTGGCCTCATTTATCTTCTCTGATCCTCACTCTCTGTTGGG	449
DB	405	GTGGCGCTGGCCTCATTTATCTTCTCTGATCCTCACTCTCTGTTGGG	449
RESULT 15			
AA170315			
ID	AA170315	standard: cDNA: 7260 BP.	
XX	AA170315:		
AC			
XX			
DE	07-JAN-2002 (first entry)		
XX	Human ATP binding cassette transporter 1 (ABCL1) cDNA.		
XX			
KW	ATP binding cassette transporter 1; ABCL1; human; lipid disorder;		
KW	cholesterol; cardiovascular disease; inflammatory disease;		
KW	antiinflammatory; antilipemic; antipsoriatic; dermatological;		
KW	Tangier disease; coronary heart disease; diagnosis; gene therapy;		
KW	polymorphism; ss.		
XX			
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
FT	CDS	321..7106	
FT		/*tag= a	
FT	CDS	501..7106	
FT		/*tag= b	
FT	variation	/note= "alternative open reading frame:: AA170314"	
FT		replace(976,A)	
FT	variation	/*tag= c	
FT		replace(1516,C)	
FT	variation	/*tag= d	
FT		replace(2969,G)	
FT	variation	/*tag= e	
FT		replace(3836,C)	
FT		/*tag= f	
XX			
XX	EP1136554-A1.		
XX			
PD	26-SEP-2001.		
XX			
PF	24-MAR-2000: 2000EP-0106401.		
XX			
PK	24-MAR-2000: 2000EP-0106401.		
XX			
PA	(FARK) BAYER AG.		
XX			
PI	Schmitz G, Bodzioch M;		
XX			
DR	WPI: 2001-640389/74.		
DR	P-PSDB: AAM50228.		
XX			
PT	New adenosine triphosphate binding cassette transporter gene		
PT	polymorphisms, useful for diagnosing and treating lipid disorders,		
PT	cardiovascular diseases and inflammatory diseases		
XX			
PS	Disclosure: Page 26-28; 41pp; English.		
XX			
CC	The present sequence is that of cDNA encoding the human adenosine		
CC	triphosphate (ATP) binding cassette transporter 1 (ABCL1) protein		
CC	(see AAM50227). The sequence includes an extended open reading		
CC	frame (ORF) to that provided by the sequence in AA170314, using		
CC	an alternative ATG codon as initiation codon and thereby adding an		
CC	extra 40 N-terminal amino acids to the encoded ABC1 protein (see		
CC	AAM50228). The invention provides 4 common polymorphisms in the		
CC	ABCL1 gene. These were identified by sequencing the ABC1 gene in		
CC	different Tangier kindreds. In the variant genes (numbered as in		
CC	AA170314), G is changed to A at position 596, T is changed to C at		
CC	position 1136, A is changed to G at position 2589 or G is changed		
CC	to C at position 3456, or any combination of these. All of these		

```

CC polymorphisms alter the amino acid sequence of ABC1 and therefore
CC may affect its function. The 2 most common polymorphisms (G596A)
CC and A2589G) are both associated with a decreased in vitro ApoA-I
CC mediated efflux of cholesterol from mononuclear phagocytes, a
CC feature typical of Tangier disease. 3 Of the variants (G596A,
CC A2589G and G3456C) are significantly increased in a population of
CC men having low high density lipoprotein-cholesterol levels and
CC established coronary heart disease (CHD) relative to CHD-free
CC control subjects. The use of the provided ABC1 polymorphisms for
CC the diagnosis and treatment of lipid disorders, cardiovascular
CC diseases, and inflammatory diseases (e.g. psoriasis, lupus
CC erythematoses) is claimed. Modulation of ABC1 transcripts or
CC proteins by antisense or ribozyme technology or RNA decoys is also
CC claimed.
XX
SQ Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
Query Match 40.8%; Score 145.8; DB 22; Length 7260;
Best Local Similarity 80.9%; Pred. No. 1.7e-34;
Matches 182; Conservative 0; Mismatches 42; Indels 1; Gaps 1;
QY 97 CAGTTAATGACCAACCCACGGG;GTCCCTGCTGTGACGCTCGCGCGTGCCTTCAGGGCT 156
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 226 CAGTTAATGATCAGCACAC-GCGGTCCCTGCTGTGAGCTCGCGCGTGCCTTCAGGGCT 284
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 157 CCCGAGCCACACGCTGGGGTGTGGCTGAGGGAACATGGCATGTGGCCCTCAGTGTAGG 216
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 285 CCCGAGCCACACGCTGGGGTGTGGCTGAGGGAACATGGCTGTGGCCCTCACTCAGG 344
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 217 TTGCTGCTGTGGAGAAGCCTCACTTTTCAGAGAAGACAAACAGTAAGCTTGGGTTTTTCA 276
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 345 TTGCTGCTGTGAGAGACCTCACITTCAGAGAAGACAAACATGTCAGCTGTACTGGAA 404
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 277 GCAGCGGGGGGTTCTGTCAITTTTCTTTGTGGTTTGAAGTTGGG 321
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 405 GTGGCCTGGCGCTATTATTTCTCTGATCCTGATCTCTGTTCGG 449
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Search completed: May 9, 2003, 13:08:12
Job time : 127.812 secs

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Search completed: May 9, 2003, 13:08:12
Job time : 127.832 secs

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OM nucleic - nucleic search, using sw model

Run on: May 9, 2003, 11:17:01 : Search time 1066.03 seconds
(without alignments)
9746.207 Million cell updates/sec

Title: US-09-846-456-2

Perfect score: 357

Sequence: 1 tggaggtctcagctgagagg.....gagaggaaggaatgtatttg 357

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109250

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_pro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_or:*

21: em_ov:*

22: em_pat:*

23: em_pi:*

24: em_pi:*

25: em_pi:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rtd:*

36: em_htg_nam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	357	100.0	357	6	AX351030 Sequence
2	353.8	99.1	149034	9	AF275948 Homo sapi
3	351.2	98.4	183999	6	AX092589 Sequence
4	340.2	95.3	480	9	HA252277 Homo sapi
5	340.2	95.3	124608	9	AL353685 Human DNA
6	340.2	95.3	175064	2	AC012230 Homo sapi
7	340.2	95.3	201144	9	AF287262 Homo sapi
8	251.2	70.4	90698	2	AC021345 Homo sapi
9	184.2	51.6	200	9	AF258624 Homo sapi
10	159.4	44.6	10442	6	AX060713 Sequence
11	159.4	44.6	10442	6	AX060892 Sequence
12	159.4	44.6	10442	9	AF285167 Homo sapi
13	159.4	44.6	10474	6	AX060719 Sequence
14	159.4	44.6	10474	6	AX060721 Sequence
15	159.4	44.6	10474	6	AX060898 Sequence
16	159.4	44.6	10474	6	AX060900 Sequence
17	159	44.5	159	6	AX351033 Sequence
18	147	41.2	647	9	AF258627 Homo sapi
19	145.8	40.8	446	6	AX127764 Sequence
20	145.8	40.8	446	6	AX139751 Sequence
21	145.8	40.8	7260	6	AX253452 Sequence
22	145.8	40.8	9741	6	AX127830 Sequence
23	145.8	40.8	9741	6	AX139817 Sequence
24	145.8	40.8	9741	6	AX351038 Sequence
25	145.8	40.8	9854	6	AX127831 Sequence
26	145.8	40.8	9854	6	AX139818 Sequence
27	144.2	40.4	1556	9	AK024328 Homo sapi
28	136.8	38.3	298	9	AB037924 Homo sapi
29	135.8	38.0	7860	6	AX092594 Sequence
30	135.8	38.0	7862	6	AX135712 Sequence
31	101.8	28.5	179611	2	AL813806 Mus muscu
32	101.8	28.5	186889	2	AL807243 Mus muscu
33	101.8	28.5	206695	2	AC091466 Mus muscu
34	101.8	28.5	278572	10	AF287263 Mus muscu
35	99	27.7	99	6	AX351035 Sequence
36	97	27.7	99	6	AX351036 Sequence
37	67	18.8	7878	10	MMAB01 Mus musculu
38	65	18.2	6786	9	AB055582 Homo sapi
39	54.8	15.4	7074	5	AF362377 Gallus ga
40	42.6	11.9	22881	10	AF287142 Mus muscu
41	42.6	11.9	23024	6	AX080494 Sequence
42	42.6	11.9	185825	10	AC087114 Mus muscu
43	42.6	11.9	200143	2	AC073805 Mus muscu
44	39.4	11.0	226394	2	AC025794 Mus muscu
45	39	10.9	135091	2	AC107062 Bos tauru

ALIGNMENTS

RESULT 1
AX351030
LOCUS AX351030
DEFINITION Sequence 2 from Patent WO0183746.
ACCESSION AX351030
VERSION AX351030.1 GI:18616386
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
Rosier-Montus, M.F., Prados, C., Lemoine, C., Naudin, L., Denoefle, P.,
Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S.
Regulatory nucleic acid sequences of the abcl gene

linear PAI 06-FEB-2002

JOURNAL	Patent: WO 0183746-A 2 08-NOV-2001;
FEATURES	Aventis Pharma S.A. (FR)
Source	Location/Qualifiers
	1..357
BASE COUNT	64 a 78 c 116 g 59 t
ORIGIN	
Query Match	100.0%; Score 357; DB:6; Locs:1; 357;
Best Local Similarity	100.0%; Pred. No. 1e-95;
Matches 357; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY 1	TGGAGGCTCAGCTGAGGAGGCTGATTAGCAGTCCCTCATTTGGTGTATGGTTTCGACGA 60
DB 1	TGGAGGCTCAGCTGAGGAGGCTGATTAGCAGTCCCTCATTTGGTGTATGGTTTCGACGA 60
QY 61	ATACTGATGGCTGTTCCCTCCTGCTTTATCTTTTCACTTAATGATGATGATGATGATGATG 120
DB 61	ATACTGATGGCTGTTCCCTCCTGCTTTATCTTTTCACTTAATGATGATGATGATGATGATG 120
QY 121	CCCTGCTGCTGAGCTGCTGCCCTGCTTCCAGGCTCCCGAGCCACACGCTGGCGGCTGCT 180
DB 121	CCCTGCTGCTGAGCTGCTGCCCTGCTTCCAGGCTCCCGAGCCACACGCTGGCGGCTGCT 180
QY 181	GGCTAGGAGCATGGCATGTTGGCCCTCAGCTGAGTGTGCTGTGCTGAGAAATCACT 240
DB 181	GGCTAGGAGCATGGCATGTTGGCCCTCAGCTGAGTGTGCTGTGCTGAGAAATCACT 240
QY 241	TTCAGAACAGCAACAGTAGTGGTTTTCAGCAGCGGGGCTTCCTCATTTT 300
DB 241	TTCAGAACAGCAACAGTAGTGGTTTTCAGCAGCGGGGCTTCCTCATTTT 300
QY 301	TCTTTGCTGTTTGGTTGAGTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 357
DB 301	TCTTTGCTGTTTGGTTGAGTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 357
RESULT 2	
AF275948	149034 bp DNA Linear PRI 17-JUL-2000
LOCUS	AF275948 Homo sapiens ABCA1 (ABCA1) gene, complete cds.
DEFINITION	AF275948
ACCESSION	AF275948
VERSION	AF275948.1 GI:9247085
KEYWORDS	
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 149034) Santamarina-Fojo, S., Peterson, K., Knapper, C., Qian, Y., Freeman, L., Cheng, J.F., Osorio, J., Remaley, A., Yang, X.P., Haudenschild, C., Prades, C., Chimini, G., Blackmon, E., Blackmon, E., Francois, T., Buvelot, N., Rubin, E.M., Rosier, M., Deneffe, P., Fredrickson, T.S. and Brewer, H.B., Jr.
TITLE	Complete genomic sequence of the human ABCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
MEDLINE	20345099
PUBMED	10884428
REFERENCE	2 (bases 1 to 149034) Santamarina-Fojo, S., Peterson, K.M., Knapper, C.L., Freeman, L.A., Remaley, A.T., Yang, X.-P., Haudenschild, C.C., Blackmon, E.F., Francois, T.L. and Brewer, H.B., Jr.
AUTHORS	Direct Submission
TITLE	Submitted (08-JUN-2000) Molecular Disease Branch, National Institutes of Health, National Heart, Lung and Blood Institute, Bethesda, MD 20892, USA
JOURNAL	
FEATURES	Location/Qualifiers
Source	1..149034
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	/db_xref="taxon:9606"
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	/gene="ABCA1"
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repeat_region	4998..5278
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repeat_region	25038..25314
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	/gene="ABCA1"
	/codon_start=1
	/product="ABCA1"
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	/db_xref="GI:9247086"
	/translation="MAFWPQLRLWKNNLTFRRTQCLLELVKAPLFLELLISVRLSYPEQHECFNKNPFSAGTLPVQGLTCNANNPCFRPTGKFWVGNFKSIVARLFSARLLYSQKTSNKKMRKVLRTLOQIKSSSNKLIQLFVNDFTSGFLYHNLSPKSTVDKMLRADVILHKVFLQCYQLHLSLNCNGSKSEMIQLGQJFVSELCPL

was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr9>

RP11-31J20 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBAC3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-31J20. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true right end of clone RP11-31J20 is at 129608 in this sequence. The true right end of clone RP11-41K16 is at 2500 in this sequence.

FEATURES

Location/Qualifiers

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"

/clone="RP11-31J20"
/clone.lib="RPCI-11.1"

1358..1653

repeat_region

/note="AluSc repeat: matches 1..238 of consensus"

repeat_region

1828..1877

repeat_region

/note="L2 repeat: matches 2649..2698 of consensus"

repeat_region

2496..2714

repeat_region

/note="MIR repeat: matches 12..250 of consensus"

repeat_region

2777..2896

repeat_region

/note="MIR repeat: matches 6..128 of consensus"

repeat_region

3237..3415

repeat_region

/note="L1ME repeat: matches 5696..5821 of consensus"

repeat_region

5522..6818

repeat_region

/note="AluSq repeat: matches 1..245 of consensus"

repeat_region

7282..7415

repeat_region

/note="L1MB8 repeat: matches 6040..6173 of consensus"

repeat_region

8145..8434

repeat_region

/note="AluSc repeat: matches 1..238 of consensus"

repeat_region

12145..12713

repeat_region

/note="L2 repeat: matches 1363..1940 of consensus"

repeat_region

13890..13969

repeat_region

/note="L2 repeat: matches 2611..2701 of consensus"

repeat_region

15380..15411

repeat_region

/note="16 copies 2 mer ac 87% conserved"

repeat_region

16105..16144

repeat_region

/note="10 copies 4 mer caca 100% conserved"

repeat_region

16868..17049

repeat_region

/note="MIR repeat: matches 64..246 of consensus"

repeat_region

17941..18229

repeat_region

/note="AluSq repeat: matches 1..287 of consensus"

repeat_region

18259..18553

repeat_region

/note="AluSq repeat: matches 1..293 of consensus"

repeat_region

20310..20616

repeat_region

/note="AluSq repeat: matches 1..308 of consensus"

repeat_region

20957..21107

repeat_region

/note="MIR repeat: matches 49..212 of consensus"

repeat_region

21783..22078

repeat_region

/note="AluSc repeat: matches 7..302 of consensus"

repeat_region

22320..22439

repeat_region

/note="MIR repeat: matches 10..146 of consensus"

repeat_region

22533..22839

repeat_region

/note="AluSc repeat: matches 1..307 of consensus"

repeat_region

23427..23945

repeat_region

/note="L2 repeat: matches 2137..2750 of consensus"

repeat_region

24245..24344

repeat_region

/note="AluSq repeat: matches 2..302 of consensus"

repeat_region

24556..24587

repeat_region

/note="8 copies 4 mer acac 96% conserved"

repeat_region

26504..26561

repeat_region

/note="29 copies 2 mer ta 69% conserved"

repeat_region

26849..26892

repeat_region

/note="11 copies 4 mer tata 81% conserved"

repeat_region

28935..28626

/note="MIR repeat: matches 17..129 of consensus"

28986..29213

/note="MIR repeat: matches 2..245 of consensus"

30141..30422

/note="AluSq repeat: matches 1..302 of consensus"

31424..31734

/note="AluSp repeat: matches 1..308 of consensus"

31987..32116

/note="MERSA repeat: matches 60..188 of consensus"

32450..32536

/note="MERSA repeat: matches 14..106 of consensus"

33293..33380

/note="22 copies 4 mer atgg 79% conserved"

34435..34588

/note="MERSA repeat: matches 13..189 of consensus"

34729..34873

/note="MIR repeat: matches 49..198 of consensus"

35802..35951

/note="MIR repeat: matches 77..248 of consensus"

37184..37260

/note="2 copies 39 mer 92% conserved"

37673..37980

/note="AluSc repeat: matches 1..308 of consensus"

39674..40243

/note="L1MB2 repeat: matches 5774..6341 of consensus"

40256..40534

/note="L2 repeat: matches 2256..2533 of consensus"

41476..41615

/note="MIR repeat: matches 30..185 of consensus"

42010..42194

/note="MIR repeat: matches 49..234 of consensus"

44805..45239

/note="L1R16A repeat: matches 6..450 of consensus"

45359..45486

/note="MIR repeat: matches 1..139 of consensus"

46654..46693

/note="10 copies 4 mer acac 97% conserved"

47118..47429

/note="AluSc repeat: matches 1..312 of consensus"

47915..48283

/note="AluSq repeat: matches 145..313 of consensus"

49047..49181

/note="L2 repeat: matches 2625..2710 of consensus"

49578..49758

/note="MIR repeat: matches 9..188 of consensus"

49847..49873

/note="MIR repeat: matches 155..182 of consensus"

49874..50188

/note="AluSp repeat: matches 3..311 of consensus"

50189..50347

/note="MIR repeat: matches 5..155 of consensus"

51677..51977

/note="AluSc repeat: matches 1..303 of consensus"

52025..52123

/note="L2 repeat: matches 1655..1753 of consensus"

54337..54544

/note="MIR repeat: matches 25..246 of consensus"

54754..55042

/note="AluSp repeat: matches 1..302 of consensus"

55042..55143

/note="AluY repeat: matches 5..298 of consensus"

56027..56232

/note="MIR repeat: matches 21..259 of consensus"

56233..56286

/note="18 copies 3 mer tgt 72% conserved"

56342..56673

/note="L1MA9 repeat: matches 5893..6307 of consensus"

56750..56889

/note="L2 repeat: matches 2565..2710 of consensus"

57406..57567

/note="MERSA repeat: matches 4..187 of consensus"

57864..58174

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exon /number=17
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exon /number=19
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/gene="ABCA1"
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Db 58220 TGGAGGCTCAGCTGAGGGCTGGATTAGCAGTCTCATTGGTGTATGGTTTCAGCA 58279
QY 61 ATAAGTATGCTGTTTCCCTCTCTCTTATCTTACGTTAATGACAGGACGGGGT 120
Db 58280 ATAAGTATGCTGTTTCCCTCTCTCTTATCTTACGTTAATGACAGGACGGGGT 58338
QY 121 CCCTGCTGACGCTGCGCGCTGCGCTTCAGGGCTCCGAGCCACAGCTGGGCTGCT 180
Db 58339 CCCTGCTGACGCTGCGCGCTGCGCTTCAGGGCTCCGAGCCACAGCTGGGCTGCT 58398
QY 181 GGCTAGGGAACATGGCATTTGGCCTCAGCTGAGGTTGCTGTGGAAGAACATCTACT 240
Db 58399 GGCTAGGGAACATGGCTTGTGGCTCAGCTGAGGTTGCTGTGGAAGAACATCTACT 58458
QY 241 TTCAGAGACACAAACAGTAAGCTTGGGTTTTTCAGACGGGGGGTCTCTCATTTT 300
Db 58459 TTCAGAGACACAAACAGTAAGCTTGGGTTTTTCAGACGGGGGGTCTCTCATTTT 58518
QY 301 TCTTTGTTGTTTTCAGTTGGGATTTGGAGGAGGGAGGAGGAAGCAAGCTGTGTG 357
Db 58519 TCTTTGTTGTTTTCAGTTGGGATTTGGAGGAGGGAGGAGGAAGCAAGCTGTGTG 58575

RESULT 8

AC021345/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AC021345 90698 bp DNA linear HTS 13-101-2060
Homo sapiens clone RP1124J9, LOW-PASS SEQUENCE SAMPLING.
AC021345
AC021345.2 GI:9130845
HTG: HTGS_PHASE0.
Homo sapiens
Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 90698)
Birren, B., Linton, J., Nussbaum, C. and Lander, E.
Homo sapiens, clone RP1124J9
Unpublished
2 (bases 1 to 90698)

Birren, B., Linton, J., Nussbaum, C., Lander, E., Abraham, B., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckert, R., Bada, P.,
Boguslavsky, L., Brinkman, R., Brown, A., Burkett, A., Castle, A.,
Choe, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArelano, K., Dewar, K., Domino, M., Doyle, M., Feinstein, J.,
Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hayes, B., Heaford, A., Horton, L.,
Boeland, J. C., Johnson, R., Jones, C., Kann, L., Karas, A., Klein, J.,
Landers, J., Lechek, J., Levine, R., Lien, C., Liu, S., Locke, K.,
MacDonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
McPherson, R., Melnick, J., Menees, L., Morrow, J., Nayak, J.,
Norman, C. H., O'Connor, T., O'Donnell, P., Oliver, T. M., Peterson, K.,
Piette, N., Pisan, C., Pollara, V., Raymond, C., Riley, P., Rothman, B.,
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Hermann, N.,
Stojanovic, N., Subramanian, A., Talamas, J., Testa, S., Theodorescu, J.,
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Yan, W., J.,
Zimmer, A. and Zody, M.

TITLE

JOURNAL

COMMENT

Submitted (16-JAN 2000) Whitehead Institute/MIT Center for Genome
Research, 420 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced q1:5765761.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WTHR
Web site: http://www-seq.wi.mit.edu
Contact: sequence-submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4483
Center clone name: 24_J_9

NOTE: This record contains 92 individual
sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allow
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.

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911 1010: gap of 100 bp
1011 1873: contig of 863 bp in length
1874 1973: gap of 100 bp
1974 2824: contig of 851 bp in length
2825 2924: gap of 100 bp
2925 3802: contig of 878 bp in length
3803 3902: gap of 100 bp
3903 4816: contig of 914 bp in length
4817 4916: gap of 100 bp
4917 5759: contig of 843 bp in length

* 5760 5859: gap of 100 bp
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* 6865 7747: contig of 883 bp in length
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* 9854 10757: contig of 904 bp in length
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* 11733 11832: gap of 100 bp
* 11833 12739: contig of 907 bp in length
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* 12840 13710: contig of 871 bp in length
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* 15663 15762: gap of 100 bp
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* 19633 19732: gap of 100 bp
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* 38403 38502: gap of 100 bp
* 38503 39380: contig of 878 bp in length
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* 64127 65015: contig of 889 bp in length
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DB 13169 TGGAGGCTTCAGTTCAGAGGGTGGATTAGCAGTCTCTATGGTATGGTTTGCAGCA 13160
QY 61 ATAACGTATGGTGTTCCTCTCTGCTTATCTTTTCAGTTAATCACCAGGTCAGGGGCT 120
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DB 13109 ATAACGTATGGTGTTCCTCTCTGCTTATCTTTTCAGTTAATCACCAGGTCAGGGGCT 13050
QY 121 CCTGTGTCAGTCTTGGGCTGTGCTTTCAGGGGCTCCGAGGCTCCGAGGCTGGTGGTGGT 180
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QY 157 CCCGAGCCACACGCTGGGGCTGCTGGCTGAGGAGAACATCGCATCTGGCTTACGTTAGTTAGG 214
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QY 217 TTGCTGCTGTGGAAGACCTCACTTTCACAGAGACACAAACAGTAGTATGTTGTTTCTCA 236
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Db 315 TTGCTGCTGTGGAAGACCTCACTTTCACAGAGACACAAACAGTAGTATGTTGTTTCTCA 374
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QY 277 GCAGCGGGGGTCTCTCTCAATTTTCTTTGGTTGGTTTCAGTGGG 311
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RESULT 12
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Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA,
complete cds.
AF285167
AF285167.1 GI:9755158
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Hominidae;
Homo sapiens.
REFERENCE
1 (bases 1 to 10442)
Schwartz, K., Lawn, R.M. and Wade, D.P.
ABCA1 gene expression and apoA-I-mediated cholesterol efflux are
regulated by LXR
Unpublished
JOURNAL
2 (bases 1 to 10442)
Lawn, R.M., Wade, D.P., Garvin, M.R., Wang, X., Schwartz, K.,
Porter, J.G., Seilhamer, J.J., Vaughan, A.M. and Oram, J.F.
Direct Submission
Submitted (06-JUL-2000) Discovery Research, CV Therapeutics Inc.,
3172 Porter drive, Palo Alto, CA 94304, USA
JOURNAL
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Best Local Similarity 81.8%; Pred. No. 2e-36;
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Db 195 CAGTTAATGACGACGACGCGCTGCTGCTGATCGATCTGGCGCTGCGCTTACGTTAGTGGG 254
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QY 157 CCCGAGCCACACGCTGGGGCTGCTGGCTGAGGAGAACATCGCATCTGGCTTACGTTAGTGG 216
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Db 255 CCCGAGCCACACGCTGGGGCTGCTGGCTGAGGAGAACATCGCATCTGGCTTACGTTAGTGG 314
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QY 217 TTGCTGCTGTGGAAGACCTCACTTTCACAGAGACACAAACAGTAGTATGTTGTTTCTCA 276
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QY 277 GCAGCGGGGGTCTCTCTCAATTTTCTTTGGTTGGTTTCAGTGGG 321
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Db 375 GTGGCGTGGCCTCTATTTAICTTCTGATGCTGATCTCTGTTGGG 419
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RESULT 13
AX060719 10474 bp DNA linear 141 22-JAN-2001
LOCUS
DEFINITION
Sequence 7 from Patent WO0078972.
ACCESSION
AX060719
VERSION
AX060719.1 GI:12406108
KEYWORDS
human.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 10474)
Lawn, R.M., Wade, D. and Garvin, M.
Regulation with binding cassette transporter protein abc1
JOURNAL
CV THERAPEUTICS, INC. (US)
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
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Best Local Similarity 81.8%; Pred. No. 2e-36;
Matches 184; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 97 CAGTTAATGACGACGACGCGCTGCTGCTGATCGATCTGGCGCTGCGCTTACGTTAGTGGG 156
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QY 217 TTGCTGCTGTGGAGACCTCAGCTTTCAGAGAGACAAACAGTAACTTGGGTTTCA 276
Db 347 TTGCTGCTGTGGAGACCTCAGCTTTCAGAGAGACAAACAGTAACTTGGGTTTCA 406
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Db 407 GTGGCTGGGCTCTATTATCTCTCTGATCTCTGTTGCTGG 451

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AX060721
LOCUS AX060721 10474 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 9 from Patent WO0078972.
ACCESSION AX060721
VERSION AX060721.1 GI:12406109
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn, R.M., Wade, D., and Garvin, M.
TITLE Regulation with binding cassette transporter protein abcl
JOURNAL Patent: WO 0078972-A 9 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
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/db_xref="taxon:9606".

BASE COUNT 2907 a 2304 c 2415 g 2844 t 4 others
ORIGIN

Query Match 44.6%; Score 159.4; DB 6; Length 10474;
Best Local Similarity 81.8%; Pred. No. 2e-36;
Matches 184; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 97 CAGTTAATGACACGACGCGGCTCCCTGCTGCAGCTCTGCGCGCTGCTCCAGGCGT 156
Db 227 CAGTTAATGACACGACGCGGCTCCCTGCTGCAGCTCTGCGCGCTGCTCCAGGCGT 286
QY 157 CCCAGCCACACGCTGGGCTGCTGGCTCAGGACATGGCATGTGGCTCAGCTGAGG 216
Db 287 CCCAGCCACACGCTGGGCTGCTGGCTCAGGACATGGCATGTGGCTCAGCTGAGG 346
QY 217 TTGCTGCTGTGGAGACCTCAGCTTTCAGAGAGACAAACAGTAACTTGGGTTTCA 276
Db 347 TTGCTGCTGTGGAGACCTCAGCTTTCAGAGAGACAAACAGTAACTTGGGTTTCA 406
QY 277 GCACGGGGGTTCTCTCATTTTTCTTTGTTGTTTGGCTGGG 321
Db 407 GTGGCTGGGCTCTATTATCTCTCTGATCTCTGTTGCTGG 451

RESULT 15
AX060898
LOCUS AX060898 10474 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 7 from Patent WO0078971.
ACCESSION AX060898
VERSION AX060898.1 GI:12406275
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
TITLE ATP binding cassette transporter protein abcl polypeptides
JOURNAL Patent: WO 0078971-A 7 28-DEC-2000;

CV THERAPEUTICS, INC. (US)
Location/Qualifiers
1. 10474
/organism="Homo sapiens"
/db_xref="taxon:9606".

BASE COUNT 2906 a 2305 c 2416 g 2843 t 4 others
ORIGIN

Query Match 44.6%; Score 159.4; DB 6; Length 10474;
Best Local Similarity 81.8%; Pred. No. 2e-36;
Matches 184; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 97 CAGTTAATGACACGACGCGGCTCCCTGCTGCAGCTCTGCGCGCTGCTCCAGGCGT 256
Db 227 CAGTTAATGACACGACGCGGCTCCCTGCTGCAGCTCTGCGCGCTGCTCCAGGCGT 286
QY 157 CCCAGCCACACGCTGGGCTGCTGGCTCAGGACATGGCATGTGGCTCAGCTGAGG 216
Db 287 CCCAGCCACACGCTGGGCTGCTGGCTCAGGACATGGCATGTGGCTCAGCTGAGG 346
QY 217 TTGCTGCTGTGGAGACCTCAGCTTTCAGAGAGACAAACAGTAACTTGGGTTTCA 276
Db 347 TTGCTGCTGTGGAGACCTCAGCTTTCAGAGAGACAAACAGTAACTTGGGTTTCA 406
QY 277 GCACGGGGGTTCTCTCATTTTTCTTTGTTGTTTGGCTGGG 321
Db 407 GTGGCTGGGCTCTATTATCTCTCTGATCTCTGTTGCTGG 451

Search completed: May 9, 2003, 16:20:25
Job time : 1199.03 secs

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DN nucleic nucleic search, using sw model

Run on: May 9, 2003, 11:21:45 : Search time 50.941 seconds

(without alignments)
8708.843 Million cell updates/sec

Title: us-09-846-456-2

Perfect score: 357

Sequence: 1 tggaggctcagctgagagg.....gagggaacaaagctatcttc 357

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 783854 seqs, 621352466 residues 1567768

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA.*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCMB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	357	100.0	357	9	US-09-846-827-4
2	357	100.0	357	10	US-09-846-456-2
3	203.8	57.1	1062	9	US-09-924-140-101
4	203.8	57.1	1062	9	US-09-952-600A-101
5	159	44.5	159	10	US-09-846-456-5
6	157.4	44.1	159	9	US-09-846-827-26
7	147	41.2	158	9	US-09-846-827-25
8	145.8	40.8	9741	9	US-09-846-827-1
9	145.8	40.8	9741	10	US-09-846-456-10
10	145.8	40.8	9870	9	US-09-846-827-92
11	145.8	40.8	9870	9	US-09-846-827-93
12	145.8	40.8	9870	9	US-09-846-827-94
13	145.8	40.8	9870	9	US-09-846-827-95
14	145.8	40.8	9870	9	US-09-846-827-96
15	145.8	40.8	9870	9	US-09-846-827-97
16	145.8	40.8	9870	9	US-09-846-827-98
17	145.8	40.8	9870	9	US-09-846-827-99
18	145.8	40.8	9870	9	US-09-846-827-100
19	145.8	40.8	9870	9	US-09-846-827-101

20	145.8	40.8	9870	9	US-09-846-827-102
21	145.8	40.8	9870	9	US-09-846-827-103
22	145.8	40.8	9870	9	US-09-846-827-104
23	145.8	40.8	9870	9	US-09-846-827-105
24	145.8	40.8	9870	9	US-09-846-827-106
25	145.8	40.8	9870	9	US-09-846-827-107
26	145.8	40.8	9870	9	US-09-846-827-108
27	145.8	40.8	9870	9	US-09-846-827-109
28	145.8	40.8	9870	9	US-09-846-827-110
29	145.8	40.8	9870	9	US-09-846-827-111
30	145.8	40.8	9870	9	US-09-846-827-112
31	145.8	40.8	9870	9	US-09-846-827-113
32	145.8	40.8	9870	9	US-09-846-827-114
33	145.8	40.8	9870	9	US-09-846-827-115
34	145.8	40.8	9870	9	US-09-846-827-116
35	145.8	40.8	9870	9	US-09-846-827-117
36	145.8	40.8	9870	9	US-09-846-827-118
37	145.8	40.8	9870	9	US-09-846-827-119
38	145.8	40.8	9870	9	US-09-846-827-120
39	145.8	40.8	9870	9	US-09-846-827-121
40	145.8	40.8	9870	9	US-09-846-827-122
41	145.8	40.8	9870	9	US-09-846-827-123
42	145.8	40.8	9870	9	US-09-846-827-124
43	145.8	40.8	9870	9	US-09-846-827-125
44	145.8	40.8	9870	9	US-09-846-827-126
45	99	27.7	99	10	US-09-846-456-7

ALIGNMENTS

RESULT 1

US-09-846-827-4

Sequence 4, Application US/0984827

Publication No. US20030056234A1

GENERAL INFORMATION:

APPLICANT: DENEFFLE, PATRICE

APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE

APPLICANT: ARNOULD-REGUINE, ISABELLE

APPLICANT: DUVERGER, FRANCOIS

APPLICANT: CAMBIEN, NICOLAS

TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN AB21 GENE, THEIR USES,

DETECTION METHODS AND KITS THEREFOR

FILE REFERENCE: 03806.0522-00000

CURRENT APPLICATION NUMBER: US/09/984,827

CURRENT FILING DATE: 2002-04-01

PRIOR APPLICATION NUMBER: 60/254,108

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: FR 00/14037

PRIOR FILING DATE: 2000-10-31

NUMBER OF SEQ ID NOS: 161

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 357

TYPE: DNA

ORGANISM: Homo sapiens

US-09-846-827-4

Query Match 100.0%; Score 357; DB 9; Length 357;

Best Local Similarity 100.0%; Pred No. 1.6e-108;

Matches 357; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TGGAGGCTCAGCTGAGAGGGCTGGATTAGCAGTCCCTCATTTGGTGTATGGCTTTTCAGCA 60

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Db 1 TGGAGGCTCAGCTGAGAGGGCTGGATTAGCAGTCCCTCATTTGGTGTATGGCTTTTCAGCA 60

Oy 61 ATAACATGCTGCTTCCCTCCTCTTATCTTTTACGTAAATGACACGACCCAGCGGT 120

|||||

Db 61 ATAACATGCTGCTTCCCTCCTCTTATCTTTTACGTAAATGACACGACCCAGCGGT 120

Oy 121 CCCTGCTGTCAGCTCTGGCGCTGCCCTCCAGGGCTCCGAGCCACACGCTGGGGTGT 180

|||||

Db 121 CCCTGCTGTCAGCTCTGGCGCTGCCCTCCAGGGCTCCGAGCCACACGCTGGGGTGT 180

APPLICANT: Fojta, Silvia
TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modif
Activity and Therapeutic Uses
FILE REFERENCE: 3866,0505
CURRENT APPLICATION NUMBER: US/09/846,456
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/201,280
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patent in version 3.0
SEQ ID NO 5
LENGTH: 159
TYPE: DNA
ORGANISM: Homo sapiens
US-09-846-456-5

Query Match 44.5%; Score 159; DB 10; Length 159;
Best Local Similarity 100.0%; Pred. No. 6e-43;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 TTAATGACACGACGAGGCGTCTGTCAGCTCTGGCGGCTGCTTCCAGGCTCC 159
DB 1 TTAATGACACGACGAGGCGTCTGTCAGCTCTGGCGGCTGCTTCCAGGCTCC 60
QY 160 GAGCAGACGCTGGGGCTGCTGCTGAGGAGACATGGCATGTTGGCTCAGCTGAGGTTG 219
DB 61 GAGCAGACGCTGGGGCTGCTGCTGAGGAGACATGGCATGTTGGCTCAGCTGAGGTTG 120
QY 220 CTGCTGTGGAGAACTTCACCTTTTCAGAGAGAGACAACA 258
DB 121 CTGCTGTGGAGAACTTCACCTTTTCAGAGAGAGACAACA 159

RESULT 6
US-09-984-827-26
Sequence 26, Application US/09/984827
Publication No. US2003005624A1
GENERAL INFORMATION:
APPLICANT: DENEFL, PATRICE
APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBLEN, FRANCOIS
TITLE OF INVENTION: "PROMOTER" SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,
TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
FILE REFERENCE: 03866,0522-00000
CURRENT APPLICATION NUMBER: US/09/984,827
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: FR 06/14037
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 26
LENGTH: 159
TYPE: DNA
ORGANISM: Homo sapiens
US-09-984-827-26

Query Match 44.1%; Score 157.4; DB 9; Length 159;
Best Local Similarity 99.4%; Pred. No. 2e-42;
Matches 158; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 100 TTAATGACACGACGAGGCGTCTGTCAGCTCTGGCGGCTGCTTCCAGGCTCC 159
DB 1 TTAATGACACGACGAGGCGTCTGTCAGCTCTGGCGGCTGCTTCCAGGCTCC 60
QY 160 GAGCAGACGCTGGGGCTGCTGCTGAGGAGACATGGCATGTTGGCTCAGCTGAGGTTG 219
DB 61 GAGCAGACGCTGGGGCTGCTGCTGAGGAGACATGGCATGTTGGCTCAGCTGAGGTTG 120
QY 220 CTGCTGTGGAGAACTTCACCTTTTCAGAGAGAGACAACA 258

PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/105,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 114
SOFTWARE: JPatent
SEQ ID NO 101
LENGTH: 1062
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..153
FEATURE:
NAME/KEY: CDS
LOCATION: 154..639
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 640..1062
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 1023..1028
FEATURE:
NAME/KEY: polyA_site
LOCATION: 1047..1062
US-09-992-600A-101

Query Match 57.1%; Score 203.8; DB 9; Length 1062;
Best Local Similarity 84.8%; Pred. No. 1.6e-57;
Matches 240; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 39 ATTGGTGATGGCTTTCAGCAATACATGATGCTGTTTCCGCTGTTTTCATCTCA 98
DB 1 ATTGGTGATGGCTTTCAGCAATACATGATGCTGTTTCCGCTGTTTTCATCTCA 60
QY 99 GTTAATGACACGACGAGGCGTCTGTCAGCTCTGGCGGCTGCTTCCAGGCTCC 159
DB 61 GTTAATGACACGACGAGGCGTCTGTCAGCTCTGGCGGCTGCTTCCAGGCTCC 119
QY 159 CGAGCCACAGCTGGGGCTGCTGCTGAGGAGACATGGCATGTTGGCTCAGCTGAGGTTG 219
DB 120 CGAGCCACAGCTGGGGCTGCTGCTGAGGAGACATGGCATGTTGGCTCAGCTGAGGTTG 179
QY 219 GGTGGTGTGGAAGAACTTCATTTTCAGAGAGAGACAACA 279
DB 180 GGTGGTGTGGAAGAACTTCATTTTCAGAGAGAGACAACA 249
QY 279 AGGAGGAGGCTCTCATTTTCTTGGTGTGAGTCTG 300
DB 249 GGTGGTGTGATTTTATCTTCAGATGTTGTTGTTG 279

RESULT 5
US-09-846-456-5
Sequence 5, Application US/09/846456
Patent No. US20020146792A1
GENERAL INFORMATION:
APPLICANT: Rosier, Marie
APPLICANT: Prades, Catherine
APPLICANT: Lemoine, Cendrine
APPLICANT: Naudin, Laurent
APPLICANT: Deneffe, Patrice
APPLICANT: Duverger, Nicolas
APPLICANT: Brewer, Bryan
APPLICANT: Remaley, Alan

Db 121 CTGCTGTGGGAACCTCATTTCAGAGAACACAA 159

RESULT 7

US-09-984-827-25
Query Match 41.2% Score 147; DB 9; Length 159;
Best Local Similarity 99.4%; Pred. No. 5.7e-39;
Matches 158; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
: Sequence 25, Application US/09984827
: Publication No. US20030056234A1
: GENERAL INFORMATION:
: APPLICANT: DENEFELE, PATRICE
: APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
: APPLICANT: ARNOULD-REGUIGNE, ISABELLE
: APPLICANT: DUVERGER, NICOLAS
: APPLICANT: CAMBIEN, FRANCOIS
: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABC1 GENE, THEIR USES, AND
: FILE REFERENCE: 03806.0522-00000
: CURRENT APPLICATION NUMBER: US/09/984.827
: PRIOR FILING DATE: 2002-04-01
: PRIOR APPLICATION NUMBER: 60/254.108
: PRIOR FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: FR 00/14037
: PRIOR FILING DATE: 2000-10-31
: NUMBER OF SEQ ID NOS: 161
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 25
: LENGTH: 158
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-984-827-25

Query Match 41.2% Score 147; DB 9; Length 159;
Best Local Similarity 99.4%; Pred. No. 5.7e-39;
Matches 158; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 100 TTAATGACCAAGCAGCGGGTCTCTGCTGAGGGAACATGGCATGTTCAGAGAACACAA 259

Db 1 TTAATGACCAAGCAGCGGGTCTCTGCTGAGGGAACATGGCATGTTCAGAGAACACAA 159

QY 160 GAGGACACAGCTGGCGTCTGCTGAGGGAACATGGCATGTTCAGAGAACACAA 219

Db 60 GAGGACACAGCTGGCGTCTGCTGAGGGAACATGGCATGTTCAGAGAACACAA 119

QY 220 CTGCTGTGGGAACCTCATTTCAGAGAACACAA 259

Db 120 CTGCTGTGGGAACCTCATTTCAGAGAACACAA 159

RESULT 8

US-09-984-827-1
Query Match 41.2% Score 147; DB 9; Length 159;
Best Local Similarity 99.4%; Pred. No. 5.7e-39;
Matches 158; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
: Sequence 1, Application US/09984827
: Publication No. US20030056234A1
: GENERAL INFORMATION:
: APPLICANT: DENEFELE, PATRICE
: APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
: APPLICANT: ARNOULD-REGUIGNE, ISABELLE
: APPLICANT: DUVERGER, NICOLAS
: APPLICANT: CAMBIEN, FRANCOIS
: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABC1 GENE, THEIR USES, AND
: FILE REFERENCE: 03806.0522-00000
: CURRENT APPLICATION NUMBER: US/09/984.827
: PRIOR FILING DATE: 2002-04-01
: PRIOR APPLICATION NUMBER: 60/254.108
: PRIOR FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: FR 00/14037
: PRIOR FILING DATE: 2000-10-31
: NUMBER OF SEQ ID NOS: 161
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 9741
: TYPE: DNA
: ORGANISM: Homo sapiens

: FEATURE:
: NAME/KEY: modified_base
: LOCATION: (7009)
: OTHER INFORMATION: a, t, c or g
US-09-984-827-1

Query Match 40.8% Score 145.8; DB 9; Length 9741;
Best Local Similarity 80.9%; Pred. No. 8.3e-38;
Matches 182; Conservative 0; Mismatches 42; Indels 1; Gaps 1;
QY 97 CAGTTAATGACCAAGCAGCGGTCTGCTGAGGGAACATGGCATGTTCAGAGAACACAA 156
Db 90 CAGTTAATGACCAAGCAGCGGTCTGCTGAGGGAACATGGCATGTTCAGAGAACACAA 148
QY 157 CCCGAGTCACAGCTGTGGCGTCTGCTGAGGGAACATGGCATGTTCAGAGAACACAA 216
Db 149 CCCGAGTCACAGCTGTGGCGTCTGCTGAGGGAACATGGCATGTTCAGAGAACACAA 208
QY 217 TTGCTGTGTTGGAAGACCTCATTTCAGAGAACACAAACAGTAAGCTTTTTC 276
Db 209 TTGCTGTGTTGGAAGACCTCATTTCAGAGAACACAAACAGTAAGCTTTTTC 268
QY 277 CCAGCGGGGGTCTCTCATTTCATTTCCTGTTGTTTGGTTGGG 321
Db 269 GTGCCCTGGGCTCTCTATTAATCTCTGATCTCTCTGTTCCG 313

RESULT 9

US-09-846-456-10
Query Match 40.8% Score 145.8; DB 10; Length 9741;
Best Local Similarity 80.9%; Pred. No. 8.3e-38;
Matches 182; Conservative 0; Mismatches 42; Indels 1; Gaps 1;
: Sequence 10, Application US/09846456
: Patent No. US20020146792A1
: GENERAL INFORMATION:
: APPLICANT: ROSIER, Marie
: APPLICANT: Prades, Catherine
: APPLICANT: Lemoine, Cendrine
: APPLICANT: Naudin, Laurent
: APPLICANT: Deneffe, Patrice
: APPLICANT: Duverger, Nicolas
: APPLICANT: Brewer, Bryan
: APPLICANT: Remaley, Alan
: APPLICANT: Fojo, Silvia
: TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modify
: FILE REFERENCE: 3806.G505
: CURRENT APPLICATION NUMBER: US/09/846.456
: CURRENT FILING DATE: 2001-05-02
: PRIOR APPLICATION NUMBER: US 60/201.280
: PRIOR FILING DATE: 2000-05-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 10
: LENGTH: 9741
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: "b" is chosen from g, a, t and c
US-09-846-456-10

Query Match 40.8% Score 145.8; DB 10; Length 9741;
Best Local Similarity 80.9%; Pred. No. 8.3e-38;
Matches 182; Conservative 0; Mismatches 42; Indels 1; Gaps 1;
QY 97 CAGTTAATGACCAAGCAGCGGTCTGCTGAGGGAACATGGCATGTTCAGAGAACACAA 156
Db 90 CAGTTAATGACCAAGCAGCGGTCTGCTGAGGGAACATGGCATGTTCAGAGAACACAA 148
QY 157 CCCGAGTCACAGCTGTGGCGTCTGCTGAGGGAACATGGCATGTTCAGAGAACACAA 216
Db 149 CCCGAGTCACAGCTGTGGCGTCTGCTGAGGGAACATGGCATGTTCAGAGAACACAA 208
QY 217 TTGCTGTGTTGGAAGACCTCATTTCAGAGAACACAAACAGTAAGCTTTTTC 276
Db 209 TTGCTGTGTTGGAAGACCTCATTTCAGAGAACACAAACAGTAAGCTTTTTC 268

269 TCCGCTGCTGGGAACCTCAGTTTCAGAGAGACAAACATGTCAGCTCTCTGGAA 268

277 GACAGCGGGGTTCTCTCATTTTCTTTTGGTTTGGTTGGG 321

269 GCGGCGCGCCCTATTATCTCTGATCCCTGATCTGCTGG 313

RESULT 10

US-09-984-827-92

Sequence 92, Application US/09984827

Publication No. US20030056234A1

GENERAL INFORMATION:

APPLICANT: DENEUF, PATRICE

APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE

APPLICANT: ARNOULD-REGUIGNE, ISABELLE

APPLICANT: DUVERGER, NICOLAS

APPLICANT: CAMBIEN, FRANCOIS

TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND

FILE REFERENCE: 03806.0522-00000

CURRENT APPLICATION NUMBER: US/09/984.827

PRIOR FILING DATE: 2002-04-01

PRIOR APPLICATION NUMBER: 60/254,108

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: FR 00/14037

NUMBER OF SEQ ID NOS: 161

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 92

LENGTH: 9870

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: modified_base

LOCATION: (7138)

OTHER INFORMATION: a, t, c or g

US-09-984-827-92

Query Match 40.8%; Score 145.8; DB 9; Length 9870;

Best Local Similarity 80.9%; Pred. No. 8.3e-38;

Matches 182; Conservative 0; Mismatches 42; Indels 1; Gaps 2;

269 TCCGCTGCTGGGAACCTCAGTTTCAGAGAGACAAACATGTCAGCTCTCTGGAA 268

277 GACAGCGGGGTTCTCTCATTTTCTTTTGGTTTGGTTGGG 321

269 GCGGCGCGCCCTATTATCTCTGATCCCTGATCTGCTGG 313

277 GACAGCGGGGTTCTCTCATTTTCTTTTGGTTTGGTTGGG 321

269 GCGGCGCGCCCTATTATCTCTGATCCCTGATCTGCTGG 313

277 GACAGCGGGGTTCTCTCATTTTCTTTTGGTTTGGTTGGG 321

269 GCGGCGCGCCCTATTATCTCTGATCCCTGATCTGCTGG 313

277 GACAGCGGGGTTCTCTCATTTTCTTTTGGTTTGGTTGGG 321

269 GCGGCGCGCCCTATTATCTCTGATCCCTGATCTGCTGG 313

277 GACAGCGGGGTTCTCTCATTTTCTTTTGGTTTGGTTGGG 321

269 GCGGCGCGCCCTATTATCTCTGATCCCTGATCTGCTGG 313

277 GACAGCGGGGTTCTCTCATTTTCTTTTGGTTTGGTTGGG 321

269 GCGGCGCGCCCTATTATCTCTGATCCCTGATCTGCTGG 313

277 GACAGCGGGGTTCTCTCATTTTCTTTTGGTTTGGTTGGG 321

269 GCGGCGCGCCCTATTATCTCTGATCCCTGATCTGCTGG 313

277 GACAGCGGGGTTCTCTCATTTTCTTTTGGTTTGGTTGGG 321

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RESULT 14
US-09-984-827-95
? Sequence 45, Application US/09984827
? Publication No. US2003005624A1
? GENERAL INFORMATION:
? APPLICANT: DENEPIE, PATRICE
? APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE
? APPLICANT: ARNOULD-REQUIGNE, ISABELLE
? APPLICANT: DUVERGER, NICOLAS
? APPLICANT: CAMBIEN, FRANCOIS
? TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,
? FILE REFERENCE: 03806.0522-00000
? CURRENT FILING DATE: 2002-04-01
? PRIOR APPLICATION NUMBER: 60/254,108
? PRIOR FILING DATE: 2000-12-11
? PRIOR APPLICATION NUMBER: FR 00/14037
? PRIOR FILING DATE: 2000-10-31
? NUMBER OF SEQ ID NOS: 161
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 95
? LENGTH: 9870
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: modified_base
? LOCATION: (7138)
? OTHER INFORMATION: a, t, c or g
US-09-984-827-96

Query Match 40.8%; Score 145.8; DB 9; Length 9870;
Best Local Similarity 80.9%; Pred. No. 8.3e-38;
Matches 182; Conservative 0; Mismatches 42; Indels 1; Gaps 1;

QY 97 CATTAAATGACGACGACGGGGCTCCCTGCTGTGACGCTCTGGCGCTACGCTTCTGAGAGGCT 156
DB 219 CATTAAATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 277
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Query Match 40.8%; Score 145.8; DB 9; Length 9870;
Best Local Similarity 80.9%; Pred. No. 8.3e-38;
Matches 182; Conservative 0; Mismatches 42; Indels 1; Gaps 1;

QY 97 CATTAAATGACGACGACGGGGCTCCCTGCTGTGACGCTCTGGCGCTACGCTTCTGAGAGGCT 156
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RESULT 14
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? Sequence 46, Application US/09984827
? Publication No. US2003005624A1
? GENERAL INFORMATION:
? APPLICANT: DENEPIE, PATRICE
? APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE
? APPLICANT: ARNOULD-REQUIGNE, ISABELLE
? APPLICANT: DUVERGER, NICOLAS
? APPLICANT: CAMBIEN, FRANCOIS
? TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,
? FILE REFERENCE: 03806.0522-00000
? CURRENT APPLICATION NUMBER: US/09/984,827
? PRIOR FILING DATE: 2002-04-01
? PRIOR APPLICATION NUMBER: 60/254,108
? PRIOR FILING DATE: 2000-12-11
? PRIOR APPLICATION NUMBER: FR 00/14037
? PRIOR FILING DATE: 2000-10-31
? NUMBER OF SEQ ID NOS: 161
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 97
? LENGTH: 9870
? TYPE: DNA
? ORGANISM: Homo sapiens
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DB 219 CATTAAATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 277
QY 157 GCGAGACACACGCTGGGGCTGCTGTGAGGAGACATGATGATGATGATGATGATGATGATGATG 216
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RESULT 15
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? Sequence 97, Application US/09984827
? Publication No. US2003005624A1
? GENERAL INFORMATION:
? APPLICANT: DENEPIE, PATRICE
? APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE
? APPLICANT: ARNOULD-REQUIGNE, ISABELLE
? APPLICANT: DUVERGER, NICOLAS
? APPLICANT: CAMBIEN, FRANCOIS
? TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,
? FILE REFERENCE: 03806.0522-00000
? CURRENT APPLICATION NUMBER: US/09/984,827
? PRIOR FILING DATE: 2002-04-01
? PRIOR APPLICATION NUMBER: 60/254,108
? PRIOR FILING DATE: 2000-12-11
? PRIOR APPLICATION NUMBER: FR 00/14037
? PRIOR FILING DATE: 2000-10-31
? NUMBER OF SEQ ID NOS: 161
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 97
? LENGTH: 9870
? TYPE: DNA
? ORGANISM: Homo sapiens
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OM nucleic - nucleic search, using SW model

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(without alignments)
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Title: US-09-846-456-1

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Gapop 60.0 , Gapext 60.0

Searchcd: 2054640 seqs, 14551402878 residues

Word size : 30 *or more*
Total number of hits satisfying chosen parameters: 90357

Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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c 410	52	1.6 160915	2	AP001084	c 483	52	1.6 260967	2	AC068769	AC068769 Homo sapi
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1 (bases 1 to 201144)
Qiu, Y., Cavelier, L., Chiu, S., Yang, X., Rubin, E. and Cheng, J. F.
Human and mouse ABCA1 comparative sequencing and transgenesis
studies revealing novel regulatory sequences
Genomics 73 (1), 66-76 (2001)
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Qiu, Y., Cavelier, L., Chiu, S., Rubin, E. and Cheng, J. F.
Direct Submission
Submitted (13-JUL-2000) Genome Science Department, Lawrence
Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,
CA 94720, USA
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Prades, C., Chimini, G., Blackmon, E., Francois, I., Raverger, N.,
Rubio, E.M., Rosier, M., Deneffe, P., Fredrickson, D.S. and Brewer, H.B.
Jr.
TITLE Complete genomic sequence of the human ABCA1 gene: analysis of the
human and mouse ATP-binding cassette A Promoter
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
MEDLINE 20345099
PUBMED 10684428
REFERENCE 2 (bases 1 to 149034)
AUTHORS Santamarina-Fojo, S., Peterson, K.M., Knapper, C.L., Freeman, L.A.,
Remaley, A.T., Yang, X.-P., Haudenschild, C.C., Blackmon, E.E.,
Francois, T.L. and Brewer, H.B. Jr.
TITLE Direct Submission
JOURNAL Submitted (08-JUN-2000) Molecular Disease Branch, National
Institutes of Health, National Heart, Lung and Blood Institute,
Bethesda, MD 20892, USA
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Brown, A., Castle, A., Colangelo, M., Collins, S., Collamore, A.,
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 Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,
 Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heatford, A., Horton, L.,
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 Lehoczy, J., Lieu, C., Locke, K., MacDonald, P., Marquis, N.,
 McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Melnick, J.,
 Morrow, J., Naylor, J., Norman, C. H., O'Connor, L., O'Donnell, P.,
 Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
 Testa, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
 Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Direct Submission
 Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Apr 22, 2000 this sequence version replaced g1:6454031.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: L2510

Center Clone name: L_M10

----- Summary Statistics

Sequencing vector: M13: M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.9607s

Consensus quality: 117571 bases at least Q40

Consensus quality: 145749 bases at least Q40

Consensus quality: 166940 bases at least Q20

Insert size: 185000; agarose-gel

Insert size: 171264; sum-of-contents

Quality coverage: 2.9 in Q20 bases; agarose-gel

Quality coverage: 3.2 in Q20 bases; sum-of-contents

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 39 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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 1004 1103: gap of 100 bp
 1104 2634: contig of 1531 bp in length
 2635 2734: gap of 100 bp
 2735 4415: contig of 1681 bp in length
 4416 4515: gap of 100 bp
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 5886 7879: contig of 1994 bp in length
 7880 7979: gap of 100 bp
 7980 9686: contig of 1707 bp in length
 9687 9786: gap of 100 bp
 9787 12253: contig of 2467 bp in length
 12254 12353: gap of 100 bp
 12354 15228: contig of 2875 bp in length
 15229 15328: gap of 100 bp
 15329 17200: contig of 1872 bp in length
 17201 17300: gap of 100 bp
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 20132 20231: gap of 100 bp
 20232 22587: contig of 2356 bp in length
 22588 22687: gap of 100 bp
 22688 25707: contig of 3020 bp in length
 25708 25807: gap of 100 bp
 25808 28184: contig of 2177 bp in length
 28185 28284: gap of 100 bp

28285 31338: contig of 3054 bp in length
 31339 31438: gap of 100 bp
 31439 34299: contig of 2861 bp in length
 34300 34399: gap of 100 bp
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 38319 38418: gap of 100 bp
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 45549 48116: contig of 2568 bp in length
 48117 48216: gap of 100 bp
 48217 52618: contig of 4402 bp in length
 52619 52718: gap of 100 bp
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 56593 56692: gap of 100 bp
 56693 59635: contig of 2943 bp in length
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 59736 63661: contig of 3926 bp in length
 63662 63761: gap of 100 bp
 63762 68437: contig of 4676 bp in length
 68438 68537: gap of 100 bp
 68538 71456: contig of 2921 bp in length
 71459 71558: gap of 100 bp
 71559 76888: contig of 5330 bp in length
 76889 76988: gap of 100 bp
 76989 82113: contig of 5125 bp in length
 82114 82213: gap of 100 bp
 82214 88220: contig of 6007 bp in length
 88221 88320: gap of 100 bp
 88321 93499: contig of 5179 bp in length
 93500 93599: gap of 100 bp
 93600 97901: contig of 4302 bp in length
 97902 98001: gap of 100 bp
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 103017 103116: gap of 100 bp
 103117 109178: contig of 6062 bp in length
 109179 109278: gap of 100 bp
 109279 117307: contig of 8029 bp in length
 117308 117407: gap of 100 bp
 117408 124079: contig of 6672 bp in length
 124080 124179: gap of 100 bp
 124180 131283: contig of 7102 bp in length
 131282 131381: gap of 100 bp
 131382 148059: contig of 6678 bp in length
 148060 148159: gap of 100 bp
 148160 145491: contig of 7332 bp in length
 145492 145591: gap of 100 bp
 145592 157391: contig of 11800 bp in length
 157392 157491: gap of 100 bp
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location/Qualifiers

FEATURES

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4516..5785

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7980..9686

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 1581 AATAGTAGGAGAGAGAGAGAGATGGAAGGTGAGGAGATCTAAATATCTCTA 214

DB 1 AATTGGAGATGAGAGTGGATGGGGGGGACCGGAGAGCGGAGCGGACCGCTTCTCTCCG 60

QY 2956 GGCTGTGGTACAGGAGAGGAGGAGGAGTCTGCGGACCAACAGAGCGCGGTCTCTCAGGCGG 3015

* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be genetically and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved. 910: contig of 910 bp in length
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* 62152 63022: contig of 871 bp in length
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Best Local Similarity 99.7%; Pred. No. 1.1e-149;
Matches 342; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2895 IGGCAGCAGAGTGGGGCGGAGCCGAGAGCCGAGAGCGGAGGCTTCTCCGGG 2953
DB 87529 TGGAGCGAGTGGGGCGGAGCCGAGAGCCGAGAGCGGAGGCTTCTCCGGG 87470
QY 2959 CTCGGCAGGCGGAGGCTCCGGCGACCAACAGAGCGGCTTCTCCGGG 87418
DB 87469 CTCGGCAGGCGGAGGCTCCGGCGACCAACAGAGCGGCTTCTCCGGG 87410
QY 3019 CTCCTGTGTTTTCGGGCTTCTGTTTCTCCGCTTCCGAGGCTTCTCCGGG 3078
DB 87409 CTCCTGTGTTTTCGGGCTTCTGTTTCTCCGCTTCCGAGGCTTCTCCGGG 87350
QY 3079 AGGAGAAAGAGCGCAACACAAAGTGGAAACAGGTAAAGGCTTCTCCGGG 3138
DB 87349 AGGAGAAAGAGCGCAACACAAAGTGGAAACAGGTAAAGGCTTCTCCGGG 87290
QY 3139 TTGGCGTTATTGTTTTCGAGGCGAGGAGGCTTCCGAAAGGCTTCTCCGGG 3198
DB 87289 TTGGCGTTATTGTTTTCGAGGCGAGGAGGCTTCCGAAAGGCTTCTCCGGG 87230
QY 3199 ACTTTGATCGGAGCCCATCCCGGAGCTT 3231
DB 87229 ACTTTGATCGGAGCCCATCCCGGAGCTT 87197

RESULT 17
AX253452 AX253452 7260 bp DNA linear PAT 10-OCT-2001
DEFINITION Sequence 3 from Patent WO0170810.
ACCESSION AX253452
KEYWORDS AX253452.1 GI:16073979
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 7260)
AUTHORS Schmitz,G. and Bodzioch,M.
TITLE ATP binding cassette transporter 1 (abc1) gene polymorphisms and uses thereof for the diagnosis and treatment of lipid, cardiovascular or inflammatory disorders
JOURNAL Patent: WO 0170810-A 3 27-Sep-2001;
Hayer Aktiengesellschaft (DE)
FEATURES
Source location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 1834 a 1765 c 1905 g 1756 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.4e-119;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2887 AAACCCCGTAATTCGAGCGAGAGTGGGGCGGAGCCGAGAGCGGAGGAGCC 2946
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QY 2947 TTCTCTCCCGGCTCGGCGAGGCGAGGCGGAGGCTTCCGCAACAGAGAGCGGCTTC 3006
DB 61 TTCTCTCCCGGCTCGGCGAGGCGAGGCGGAGGCTTCCGCAACAGAGAGCGGCTTC 120

QY 3007 TCAGGGCGCTTGGCTCTCTGTTTTCGGGCTTCTGTTTTCGGGAGGC 3066
DB 121 TCAGGGCGCTTGGCTCTCTGTTTTCGGGCTTCTGTTTTCGGGAGGC 180
QY 3067 TTGTCAAGGGCTAGGAGAAAGAGACCAACACAAAAGTGGAAACAG 3114
DB 181 TTGTCAAGGGCTAGGAGAAAGAGACCAACACAAAAGTGGAAACAG 228

RESULT 18
AX351032 AX351032 221 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 4 from Patent WO0183746.
ACCESSION AX351032
VERSION AX351032.1 GI:18616388
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE Rosier-Montus,M.F., Prades,C., Lemoline,C., Naudin,L., Deneffe,P., Brewer,B., Duverger,N., Remaley,A. and Santamarina-Fojo,S.
JOURNAL Regulatory nucleic acid sequences of the abc1 gene
Patent: WO 0183746-A 4 08-NOV-2001;
Aventis Pharma S.A. (FR)
FEATURES
Source location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 44 a 62 c 73 g 42 t
ORIGIN

Query Match 6.8% Score 221; DB 6; Length 221;
Best Local Similarity 100.0%; Pred. No. 7.1e-115;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2894 GTAATTCGAGCGAGAGTGGGGCGGAGCCGAGAGCGGAGCCGAGCCCTTCTCTC 2953
DB 1 GTAATTCGAGCGAGAGTGGGGCGGAGCCGAGAGCGGAGCCCTTCTCTC 60
QY 2954 CCGGCTCGGCGAGGCGGAGGCTCCGCGACCAACAGAGCGGTTCTCAGGCG 3013
DB 61 CCGGCTCGGCGAGGCGGAGGCTCCGCGACCAACAGAGCGGTTCTCAGGCG 120
QY 3014 GCCTTGTCTCTGTTTTCGGGCTTCTGTTTTCGGGAGGCTTCTCAA 3073
DB 121 GCCTTGTCTCTGTTTTCGGGCTTCTGTTTTCGGGAGGCTTCTCAA 180
QY 3074 GGGTAGAGAAAGAGAGCGCAACACAAAAGTGGAAACAG 3114
DB 181 GGGTAGAGAAAGAGAGCGCAACACAAAAGTGGAAACAG 221

RESULT 19
AK024328 AK024328 1556 bp mRNA linear PRI 01-AUG-2002
DEFINITION Homo sapiens CDNA FLJ14266 fis, clone PLACE1002437, highly similar to ATP-BINDING CASSETTE TRANSPORTER 1.
ACCESSION AK024328
VERSION AK024328.1 GI:10436685
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens placenta cDNA to mRNA, clone PLACE1002437.
clone:PLACE1002437.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

QY 3074 GGGTAGAGAAAGAGAGCGCAACACAAAAGTGGAAACAG 3114
DB 181 GGGTAGAGAAAGAGAGCGCAACACAAAAGTGGAAACAG 221


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QY 3090 ACGCAACACAAAAGTGGAAACAG 3114
Db 181 ACGCAACACAAAAGTGGAAACAG 205

RESULT 22
AX060713 10442 bp DNA linear PAT 22-JAN-2001
LOCUS Sequence 1 from Patent W00078972.
DEFINITION
ACCESSION AX060713
VERSION AX060713.1 GI:12406103
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 10442)
AUTHORS Lawn,R.M., Wade,D., and Garvin,M.
TITLE Regulation with binding cassette transporter protein abcl
JOURNAL Patent: WO 0078972-A 1 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
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/db_xref="taxon:9606"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.4e-101;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCGCGGACCGGACGAGCGGACCGCTTCTCTCCGGGCTGCGGAGCGAGCGGGCGG 60

QY 2978 GGAGCTCCCGGACCAACAGCGGCTTCTCAGGGCGCTTTGCTCTCTTTTCCCGG 3037
Db 61 GGAGCTCCCGGACCAACAGCGGCTTCTCAGGGCGCTTTGCTCTCTTTTCCCGG 120

QY 3038 GTTCTGTTTTCCTCCCTTCTCCGGAGCGCTTGTCAAGGGGTAGGAAAGACGCAAC 3097
Db 121 GTTCTGTTTTCCTCCCTTCTCCGGAGCGCTTGTCAAGGGGTAGGAAAGACGCAAC 180

QY 3098 ACAAAGTGGAAACAG 3114
Db 181 ACAAAGTGGAAACAG 197

RESULT 24
AF285167 10442 bp mRNA linear PRI 09-AUG-2000
LOCUS Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA.
DEFINITION complete cds.
ACCESSION AF285167
VERSION AF285167.1 GI:9755158
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 10442)
AUTHORS Schwartz,K., Lawn,R.M. and Wade,D.P.
TITLE ABCA1 gene expression and apoA-I-mediated cholesterol efflux are
regulated by LXR
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 10442)
AUTHORS Lawn,R.M., Wade,D.P., Garvin,M.R., Wang,X., Schwartz,K.,
Porter,J.G., Seilhamer,J.J., Vaughan,A.M. and Oram,J.F.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-2000) Discovery Research, CV Therapeutics Inc.,
3172 Porter Drive, Palo Alto, CA 94304, USA
FEATURES
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291..7076
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KEKLAARVLRSDILKPIRLTLNSTSPRPSKLEAATKTLHSLCTLAQLFSMR
SHSDMRQEVMLFTNVNSSSTOITQAVSRVCGHPEGGGLKIKSLNWDNNTKALF
GGNGTEEDAEETFDVNSTTPYCNDLKNLESPKTIWKALKPLLVKRLDTPDPAT
RQVMAEVNKTFOELAVFHDLCEHMEELSPKTIWTFMNSQENDLYRMCLDSNDHFWE
CQLGLDVTADIVAFIAKHPEDVDSNGSVITWREAFNETNOAIRTISRMECVNLN
KLEPIATEVMJLNKSMELLDERKFWAGIVFTGPTGSELPHVYKIKRMDIDNVRT
NKIKDGYWUPGPRADPFEDMRVWGGFAYLDQVYEOAIIPLVTCTEKTGTYVMQMPY
PCYVDIIFLRVMSRSHPLMTLAWIYSVAVIKIGIVTEKARLKETMHRIMGLDNLILW
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Db 121 TTTCCCGGCTTCTGTTTCTCCCTTCTCCGGAGCGCTTGTCAAGGGGTAGGAAAGAG 180
QY 3090 ACGCAACACAAAAGTGGAAACAG 3114
Db 181 ACGCAACACAAAAGTGGAAACAG 205

RESULT 22
AX060713 10442 bp DNA linear PAT 22-JAN-2001
LOCUS Sequence 1 from Patent W00078972.
DEFINITION
ACCESSION AX060713
VERSION AX060713.1 GI:12406103
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 10442)
AUTHORS Lawn,R.M., Wade,D., and Garvin,M.
TITLE Regulation with binding cassette transporter protein abcl
JOURNAL Patent: WO 0078972-A 1 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
Source
1..10442
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2898 a 2297 c 2408 g 2835 t 4 others
ORIGIN

Query Match 6.1%; Score 197; DB 6; Length 10442.
Best Local Similarity 100.0%; Pred. No. 6.4e-101;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2918 GCGCGGACCGGACGAGCGGACCGCTTCTCTCCGGGCTGCGGAGCGAGCGGGCGG 2977
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QY 2978 GGAGCTCCCGGACCAACAGCGGCTTCTCAGGGCGCTTTGCTCTCTTTTCCCGG 3037
Db 61 GGAGCTCCCGGACCAACAGCGGCTTCTCAGGGCGCTTTGCTCTCTTTTCCCGG 120

QY 3038 GTTCTGTTTTCCTCCCTTCTCCGGAGCGCTTGTCAAGGGGTAGGAAAGACGCAAC 3097
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QY 3098 ACAAAGTGGAAACAG 3114
Db 181 ACAAAGTGGAAACAG 197

RESULT 24
AX060892 10442 bp DNA linear PAT 22-JAN-2001
LOCUS Sequence 1 from Patent W00078971.
DEFINITION
ACCESSION AX060892
VERSION AX060892.1 GI:12406270
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 10442)
AUTHORS Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
TITLE ATP binding cassette transporter protein abcl polypeptides
JOURNAL Patent: WO 0078971-A 1 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
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BASE COUNT 2898 a 2297 c 2408 g 2835 t 4 others
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 3903 3902: gap of 100 bp
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 4917 5759: contig of 843 bp in length
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 5860 6764: contig of 905 bp in length
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 6865 7747: contig of 883 bp in length
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 8856 9753: contig of 898 bp in length
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 49381 50250: contig of 870 bp in length
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 50351 51209: contig of 859 bp in length
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Query Match
 Best Local Similarity 99.28; Score 152; DB 2; Length 90698;
 Matches 252; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Db 10237 ACAAAGGTGAACTCCATCTCAATTAAAAAAGAAAGATTTTGGTGGTCACTTCA 10296
 QY 155 AATAGTAGCAGAGAGAGAGAGAGAGAGATGGAGGTCACAGAGACTAATTATCTCTCA 214
 Db 10297 AATAGTAGCAGAGAGAGAGAGAGAGATGGAGGTCACAGAGACTAATTATCTCTCA 10356
 QY 215 AATATCATCTAGGAAGATAACACCTTTTAAATACACTCTCTGCTTTTATAACATCATTC 274
 Db 10457 AATATCATCTAGGAAGATAACACCTTTTAAATACACTCTCTGCTTTTATAACATCATTC 10416
 QY 275 TGCCAAGGACTCA 288
 Db 10417 TGCCAAGGACTCA 10430

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 DEFINITION Sequence 6 from Patent WO0183746.
 ACCESSION AX351034
 VERSION AX351034.1 GI:18616390
 KEYWORDS human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 Rosier-Montus,M.F., Prades,C., Lemoine,C., Naudin,L., Deneffe,P.,
 Brewer,B., Duverger,N., Remaley,A. and Santamarina-Fojo,S.
 Regulatory nucleic acid sequences of the abcl gene
 Patent: WO 0183746-A 6 08 NOV-2001;
 Aventis Pharma S.A. (FR)

FEATURES
 source
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 20 a 30 c 34 g 13 t
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 DEFINITION Sequence 3 from Patent WO0130848.
 ACCESSION AX127764
 VERSION AX127764.1 GI:14134411
 KEYWORDS
 SOURCE
 synthetic construct.
 synthetic construct
 artificial sequences.
 1 (bases 1 to 446)
 Deneffe,P., Rosier-Montus,M.F., Arnould-Reguinne,I., Prades,C.,
 Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,G.H.,
 Remaley,A., Brewer,H.B. and Dean,M.
 Nucleic acids of the human abcl gene and their therapeutic and
 diagnostic application
 Patent: WO 0130848-A 3 03-MAY-2001;
 Aventis Pharma S.A. (FR)

FEATURES
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RESULT 32
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 DEFINITION Sequence 3 from Patent EP1096012.
 ACCESSION AX139751
 VERSION AX139751.1 GI:14275333
 KEYWORDS
 SOURCE
 synthetic construct.
 synthetic construct
 artificial sequences.
 1 (bases 1 to 446)
 Deneffe,P., Rosier-Montus,M.F., Arnould-Reguinne,I., Prades,C.,
 Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,I.,G.H.,
 Remaley,A., Brewer,H.B. and Dean,M.
 Nucleic acids of the human abcl gene and their therapeutic and
 diagnostic application
 Patent: EP 1096012-A 3 02-MAY-2001;
 Aventis Pharma S.A. (FR)

FEATURES
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QY 3023 CTTCCTTTTCCCGGGTCTGCTTTCTCCCTTCTCCGAGGCTTGTCAAGGGGTAGCA 3082
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RESULT 33
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 DEFINITION Sequence 69 from Patent WO0130848.
 ACCESSION AX127830
 VERSION AX127830.1 GI:14134477
 KEYWORDS
 SOURCE
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 Deneffe,P., Rosier-Montus,M.F., Arnould-Reguinne,I., Prades,C.,

Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G. H.,
 Remaley, A., Brewer, H. B. and Dean, M.
 Nucleic acids of the human abcl gene and their therapeutic and
 diagnostic application
 Patent: WO 0130848-A 69 03-MAY-2001;
 Aventis Pharma S.A. (FR)
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 1. 9741
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 DEFINITION
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 1 (bases 1 to 9741)
 Rosier, P., Rosier-Montus, M.F., Arnold-Requigne, I., Prades, C.,
 Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G. H.,
 Remaley, A., Brewer, H. B. and Dean, M.
 Nucleic acids of the human abcl gene and their therapeutic and
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 Patent: EP 1096012-A 69 02-MAY-2001;
 Aventis Pharma S.A. (FR)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 9741)
 Rosier, P., Rosier-Montus, M.F., Arnold-Requigne, I., Prades, C.,
 Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G. H.,
 Remaley, A., Brewer, H. B. and Dean, M.
 Nucleic acids of the human abcl gene and their therapeutic and
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 Patent: EP 1096012-A 69 02-MAY-2001;
 Aventis Pharma S.A. (FR)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 126295)
 Birren, R., Linton, L., Nusbaum, C. and Lander, E.
 Homo sapiens chromosome 17, clone HRPC843B9, complete sequence.
 Unpublished
 2 (bases 1 to 126295)
 Birren, R., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P.,
 Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckery, R.,
 Boutwell, C., Byrne, S., Cantu, C., Castle, A., Cerny, J., Cooke, P.,
 Daly, M., Depayre, E., Devon, K., Dewar, K., Donelan, L., Durette, B.,
 Etmadi, S., Ferreira, P., Forrest, C., Funke, R., Gage, D., Gardyna, S.,
 Gensheimer, S., Geraghty, K., Gilmartin, T., Gray, D., Hagos, H.,
 Harris, K., Horton, L., Howland, J., Hul, L., Jacotot, L., Linton, L.,
 McKenzie, J., Marquis, N., McEwan, P., McGurk, A., Meidrim, J.,
 Molla, M., Morris, W., Morrow, J., Nachman, A., Naylor, J., O'Connor, T.,
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 Rollins, G., Rossello, R., Roy, A., Shyam, R., Soohoo, S.,
 Stange-Thomann, N., Stillwell, J., Stone, C., Strickland, C., Sydney, K.,
 Tang, J., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y.,
 Ye, W., Zemseval, I., Zhao, J. and Zody, M.
 Direct Submission
 Submitted (13-FEB-1998) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 126295)
 Birren, R., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
 Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckery, R., Benn, J.,
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 Devon, K., Dewar, K., Donelan, L., Ferreira, P., FitzHugb, W.,
 Forrest, C., Funke, R., Gage, D., Gardyna, S., Geraghty, K., Grant, G.,
 Hagos, H., Headford, A., Herena, L., Horton, L., Howland, J., C.,
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ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Rosier, P., Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denelle, P.,
 Brewer, H., Duverger, N., Remaley, A. and Santamarina-Fojo, S.
 Regulatory nucleic acid sequences of the abcl gene
 Patent: WO 0183746-A 10 08-NOV-2001;
 Aventis Pharma S.A. (FR)
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 QY 3023 CTGTGTTTTCCTGTTCTCTCTCCCTCTCTCGGAGGCTTGTCAAGGGGTAGGA 3082
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 DB 61 GAAAGAGCGCAACACAAAAGTGGAAACAG 92
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 KEYWORDS
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 126295)
 Birren, R., Linton, L., Nusbaum, C. and Lander, E.
 Homo sapiens chromosome 17, clone HRPC843B9
 Unpublished
 2 (bases 1 to 126295)
 Birren, R., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P.,
 Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckery, R.,
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 Daly, M., Depayre, E., Devon, K., Dewar, K., Donelan, L., Durette, B.,
 Etmadi, S., Ferreira, P., Forrest, C., Funke, R., Gage, D., Gardyna, S.,
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 Harris, K., Horton, L., Howland, J., Hul, L., Jacotot, L., Linton, L.,
 McKenzie, J., Marquis, N., McEwan, P., McGurk, A., Meidrim, J.,
 Molla, M., Morris, W., Morrow, J., Nachman, A., Naylor, J., O'Connor, T.,
 Pavlin, B., Peterson, K., Ranganath, S., Riley, R., Roberts, D.,
 Rollins, G., Rossello, R., Roy, A., Shyam, R., Soohoo, S.,
 Stange-Thomann, N., Stillwell, J., Stone, C., Strickland, C., Sydney, K.,
 Tang, J., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y.,
 Ye, W., Zemseval, I., Zhao, J. and Zody, M.
 Direct Submission
 Submitted (13-FEB-1998) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 126295)
 Birren, R., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
 Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckery, R., Benn, J.,
 Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M.,
 Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E.,
 Devon, K., Dewar, K., Donelan, L., Ferreira, P., FitzHugb, W.,
 Forrest, C., Funke, R., Gage, D., Gardyna, S., Geraghty, K., Grant, G.,
 Hagos, H., Headford, A., Herena, L., Horton, L., Howland, J., C.,
 Jacotot, L., Jones, C., Kann, L., Karatas, A., Lehoczy, J.,
 Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
 Meidrim, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J.,

Nahf, R., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P.,
 Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P.,
 Stange-Thomann, N., Stilwell, J., Stojanovic, N., Store, C.,
 Subramanian, A., Testave, S., Tichovolsky, N., Torruella-Miller, I.,
 Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D.,
 Ye, W. J., Zhao, J. and Zody, M.
 Direct Submission
 Submitted (02-SEP-1998) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Sep 2, 1998 this sequence version replaced qi:3451370.
 All repeats were identified using RepeatMasker: Smit, A.F.A. &
 Green, P. (1996-1997)
<http://ftp.genome.washington.edu/HW/RepeatMasker.html>.

FEATURES

Source

Location/Qualifiers

1..126295

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/complement(714..1012)

/rpt_family="AluSc"

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/rpt_family="L2"

/complement(2503..2646)

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/complement(2647..2954)

/rpt_family="AluJb"

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3758..4544

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4743..4873

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/complement(5068..5364)

/rpt_family="AluJb"

/complement(6403..6675)

/rpt_family="AluSx"

6782..6950

/rpt_family="MIR"

/complement(7379..7744)

/rpt_family="Tigger1"

/complement(7735..7840)

/rpt_family="(GGGA)n"

/complement(7841..7876)

/rpt_family="purine-rich"

/complement(7883..7988)

/rpt_family="Tigger1"

/complement(7989..8597)

/rpt_family="Tigger1"

/complement(8604..8741)

/rpt_family="FLAM_C"

/complement(8759..9456)

/rpt_family="Tigger1"

/complement(9467..9759)

/rpt_family="AluSx"

/complement(9820..10276)

/rpt_family="Tigger1"

10754..11095

/rpt_family="MER47A"

/complement(11106..11949)

/rpt_family="L2"

12033..12147

/rpt_family="LMC2"

12148..12235

/rpt_family="LMC2"

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 repeat_region 13224..13251
 /rpt_family="MIR"
 repeat_region 13252..13544
 /rpt_family="AluSg"
 repeat_region 13545..13769
 /rpt_family="MIR"
 repeat_region 14208..14364
 /rpt_family="MER5A"
 repeat_region complement(14835..15195)
 /rpt_family="LMC2"
 repeat_region complement(15353..15497)
 /rpt_family="L2"
 repeat_region complement(15662..15828)
 /rpt_family="MLTIC"
 repeat_region complement(16301..16607)
 /rpt_family="AluY"
 repeat_region 17500..17802
 /rpt_family="AluSx"
 repeat_region complement(18474..18774)
 /rpt_family="AluSg"
 repeat_region 18825..18902
 /rpt_family="MIR"
 repeat_region complement(19636..19771)
 /rpt_family="MER20"
 repeat_region 19834..20129
 /rpt_family="AluSp"
 repeat_region complement(20145..20168)
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 repeat_region complement(20169..20451)
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 repeat_region complement(20456..20765)
 /rpt_family="AluSg"
 repeat_region complement(21023..21343)
 /rpt_family="LIM4"
 repeat_region 21344..21630
 /rpt_family="AluSx"
 repeat_region complement(21631..21700)
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 repeat_region 22291..22526
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 repeat_region 23606..23899
 /rpt_family="AluJo"
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 repeat_region 27712..28009
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 repeat_region complement(31041..31353)
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 repeat_region complement(32362..32571)
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 repeat_region complement(33470..33781)

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complement(35504..35774)
/rpt_family="L1ME3A"
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/rpt_family="AluJo"
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36204..36516
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complement(36689..37629)

Query Match      2.0%  Score 65;  DB 9;  Length 25295;
Best local Similarity 100.0%;  Pred. No. 6.1e-25;
Matches 65;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 1017 GATCTCGACTCACTGACCTGCTCCCTCCCGGTTCAAGGATTCCTGCTGAGCTC 1076
|||||
DB 31115 GATCTCGACTCACTGACCTGACCTGCTCCCGGTTCAAGGATTCCTGCTGAGCTC 31174

QY 1077 CTGAG 1081
|||||
DB 31175 CTGAG 31179

RESULT 37
AL807243/c
LOCUS
DEFINITION
MUS MUSCULUS CHROMOSOME 4 CLONE RP23-25D17. *** SEQUENCING IN
PROGRESS ***, 24 unordered pieces.
ACCESSION
AL807243
VERSION
AL807243.5 Gi:21668234
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 186889)
Melay, K.
Direct Submission
Submitted (29-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Jul 2, 2002 this sequence version replaced qt.21668136.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: BM25D17
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% G; reads
Consensus quality: 175959 bases at least Q40
Consensus quality: 179463 bases at least Q30
Consensus quality: 182069 bases at least Q20
Insert size: 184589; sum-of-contrigs
Insert size: 189466; 5.5% error; average-tp
Quality coverage: 4.72x in Q20 bases; sum-of-contrigs Quality
coverage: 4.82x in Q20 bases; average-tp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
*
* 1 4849: contig of 4849 bp in length
* 4850 4949: gap of 100 bp

FEATURES
Source
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/db_xref="taxon:10090"
/chromosome="4"
/clone="RP23-25D17"
/clone_lib="RPC1-23"
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fragment_chain:1"
4950..22620
/note="assembly fragment:01761
fragment_chain:1"
22721..29963
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fragment_chain:1"
30064..40087
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fragment_chain:1"
40188..44438
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44539..48960
/note="assembly fragment:01430
fragment_chain:1"
49061..56007
/note="assembly fragment:01667
fragment_chain:1"
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22621 22720: gap of 100 bp
22721 29963: contig of 7243 bp in length
29964 30063: gap of 100 bp
30064 40087: contig of 10024 bp in length
40088 40187: gap of 100 bp
40188 44438: contig of 4251 bp in length
44439 44538: gap of 100 bp
44539 48960: contig of 4422 bp in length
48961 49060: gap of 100 bp
49061 56007: contig of 6947 bp in length
56008 56107: gap of 100 bp
56108 58284: contig of 2177 bp in length
58285 58384: gap of 100 bp
58385 60786: contig of 2402 bp in length
60787 60886: gap of 100 bp
60887 66707: contig of 5821 bp in length
66708 66807: gap of 100 bp
66808 92102: contig of 25295 bp in length
92103 92202: gap of 100 bp
92203 99909: contig of 7707 bp in length
99910 100009: gap of 100 bp
100010 103760: contig of 3751 bp in length
103761 103860: gap of 100 bp
103861 110765: contig of 6905 bp in length
110766 110865: gap of 100 bp
110866 114785: gap of 100 bp
114786 125959: contig of 11174 bp in length
125960 126059: gap of 100 bp
126060 128749: contig of 2690 bp in length
128750 128849: gap of 100 bp
128850 132373: contig of 3524 bp in length
132374 132473: gap of 100 bp
132474 134930: contig of 2457 bp in length
134931 135030: gap of 100 bp
135031 139301: contig of 4271 bp in length
139302 139401: gap of 100 bp
139402 144448: contig of 5047 bp in length
144449 144548: gap of 100 bp
144549 147074: contig of 2526 bp in length
147075 147174: gap of 100 bp
147175 156317: contig of 9143 bp in length
156318 156417: gap of 100 bp
156418 186889: contig of 30472 bp in length.

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3775..4559
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repeat_region 24706..24903
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repeat_region 28709..28781
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repeat_region 29420..29635
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repeat_region 29979..30116
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repeat_region 30773..31036
/rpt_family="L2"
repeat_region 31039..31722
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repeat_region 32160..32333
/rpt_family="CR1"
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repeat_region 34248..34275
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 Best Local Similarity 100.0%; Pred. No. 1.3e-22;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1017 GATCGGAGTCACTGTAACCTGCTCCCGGGTTCAAGCGATTCTCCCTCAGCCCTC 1076
 |||||||.....
 DB 45729 GATCTCGAGTACGTAACTCTGCTCCCGGGTTCAAGCGATTCTCCCTCAGCCCTC 45670

QY 1077 C 1077
 DE 45669 C 45659

RESULT 59

AF287263

LOCUS AF287263 278572 bp DNA linear ROD 23-APR-2001
 DEFINITION Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abca1)
 gene, complete cds.

ACCESSION AF287263

VERSION AF287263.1 GI:11611824

KEYWORDS

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 278572)
 AUTHORS Chou, Y., Goodfellow, L., Chiu, S., Yang, X., Rubin, E. and Chong, J. P.

Raymond, C., Retta, R., Kieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triplio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zempek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (29-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 44897)

REFERENCE
AUTHORS
Barn, N., Bastien, V., Bloom, E., Ali, A., Allen, N., Anderson, S., Camarata, J., Chang, J., Chazaro, B., Choepey, Y., Collymore, A., Cook, A., Cooke, P., DeFellano, K., Dewar, R., Diaz, J. S., Dodge, S., Fato, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, J., Levine, R., Lisblad-Toh, K., Liu, G., MacLean, C., MacDonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Meneses, J., Minoda, T., Miodini, V., Murphy, J., Naylor, J., Nguyen, C., Nicol, R., Nerbo, C., Norman, C. R., O'Connor, F., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zempek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 30, 2002 this sequence version replaced a:17149709.
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www.seq.wi.mit.edu>
Contact: submissions@genome.wi.mit.edu
Project information
Project name: 121814
Center project name: 2319_014
Center Clone name: 2319_014

NOTE: This record contains 54 individual:
• sequencing reads that have not been assembled into
• contigs. Runs of N are used to separate the reads
• and the order in which they appear is completely
• arbitrary. Low-pass sequence sampling is useful for
• identifying clones that may be over-represented and allows
• overlap relationships among clones to be deduced.
• However, it should not be assumed that this clone
• will be sequenced to completion. In the event that
• the record is updated, the accession number will
• be preserved.

1 734: contig of 74 bp in length
735 834: gap of 100 bp
835 1552: contig of 718 bp in length
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1653 2405: contig of 753 bp in length
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2506 3239: contig of 714 bp in length
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4195 4930: contig of 736 bp in length
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5854 6627: contig of 774 bp in length
6628 6727: gap of 100 bp
6728 7449: contig of 722 bp in length

7450 7549: gap of 100 bp
7550 8322: contig of 773 bp in length
8323 8422: gap of 100 bp
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9127 9226: gap of 100 bp
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9974 10073: gap of 100 bp
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15817 16563: contig of 747 bp in length
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21642 22399: contig of 758 bp in length
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23237 23336: gap of 100 bp
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* 52108 52207: gap of 100 bp
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* 52910 53009: gap of 100 bp
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Query Match 1.8%; Score 58; DB 2; Length 57662;

Best Local Similarity 100.0%; Pred. No. 6e-21;

Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGGATTACGATGAGCCACTGCGCCAGC 1244

DB 39017 CTGCCACCTTGGCTCCCAAGTCTGGGATTACGATGAGCCACTGCGCCAGC 38960

RESULT 42

HS931E15/C

LOCUS HS931E15 81874 bp DNA linear PRI 23-NOV-1999

Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSS, GSSs and genomic marker DXS8098, complete sequence.

AL023575

VERSION AL023575.1 GI:3618163

KEYWORDS HTG; DXS8098.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 81874)

Pavitt, R.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (24-SEP-1998) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

requests: clonerequest@sanger.ac.uk

On Sep 18, 1998 this sequence version replaced gi:3550203.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence has been finished according to sequence map criteria

as follows. An attempt is made to resolve all sequencing problems,

such as compressions and repeats, but not necessarily within known

annotated human repeat sequence elements (e.g. Alu). Where the

sequence is ambiguous, there is an annotation using the 'unsure'

feature key.

This sequence was generated from part of bacterial clone contigs of

human chromosome X, constructed by the Sanger Centre Chromosome X

Mapping Group. Further information can be found at

http://www.sanger.ac.uk/HGP/ChrX

931E15 is from the library RPC15 constructed at the Roswell Park

Cancer Institute by the group of Pieter de Jong. For further

details see http://bacpac.med.buffalo.edu/VECTOR: prYPAC2

IMPORTANT: This sequence is not the entire insert of clone 931E15.

It may be shorter because we only sequence overlapping sections

once, or longer because we arrange for a small overlap between

neighbouring submissions.

The true left end of 424312 (282207) is at 36643 in this sequence.

The true right end of 506G2 (282213) is at 37431.

Location/Qualifiers

1..81874

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/chromosome="X"
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/clone="RP5-931K15"
/clone_lib="RC1-5"
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complement(228..531)
/feature="AluX repeat: matches 292..3 of consensus"
569..687
/feature="AluJ repeat: matches 11..127 of consensus"
702..1002
/feature="AluSp repeat: matches 1..42 of consensus"
1010..1178
/feature="FRAM repeat: matches 5..166 of consensus"
complement(1365..1664)
/feature="match: STS G05254"
2391..2691
/feature="AluX repeat: matches 1..300 of consensus"
2767..3067
/feature="AluJ repeat: matches 1..302 of consensus"
complement(4220..4537)
/feature="AluJ repeat: matches 300..1 of consensus"
4701..5004
/feature="AluJ repeat: matches 2..302 of consensus"
5170..5497
/feature="L1 repeat: matches 3627..3956 of consensus"
5498..5643
/feature="AluS repeat: matches 1..146 of consensus"
5644..5948
/feature="AluY repeat: matches 1..301 of consensus"
5950..6115
/feature="AluS repeat: matches 133..290 of consensus"
6156..6393
/feature="L1 repeat: matches 1985..4249 of consensus"
6629..6979
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6978..7073
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complement(7078..7139)
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7238..7675
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7678..7969
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7970..8091
/feature="L1 repeat: matches 5150..5270 of consensus"
8094..8396
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8400..8615
/feature="L1 repeat: matches 47..276 of consensus"
8616..8733
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8743..8816
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8856..9146
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9152..9362
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9365..9667
/feature="AluJ repeat: matches 1..302 of consensus"
9668..10289
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10710..11004
/feature="AluX repeat: matches 7..301 of consensus"
11299..11939
/feature="L1 repeat: matches 271..910 of consensus"
11983..12087
/feature="L1 repeat: matches 6..109 of consensus"
12100..12401
/feature="AluX repeat: matches 4..302 of consensus"
12439..12940
/feature="L1 repeat: matches 166..685 of consensus"
complement(13266..13588)
/feature="match: STS L40936"
13604..13904
/feature="AluX repeat: matches 2..302 of consensus"
13958..14050
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14055..14323
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14514..14836
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15126..15428
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16118..16420
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complement(16828..16935)
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complement(17160..17224)
/feature="MIR repeat: matches 149..84 of consensus"
18120..18226
/feature="match: STS L24586"
complement(18124..18827)
/feature="match: GSS B16853 B14990"
complement(19178..19676)
/feature="AluS repeat: matches 303..2 of consensus"
19901..20160
/feature="AluY repeat: matches 39..298 of consensus"
complement(20716..20882)
/feature="MIR repeat: matches 260..69 of consensus"
complement(20824..21385)
/feature="match: GSS B94184 A010265"
21550..23628
/feature="putative CpG island"
complement(22542..22581)
/feature="MIR repeat: matches 134..95 of consensus"
complement(23094..24185)
/feature="SVA repeat: matches 1101..1 of consensus"
24186..24211
/feature="23 copies 2 mer aa 80% conserved"
24520..24884
/feature="L1 repeat: matches 517..890 of consensus"
complement(25504..25687)
/feature="MER2 repeat: matches 155..1 of consensus"
26421..26484
/feature="32 copies 2 mer tt 83% conserved"
complement(26486..26661)
/feature="AluJ repeat: matches 3..300 of consensus"
26867..27164
/feature="AluY repeat: matches 3..302 of consensus"
27165..27462
/feature="AluS repeat: matches 2..302 of consensus"
28080..28392
/feature="AluX repeat: matches 1..298 of consensus"
complement(28817..29089)
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29122..29252
/feature="L1 repeat: matches 3151..3280 of consensus"
complement(29957..30200)
/feature="L1 internal repeat: matches 5375..5124 of consensus"
complement(30513..30706)
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30728..31025
/feature="AluX repeat: matches 1..299 of consensus"
31059..31356
/feature="AluS repeat: matches 1..296 of consensus"
31359..31505
/feature="MER4B repeat: matches 11..148 of consensus"

```


Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trifunovic, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J. Young, G., Zainoun, J., Zembe, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 145264)
 Hirren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Bonaslucki, L., Boukhalter, B., Brown, A., Camarata, J., Camparano, A., Chang, A., Chazaro, B., Choepel, Y., Colanquillo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArillano, K., Dewar, K., Diaz, J., Dodge, S., Eero, S., Ferreira, P., FitzHugh, W., Gage, D., Gallant, J., Gandy, N., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hayes, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karakas, A., Kells, C., Lakoque, K., Lankar, R., Landers, T., Lehocsky, J., Levine, K., Lindblad-Toh, K., Lin, J., MacDonald, C., McDonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Melnick, J., Menees, C., Mihova, T., Mlenga, V., Murphy, T., Nayler, J., Nguyen, C., Nicol, K., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierce, N., Peltara, V., Raymond, C., Retta, R., Rieback, M., Riley, K., Riste, E., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trifunovic, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J. Young, G., Zainoun, J., Zembe, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 4 (bases 1 to 145264)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Bonaslucki, L., Boukhalter, B., Brown, A., Camarata, J., Camparano, A., Chang, A., Chazaro, B., Choepel, Y., Colanquillo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArillano, K., Dewar, K., Diaz, J., Dodge, S., Eero, S., Ferreira, P., FitzHugh, W., Gage, D., Gallant, J., Gandy, N., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hayes, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karakas, A., Kells, C., Lakoque, K., Lankar, R., Landers, T., Lehocsky, J., Levine, P., Lindblad-Toh, K., Lin, J., MacDonald, C., McDonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Melnick, J., Menees, C., Mihova, T., Mlenga, V., Murphy, T., Nayler, J., Nguyen, C., Nicol, K., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierce, N., Peltara, V., Raymond, C., Retta, R., Rieback, M., Riley, K., Riste, E., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trifunovic, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J. Young, G., Zainoun, J., Zembe, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (31-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 31, 2002 this sequence version replaced at: 14526475.
 All repeats were identified using RepeatMasker.
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/SW/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Web site: http://www.seq.w.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L24318
 Center clone name: 48_0_9

FEATURES
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 /db_xref="taxon:9606"
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 /map="11"
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 /clone_lib="RPC1-11 Human Male BAC"
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 905..1010
 /rpt_family="LIMC4"
 1129..1151
 /rpt_family="AT-rich"
 1200..1507
 /rpt_family="AluX"
 2953..3126
 /rpt_family="AluSg/x"
 3285..3573
 /rpt_family="AluX"
 3585..3886
 /rpt_family="AluSg"
 3996..4372
 /rpt_family="MLT11"
 4436..4618
 /rpt_family="MER104"
 5800..5866
 /rpt_family="AluJo"
 6046..6122
 /rpt_family="L2"
 6264..6550
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 complement(6681..6986)
 /rpt_family="AluJb"
 complement(6987..7057)
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 complement(7446..7635)
 /rpt_family="L3PA13"
 7636..7923
 /rpt_family="LIM4"
 7953..8962
 /rpt_family="AluJo/FLAM"
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 8189..8244
 /rpt_family="LIM4"
 8245..8517
 /rpt_family="AluY"
 8518..8584
 /rpt_family="LIM4"
 8585..8877
 /rpt_family="AluJb"
 8878..9031
 /rpt_family="LIM4"
 complement(9033..9150)
 /rpt_family="FLAM_A"
 9410..10353
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 complement(10428..10725)
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 13442..13525
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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: I3990
Center clone name: 21.E.12
----- Summary Statistics -----
Sequencing vector: M13; M77815; 38 of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 142529 bases at least Q4C
Consensus quality: 144014 bases at least Q30
Consensus quality: 144580 bases at least Q20
Insert size: 128000; agarose-fp
Insert size: 145212; sum-of-contigs
Quality coverage: 9.4 in Q20 bases; agarose-fp
Quality coverage: 8.3 in Q20 bas.
* NOTE: this is a working draft sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1732: contig of 1732 bp in length
* 1733 1832: gap of 100 bp
* 1833 2945: contig of 1113 bp in length
* 2946 3045: gap of 100 bp
* 3046 4116: contig of 1071 bp in length
* 4117 4216: gap of 100 bp
* 4217 5757: contig of 1541 bp in length
* 5758 5857: gap of 100 bp
* 5858 7545: contig of 1688 bp in length
* 7546 7645: gap of 100 bp
* 7646 11527: contig of 3882 bp in length
* 11528 11627: gap of 100 bp
* 11628 55477: contig of 43850 bp in length
* 55478 55577: gap of 100 bp
* 55578 66767: contig of 11190 bp in length
* 66768 66867: gap of 100 bp
* 66868 83973: contig of 17106 bp in length
* 83974 84073: gap of 100 bp
* 84073 107174: contig of 23101 bp in length
* 107175 107274: gap of 100 bp
* 107275 137395: contig of 30121 bp in length
* 137396 147495: gap of 100 bp
* 147496 146312: contig of 8817 bp in length.
* Location/Qualifiers
* 1. 146312
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* /db_xref="taxon:9606"
* /clone="RP11-21E12"
* /clone_lib="RPC1-11 Human Male BAC"
* 1. 1732
* /note="Assembly_fragment"
* clone_end:SP6
* vector_side:left
* 1833..2945
* /note="assembly_fragment"
* 3046..4116
* /note="assembly_fragment"
* 4217..5757
* /note="assembly_fragment"
* 5858..7545
* /note="assembly_fragment"
* 7646..11527
* /note="assembly_fragment"
* 11628..55477
* /note="assembly_fragment"
* 55578..66767

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misc_feature /note="assembly_fragment"
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misc_feature /note="assembly_fragment"
107275..137395
misc_feature /note="assembly_fragment"
137496..146312
misc_feature /note="assembly_fragment"
clone_end:T7
vector_side:right"

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BASE COUNT 37492 a 36284 c 35592 g 45732 t 1112 others

Query Match 1.8%; Score 58; DB 2; Length 146312;

Best local Similarity 100.0%; Pred. No. 6.6e-21; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTGTGGATTACAGCATGAGTCACGTCGCTGACG 1244

DB 142968 CTGCCACCTTGGCTCCCAAGTGTGGATTACAGCATGAGTCGCTGACG 133025

RESULT 47

AC015495

LOCUS Homo sapiens clone RP11-21E14, WORKING DRAFT SEQUENCE, 13 unordered pieces.

AC015495

VERSION AC015495.4 GI:10047765

KEYWORDS HTG; HTGS; PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 155982)

1 (bases 1 to 155982)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,

Baldwin, J., Barna, N., Beckerly, R., Bonuskavsky, L., Brockway, B.,

Brown, A., Castle, A., Collangelo, M., Collins, S., Collins, P.,

Cooke, P., DeArillano, K., Dewar, K., Domino, M., Donahue, L., Day, E.,

Perrella, P., FitzHugh, W., Forrest, C., Funke, R., Gage, P.,

Galagan, J., Gardyna, S., Grant, G., Hanks, P., Hefford, A., Horton, R.,

Hewland, J., Johnson, R., Jones, C., Kahn, L., Karas, A., Klein, L.,

Lehoczky, J., Lieu, C., Locke, K., Macdonald, J., Marquis, N.,

McEwan, P., McGuck, A., McKernan, K., McLaughlin, J., McDerm, J.,

Morrow, J., Naylor, J., Norman, C., O'Connor, J., O'Donnell, P.,

Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Subramaniam, A., Talamas, J.,

Testa, S., Tirrell, A., Vassiliev, R., Vo, A., Wheeler, J., Wu, X.,

Wyman, D., Ye, W., Zimmer, A. and Zody, M.

Direct Submission

Submitted (16-NOV-1999)

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Sep 10, 2000 this sequence version replaced 41:7249029.

All repeats were identified using RepeatMasker:

Smith, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Genome Center

Center code: W1BR

Web site: http://www.seq.wisc.edu

Contact: sequence_submission@genome.wi.mit.edu

Project Information

Center project name: L3991

Center clone name: 21E14

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big dye; 160% of reads

Assembly program: Phrap; version 0.960741

Consensus quality: 147683 bases at least Q40
 Consensus quality: 151981 bases at least Q30
 Consensus quality: 153418 bases at least Q20
 Insert size: 156000; agarose-fp
 Insert size: 154782; sum-of-contigs
 Quality coverage: 4.4 in Q20 bases; agarose-fp
 Quality coverage: 4.4 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence, as soon as it is available and the accession number will be preserved.

1 8185: contig of 8185 bp in length
 8186 8285: gap of 100 bp
 8286 9661: contig of 1376 bp in length
 9662 9761: gap of 100 bp
 9762 11131: contig of 1370 bp in length
 11132 11231: gap of 100 bp
 11232 57436: contig of 46205 bp in length
 57437 57536: gap of 100 bp
 57537 61395: contig of 3859 bp in length
 61396 61495: gap of 100 bp
 61496 65614: contig of 4119 bp in length
 65615 65714: gap of 100 bp
 65715 71509: contig of 5795 bp in length
 71510 71609: gap of 100 bp
 71610 81113: contig of 9504 bp in length
 81114 81213: gap of 100 bp
 81214 92173: contig of 10960 bp in length
 92174 92273: gap of 100 bp
 92274 103878: contig of 11605 bp in length
 103879 103978: gap of 100 bp
 103979 120091: contig of 16113 bp in length
 120092 120191: gap of 100 bp
 120192 154009: contig of 33818 bp in length
 154010 154109: gap of 100 bp
 154110 155982: contig of 1873 bp in length.

FEATURES

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 /clone_lib="RPC1-11 Human Male BAC"
 misc_feature 1..8185
 /note="assembly_fragment"
 clone_end:SP6
 vector_side:left
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/note="assembly_fragment
clone_end:17
vector:side:right"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 6.6e 21;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGGATGAGCACTGGCGTACG 1244
|||||
DB 4997 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGGATGAGCACTGGCGTACG 18054

RESULT 48
AC068988
LOCUS
DEFINITION Homo sapiens chromosome 15 clone RP11-233C13 map 15, *** SEQUENCING
IN PROGRESS ***, 2 ordered pieces.
ACCESSION AC018988
VERSION AC018988.10 GI:21307395
KEYWORDS HTG: HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEPIN.
SOURCE human.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 158071)
Homo sapiens chromosome 15, clone RP11-233C13
2 (bases 1 to 158071)
Homo sapiens
Anderson, S., Baldwin, J., Barna, N., Beckwith, S., Bedi, F.,
Boukhalil, B., Brown, A., Camparata, J., Camparata, A., Chang, J.,
Chazaro, B., Choe, P., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Fitzhugh, W., Gage, D.,
Galagan, J., Galadina, S., Ginde, S., Gord, S., Goyette, M., Graham, B.,
Grand-Pierre, N., Hago, B., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Lamazzari, R., Landers, T., Lehorzky, J., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N.,
Matthews, C., McCarthy, M., McKean, P., McKernan, K., Meldrum, J.,
Meneus, L., Mihova, T., Mienda, V., Murphy, T., Naylor, S., Nguyen, C.,
Nicoli, R., Norbu, C., Norman, C.H., O'Connor, I., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phukhang, P., Piriz, N.,
Pollara, V., Raymond, C., Retta, R., Rueback, M., Riley, R., Rise, S.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Sanes, R., Schauer, S.,
Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stajich, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,
Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (17-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 1, 2002 this sequence version replaced gi:20331004.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L5451
Center clone name: 233_C_13
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 41244: contig of 41244 bp in length
* 41245 41344: gap of 100 bp
* 41345 158071: contig of 116727 bp in length.
FEATURES
Location/Qualifiers
1..158071
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="15"
/clone="RP11-233C13"
/clone_lib="RFL-11 Human Male BAC"
BASE COUNT 41814 a 38724 c 38609 g 38824 t 100 others
ORIGIN
Query Match 1.8% Score 58; DB 2; Length 158071;
Best Local Similarity 100.0%; Pred. No. 6.6e 21;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGGATGAGCACTGGCGTACG 1244
|||||
DB 144019 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGGATGAGCACTGGCGTACG 144076

RESULT 49
AC068082/c
LOCUS
DEFINITION Homo sapiens chromosome 2 clone RP11-21M2 map 2, WORKING DRAFT
SEQUENCE, 23 unordered pieces.
ACCESSION AC068082
VERSION AC068082.2 GI:8247823
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 158450)
Homo sapiens chromosome 2, clone RP11-21M2
2 (bases 1 to 158450)
Homo sapiens
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedi, F.,
Boukhalil, B., Brown, A., Camparata, J., Camparata, A., Chang, J.,
Chazaro, B., Choe, P., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Fitzhugh, W., Gage, D.,
Galagan, J., Galadina, S., Ginde, S., Gord, S., Goyette, M., Graham, B.,
Grand-Pierre, N., Hago, B., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Lamazzari, R., Landers, T., Lehorzky, J., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N.,
Matthews, C., McCarthy, M., McKean, P., McKernan, K., Meldrum, J.,
Meneus, L., Mihova, T., Mienda, V., Murphy, T., Naylor, S., Nguyen, C.,
Nicoli, R., Norbu, C., Norman, C.H., O'Connor, I., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phukhang, P., Piriz, N.,
Pollara, V., Raymond, C., Retta, R., Rueback, M., Riley, R., Rise, S.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Sanes, R., Schauer, S.,
Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stajich, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,
Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (25-DEC-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 25, 1999 this sequence version replaced gi:10000000.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L5451
Center clone name: 233_C_13
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 41244: contig of 41244 bp in length
* 41245 41344: gap of 100 bp
* 41345 158071: contig of 116727 bp in length.
FEATURES
Location/Qualifiers
1..158071
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="15"
/clone="RP11-233C13"
/clone_lib="RFL-11 Human Male BAC"
BASE COUNT 41814 a 38724 c 38609 g 38824 t 100 others
ORIGIN
Query Match 1.8% Score 58; DB 2; Length 158071;
Best Local Similarity 100.0%; Pred. No. 6.6e 21;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGGATGAGCACTGGCGTACG 1244
|||||
DB 144019 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGGATGAGCACTGGCGTACG 144076

```

Bodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Haqos, R., Heaford, A., Horton, L., Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kama, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, J., Leheczy, J., Levine, R., Liu, C., Liu, S., Locke, K., MacDonald, P., Karpis, N., McCarthy, M., McEwan, P., McGurk, A., McKean, K., Mphahlele, R., Meldrum, J., Menus, L., Mihova, T., Miranda, C., Miñana, V., Morrison, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollard, V., Raymond, J., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, R., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Triolillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (28-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 4, 2000 this sequence version replaced qi:7658356.
All repeats were identified using RepeatMasker:
Snit, A. F. A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.htm>

TITLE:
JOURNAL:
COMMENT:

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www.seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
Project Information:
Center project name: L10095
Center Clone name: 21_M_2

Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.9607.1
Consensus quality: 146955 bases at least Q40
Consensus quality: 153080 bases at least Q40
Consensus quality: 155308 bases at least Q20
Insert size: 163000; agarose-gel
Insert size: 156250; sum-of-coverage
Quality coverage: 3.6 in Q20 bases; agarose-gel
Quality coverage: 3.8 in Q20 bases; sum-of-coverage

NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1749: contig of 1749 bp in length
1750 1849: gap of 100 bp
1850 3169: contig of 1320 bp in length
3170 3269: gap of 100 bp
3270 4573: contig of 1304 bp in length
4574 4673: gap of 100 bp
4674 7997: contig of 3424 bp in length
7998 8097: gap of 100 bp
8098 13045: contig of 4948 bp in length
13046 13145: gap of 100 bp
13146 16766: contig of 3621 bp in length
16767 16866: gap of 100 bp
16867 20859: contig of 3992 bp in length
20860 20959: gap of 100 bp
20960 23743: contig of 2784 bp in length
23744 23843: gap of 100 bp
23844 27652: contig of 3809 bp in length
27653 27752: gap of 100 bp
27753 31395: contig of 3643 bp in length
31396 31495: gap of 100 bp
31496 36408: contig of 4913 bp in length
36409 36508: gap of 100 bp

36509 42265: contig of 5757 bp in length
42266 42365: gap of 100 bp
42366 47307: contig of 4942 bp in length
47308 47407: gap of 100 bp
47408 52438: contig of 5031 bp in length
52439 52538: gap of 100 bp
52539 60035: contig of 7497 bp in length
60036 60135: gap of 100 bp
60136 68356: contig of 8221 bp in length
68357 68456: gap of 100 bp
68457 76898: contig of 8442 bp in length
76899 76998: gap of 100 bp
76999 85827: contig of 8829 bp in length
85828 85927: gap of 100 bp
85928 96327: contig of 10400 bp in length
96328 96427: gap of 100 bp
96428 108928: contig of 12501 bp in length
108929 109028: gap of 100 bp
109029 121274: contig of 12246 bp in length
121275 121374: gap of 100 bp
121375 141287: contig of 19913 bp in length
141288 141387: gap of 100 bp
141388 158450: contig of 17063 bp in length.

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1850..3169
/note="assembly_fragment"
3270..4573
/note="assembly_fragment"
4674..7997
/note="assembly_fragment"
8098..13045
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13146..16766
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16867..20859
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31496..36408
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42366..47307
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47408..52438
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60136..68356
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/note="assembly_fragment"
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/note="assembly_fragment"

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  /note="assembly_fragment"
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  /note="assembly_fragment"
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Best Local Similarity 100.0%; Pred. No. 6.6e-21;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGCATGACGACCTGACACAG 1244
      |||||||
DB 64666 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGCATGACGACCTGACACAG 64009
      |||||||

RESULT 50
AC093737 162419 bp DNA linear HIG 10-SEP-2001
LOCUS Homo sapiens chromosome 2 clone RP11-21M2, WORKING DRAFT SEQUENCE.
DEFINITION 2 unordered pieces.
ACCESSION AC093737.1 GI:15529775
VERSION HIG; HIGS_PHASE1; HIGS_DRAFT; HTGS_FULLTOP.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 162419)
  Waterston, R.H.
  The sequence of Homo sapiens clone
  Unpublished
  2 (bases 1 to 162419)
  Waterston, R.H.
  Direct Submission
  Submitted (10-SEP-2001) Genome Sequencing Center, Washington
  University School of Medicine, 4444 Forest Park Parkway, St. Louis,
  MO 63108, USA

COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/user/index.shtml
----- Project Information -----
Center project name: H_NIH021M22
-----
Drafting center: QC_Core
-----
----- Summary Statistics -----
Sequencing vector: M13; 368
Sequencing vector: plasmid; 648
Chemistry: Dye-primer ET; 0% of reads
Assembly program: Phrap; version 0.950319
Consensus quality: 162004 bases at least Q40
Consensus quality: 162155 bases at least Q40
Consensus quality: 162211 bases at least Q40
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 70250: contig of 70250 bp in length
* 70251 70350: gap of unknown length
* 70351 162419: contig of 92069 bp in length.

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FEATURES
  source
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        /db_xref="taxon:9606"
        /chromosome="2"
        /clone="RP11-21M2"
        l..70250
        /note="assembly_name:Contig13"
        clone_end:T7
        vector_side:right
        70451..162419
        /note="assembly_name:Contig14"
        clone_end:SP6
        vector_side:right
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      ORIGIN
        Query Match 1.8%; Score 58; DB 2: Length 162419;
        Best Local Similarity 100.0%; Pred. No. 6.6e-21;
        Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
        QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGCATGACGACCTGACACAG 1244
            |||||||
        DB 52046 CTGCCACCTTGGCTCCCAAGTCTGGATTACAGCATGACGACCTGACACAG 52103
            |||||||
        Search completed: May 10, 2003, 00:31:40
        Job time : 13938.7 secs

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GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2003, 17:55:06 : Search time 141.721 seconds

(without alignment's)

6260.245 Million cell updates/sec

Title: US-09-846-456-3

Perfect score: 2893

Sequence: 1 acaagcagggggcaggag.....ctadctcgggaacaccc 2893

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 30

Total number of hits satisfying chosen parameters: 753

Minimum DH seq length: 0

Maximum LB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	55	1.9	246240	2	US-08-724-394A-20	Sequence 20, Appl
C 2	55	1.9	246240	2	US-08-724-394A-21	Sequence 21, Appl
C 3	55	1.9	246240	2	US-08-724-394A-22	Sequence 22, Appl
C 4	51	1.8	162450	4	US-09-345-642-1	Sequence 1, Appl
C 5	50	1.7	162450	4	US-09-345-642-1	Sequence 1, Appl
C 6	49	1.7	866	4	US-09-257-179-11	Sequence 1, Appl
C 7	49	1.7	21234	4	US-09-810-671-3	Sequence 3, Appl
C 8	49	1.7	36159	4	US-09-749-588-3	Sequence 1, Appl
C 9	48	1.7	31571	1	US-08-323-443B-1	Sequence 1, Appl
C 10	48	1.7	36651	4	US-09-738-894A-3	Sequence 3, Appl
C 11	48	1.7	53526	3	US-08-658-136-2	Sequence 2, Appl
C 12	48	1.7	53577	3	US-08-658-136-2	Sequence 1, Appl
C 13	47	1.6	13158	2	US-08-667-080-105	Sequence 105, Appl
C 14	45	1.6	153	2	US-08-849-761-2	Sequence 2, Appl
C 15	45	1.6	891	4	US-09-247-155-141	Sequence 141, Appl
C 16	45	1.6	1040	4	US-09-288-143-16	Sequence 16, Appl
C 17	45	1.6	1701	4	US-09-078-294-9	Sequence 9, Appl
C 18	45	1.6	3267	2	US-08-257-463H-12	Sequence 12, Appl
C 19	45	1.6	3267	4	US-08-367-841A-12	Sequence 12, Appl
C 20	45	1.6	3267	5	PCT-US95-07201-12	Sequence 12, Appl
C 21	45	1.6	3663	4	US-09-459-884-11	Sequence 11, Appl
C 22	45	1.6	3844	4	US-09-689-423-1	Sequence 1, Appl
C 23	45	1.6	5262	4	US-08-520-373D-5	Sequence 5, Appl
C 24	45	1.6	5581	4	US-08-973-544-1	Sequence 1, Appl
C 25	45	1.6	8396	4	US-09-328-174A-1	Sequence 1, Appl
C 26	45	1.6	8409	4	US-09-167-681-37	Sequence 37, Appl
C 27	45	1.6	22481	4	US-08-367-841A-43	Sequence 43, Appl

28	45	1.6	22481	5	PCT-US95-07201-43	Sequence 43, Appl
29	45	1.6	22484	4	US-09-875-223-2	Sequence 2, Appl
30	45	1.6	84495	4	US-09-797-906-3	Sequence 3, Appl
31	45	1.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
32	45	1.6	246240	2	US-08-724-394A-21	Sequence 21, Appl
33	45	1.6	246240	2	US-08-724-394A-22	Sequence 22, Appl
C 34	44	1.5	6792	4	US-09-374-454-20	Sequence 20, Appl
C 35	44	1.5	112132	4	US-09-741-150-3	Sequence 3, Appl
C 36	44	1.5	176373	3	US-09-128-155-17	Sequence 17, Appl
C 37	43	1.5	2310	1	US-08-471-570-9	Sequence 9, Appl
C 38	43	1.5	2676	1	US-08-471-570-7	Sequence 7, Appl
C 39	43	1.5	14796	4	US-08-975-080-35	Sequence 35, Appl
40	43	1.5	14796	4	US-09-630-706-10	Sequence 10, Appl
41	43	1.5	14796	4	US-09-496-694B-3	Sequence 3, Appl
42	43	1.5	28720	4	US-09-341-587-7	Sequence 7, Appl
C 43	43	1.5	40030	4	US-09-780-049-18	Sequence 18, Appl
C 44	43	1.5	70000	4	US-09-851-896-3	Sequence 3, Appl
C 45	43	1.5	72604	4	US-09-268-992-7	Sequence 7, Appl
C 46	43	1.5	72604	4	US-09-657-474-7	Sequence 7, Appl
47	43	1.5	81001	4	US-09-750-580-1	Sequence 1, Appl
C 48	43	1.5	98844	4	US-09-791-211-10	Sequence 10, Appl
C 49	43	1.5	99500	4	US-09-798-096-10	Sequence 10, Appl
50	42	1.5	1613	2	US-08-812-204-1	Sequence 1, Appl
51	42	1.5	1656	1	US-08-324-465-2	Sequence 2, Appl
52	42	1.5	1656	2	US-08-465-981-2	Sequence 2, Appl
53	42	1.5	1656	5	PCT-US93-11915-2	Sequence 2, Appl
54	42	1.5	1725	1	US-08-324-465-5	Sequence 5, Appl
55	42	1.5	1725	5	US-08-465-981-5	Sequence 5, Appl
56	42	1.5	1725	5	PCT-US93-11915-5	Sequence 5, Appl
57	42	1.5	2086	2	US-08-655-640-5	Sequence 5, Appl
58	42	1.5	5590	4	US-09-050-159-129	Sequence 129, Appl
C 59	42	1.5	62804	4	US-09-800-960-3	Sequence 3, Appl
60	41	1.4	198	2	US-08-967-101-107	Sequence 107, Appl
61	41	1.4	198	2	US-08-592-541-107	Sequence 107, Appl
62	41	1.4	198	3	US-09-124-698-107	Sequence 107, Appl
63	41	1.4	198	4	US-09-127-480-107	Sequence 107, Appl
64	41	1.4	198	4	US-08-496-841C-107	Sequence 107, Appl
65	41	1.4	198	4	US-09-124-523-103	Sequence 103, Appl
66	41	1.4	386	2	US-08-967-101-103	Sequence 103, Appl
67	41	1.4	386	2	US-08-592-541-103	Sequence 103, Appl
68	41	1.4	386	3	US-09-124-698-103	Sequence 103, Appl
69	41	1.4	386	4	US-09-127-480-103	Sequence 103, Appl
70	41	1.4	386	4	US-08-496-841C-103	Sequence 103, Appl
71	41	1.4	386	4	US-09-124-523-103	Sequence 103, Appl
C 72	41	1.4	719	4	US-09-227-357-74	Sequence 74, Appl
73	41	1.4	893	2	US-08-967-101-13	Sequence 13, Appl
74	41	1.4	893	2	US-08-592-541-13	Sequence 13, Appl
75	41	1.4	893	3	US-09-124-698-13	Sequence 13, Appl
76	41	1.4	893	4	US-09-127-480-13	Sequence 13, Appl
77	41	1.4	893	4	US-08-496-841C-13	Sequence 13, Appl
78	41	1.4	893	4	US-09-124-523-13	Sequence 13, Appl
C 79	41	1.4	896	4	US-08-943-731-31	Sequence 31, Appl
80	41	1.4	1117	2	US-08-967-101-156	Sequence 156, Appl
81	41	1.4	1117	2	US-08-592-541-156	Sequence 156, Appl
82	41	1.4	1117	3	US-08-888-077A-6	Sequence 6, Appl
83	41	1.4	1117	3	US-09-124-698-156	Sequence 156, Appl
84	41	1.4	1117	4	US-09-127-480-156	Sequence 156, Appl
85	41	1.4	1117	4	US-08-496-841C-156	Sequence 156, Appl
86	41	1.4	1624	2	US-08-852-807-10	Sequence 10, Appl
C 88	41	1.4	2559	2	US-08-886-152-4	Sequence 4, Appl
C 89	41	1.4	2559	4	US-09-196-222-4	Sequence 4, Appl
C 90	41	1.4	11811	4	US-09-078-294-7	Sequence 7, Appl
C 91	41	1.4	13674	2	US-08-852-807-1	Sequence 1, Appl
C 92	41	1.4	18609	4	US-08-943-731-1	Sequence 1, Appl
C 93	41	1.4	19311	1	US-08-310-356-36	Sequence 36, Appl
C 94	41	1.4	19557	5	PCT-US92-06300-1	Sequence 1, Appl
C 95	41	1.4	35060	3	US-08-814-095-7	Sequence 7, Appl
C 96	41	1.4	38564	4	US-09-734-673-3	Sequence 3, Appl
C 97	41	1.4	98844	4	US-09-791-211-10	Sequence 10, Appl
C 98	41	1.4	99500	4	US-09-798-096-10	Sequence 10, Appl
C 99	41	1.4	168575	4	US-09-426-290-1	Sequence 1, Appl
C 100	40	1.4	295	2	US-08-849-701-8	Sequence 8, Appl

c 101	40	1.4	577	4	US-09-227-357-92	Sequence 92, App:	174	37	1.3	657	4	US-09-385-982-335	Sequence 335, App
c 102	40	1.4	1804	1	US-08-306-691B-40	Sequence 40, App:	175	37	1.3	668	4	US-09-347-114A-93	Sequence 93, Appl
c 103	40	1.4	1804	4	US-09-167-122-14	Sequence 14, Appl	176	37	1.3	680	4	US-09-056-285A-2	Sequence 2, Appl
c 104	40	1.4	1804	5	PCT-US93-06251-82	Sequence 82, Appl	c 177	37	1.3	819	4	US-09-337-171-13	Sequence 13, Appl
c 105	40	1.4	2896	2	US-08-709-923-1	Sequence 1, Appl	178	37	1.3	926	4	US-08-938-669A-4	Sequence 4, Appl
c 106	40	1.4	38844	4	US-09-734-675-3	Sequence 3, Appl	179	37	1.3	1000	4	US-09-018-584A-30	Sequence 30, Appl
c 107	40	1.4	80246	4	US-09-078-294-4	Sequence 4, Appl	180	37	1.3	1000	4	US-09-018-584A-31	Sequence 31, Appl
c 108	40	1.4	80595	4	US-09-078-294-3	Sequence 3, Appl	c 181	37	1.3	1145	4	US-09-078-294-17	Sequence 17, Appl
c 109	40	1.4	87350	3	US-08-781-891-79	Sequence 79, Appl	c 182	37	1.3	1460	4	US-09-257-179-23	Sequence 23, Appl
c 110	40	1.4	87543	4	US-09-791-211-3	Sequence 7, Appl	183	37	1.3	2372	1	US-07-503-103-1	Sequence 1, Appl
c 111	39	1.3	885	4	US-09-288-143-55	Sequence 55, Appl	184	37	1.3	2372	1	US-08-044-619A-1	Sequence 1, Appl
c 112	39	1.3	1164	3	US-08-755-587-32	Sequence 32, Appl	185	37	1.3	2372	1	US-08-283-911-1	Sequence 1, Appl
c 113	39	1.3	2834	4	US-09-305-384-6	Sequence 6, Appl	186	37	1.3	2372	1	US-08-245-500A-2	Sequence 2, Appl
c 114	39	1.3	3507	1	US-08-842-683-67	Sequence 67, Appl	187	37	1.3	2372	1	US-08-390-546-2	Sequence 2, Appl
c 115	39	1.3	3507	2	US-08-842-677-67	Sequence 67, Appl	188	37	1.3	2372	1	US-08-390-546-2	Sequence 2, Appl
c 116	39	1.3	6235	4	US-09-305-384-5	Sequence 5, Appl	189	37	1.3	2372	1	US-08-557-393-2	Sequence 2, Appl
c 117	39	1.3	6679	4	US-09-305-384-1	Sequence 1, Appl	190	37	1.3	2372	1	US-08-390-516C-2	Sequence 2, Appl
c 118	39	1.3	8835	3	US-08-884-324-10	Sequence 10, App:	191	37	1.3	2372	1	US-08-390-517A-2	Sequence 2, Appl
c 119	39	1.3	10684	3	US-08-618-100B-3	Sequence 3, Appl	192	37	1.3	2372	1	US-08-390-515A-2	Sequence 2, Appl
c 120	39	1.3	19736	4	US-09-740-015-3	Sequence 3, Appl	193	37	1.3	2372	2	US-08-801-718-2	Sequence 2, Appl
c 121	39	1.3	20598	4	US-09-593-955-10	Sequence 10, Appl	194	37	1.3	2372	3	US-09-073-567-1	Sequence 1, Appl
c 122	39	1.3	28994	3	US-08-884-324-14	Sequence 14, Appl	195	37	1.3	2372	4	US-09-280-805-1	Sequence 1, Appl
c 123	39	1.3	35100	5	US-08-306-691B-19	Sequence 19, Appl	196	37	1.3	2372	4	US-09-048-810-1	Sequence 1, Appl
c 124	39	1.3	35100	1	PCT-US93-06251-15	Sequence 15, App:	197	37	1.3	2372	4	US-09-170-159A-2	Sequence 2, Appl
c 125	39	1.3	112132	4	US-09-741-150-3	Sequence 3, Appl	198	37	1.3	2372	4	US-09-480-718-43	Sequence 43, Appl
c 126	39	1.3	152331	3	US-09-128-155-16	Sequence 16, App:	199	37	1.3	2455	4	US-08-406-030A-4	Sequence 4, Appl
c 127	39	1.3	152331	3	US-09-128-155-16	Sequence 16, App:	c 200	37	1.3	2713	2	US-08-916-901-6	Sequence 6, Appl
c 128	38	1.3	40	4	US-09-060-024A-2	Sequence 2, Appl	c 201	37	1.3	2713	4	US-09-154-602-6	Sequence 6, Appl
c 129	38	1.3	257	2	US-08-849-701-4	Sequence 4, Appl	c 202	37	1.3	2839	3	US-08-468-856B-5	Sequence 5, Appl
c 130	38	1.3	579	4	US-09-128-111-741	Sequence 741, App	c 203	37	1.3	2839	3	US-08-468-859A-5	Sequence 5, Appl
c 131	38	1.3	646	4	US-09-145-962-614	Sequence 14, App	c 204	37	1.3	2839	4	US-09-061-702-1	Sequence 1, Appl
c 132	38	1.3	776	4	US-09-615-008-47	Sequence 47, App	c 205	37	1.3	317	4	US-09-146-580-6	Sequence 6, Appl
c 133	38	1.3	1037	4	US-09-257-279-16	Sequence 16, App	c 206	37	1.3	4233	4	US-09-056-105-27	Sequence 27, Appl
c 134	38	1.3	1363	1	US-08-776-088-21	Sequence 21, App	207	37	1.3	4823	2	US-08-457-254-5	Sequence 5, Appl
c 135	38	1.3	1363	5	PCT-US95-09147A-21	Sequence 21, App	208	37	1.3	4823	2	US-08-484-257-20	Sequence 20, Appl
c 136	38	1.3	1381	2	US-08-443-557C-49	Sequence 49, Appl	209	37	1.3	4823	3	US-08-999-927-5	Sequence 5, Appl
c 137	38	1.3	1381	2	US-08-340-420-49	Sequence 42, Appl	210	37	1.3	4823	5	PCT-US94-08806-28	Sequence 28, Appl
c 138	38	1.3	1381	2	US-08-450-670C-49	Sequence 49, Appl	211	37	1.3	4823	5	PCT-US95-01829-5	Sequence 5, Appl
c 139	38	1.3	1381	5	PCT-US95-17111A-49	Sequence 49, App:	212	37	1.3	4823	5	PCT-US95-16626-5	Sequence 5, Appl
c 140	38	1.3	1418	5	PCT-US95-17111A-120	Sequence 120, App	213	37	1.3	4823	5	PCT-US95-16626-5	Sequence 5, Appl
c 141	49	1.3	1442	2	US-08-454-557C-120	Sequence 120, App	214	37	1.3	4922	2	US-08-330-272-5	Sequence 5, Appl
c 142	38	1.3	1442	2	US-08-340-420-120	Sequence 120, App	215	37	1.3	4922	5	PCT-US95-13663-5	Sequence 5, Appl
c 143	38	1.3	1442	2	US-08-450-670C-120	Sequence 120, App	c 216	37	1.3	5375	3	US-08-757-223-7	Sequence 7, Appl
c 144	38	1.3	5035	2	US-08-616-392-4	Sequence 4, Appl	c 217	37	1.3	5543	2	US-08-687-080-101	Sequence 101, App
c 145	38	1.3	5789	4	US-09-242-248-4	Sequence 4, Appl	218	37	1.3	7210	2	US-08-257-963B-10	Sequence 10, Appl
c 146	38	1.3	7680	4	US-09-250-748A-4	Sequence 4, Appl	219	37	1.3	7210	4	US-08-367-841A-10	Sequence 10, Appl
c 147	38	1.3	40352	3	US-08-646-113B-15	Sequence 15, Appl	220	37	1.3	7210	5	PCT-US95-07201-10	Sequence 10, Appl
c 148	38	1.3	40352	4	US-09-443-677-15	Sequence 15, Appl	221	37	1.3	9365	4	US-09-608-285A-8	Sequence 8, Appl
c 149	38	1.3	45546	4	US-09-146-015-4	Sequence 6, Appl	222	37	1.3	9365	4	US-09-350-836B-8	Sequence 8, Appl
c 150	38	1.3	80246	4	US-09-078-294-4	Sequence 4, Appl	223	37	1.3	9365	4	US-09-370-265-8	Sequence 8, Appl
c 151	38	1.3	80595	4	US-09-078-294-3	Sequence 3, Appl	224	37	1.3	9734	4	US-09-347-114A-80	Sequence 80, Appl
c 152	38	1.3	168575	4	US-09-426-290-1	Sequence 1, Appl	225	37	1.3	11811	4	US-09-078-294-7	Sequence 7, Appl
c 153	37	1.3	184	2	US-08-454-567C-47	Sequence 47, Appl	226	37	1.3	14581	4	US-08-520-373D-4	Sequence 4, Appl
c 154	37	1.3	184	2	US-08-340-420-47	Sequence 47, App:	227	37	1.3	14747	4	US-09-608-285A-42	Sequence 42, Appl
c 155	37	1.3	184	2	US-08-450-670C-47	Sequence 47, Appl	228	37	1.3	15777	4	US-09-608-285A-59	Sequence 59, Appl
c 156	37	1.3	184	5	PCT-US95-17111A-47	Sequence 47, App:	229	37	1.3	17327	1	US-07-906-871-15	Sequence 15, Appl
c 157	37	1.3	245	2	US-08-454-557C-49	Sequence 49, App:	c 230	37	1.3	17327	1	US-07-906-871-15	Sequence 15, Appl
c 158	37	1.3	245	2	US-08-450-426B-86	Sequence 86, App:	231	37	1.3	20674	4	US-09-641-638-651	Sequence 651, App
c 159	37	1.3	245	2	US-08-450-670C-86	Sequence 86, App:	c 232	37	1.3	36741	4	US-09-301-665-3	Sequence 3, Appl
c 160	37	1.3	245	5	PCT-US95-17111A-86	Sequence 86, Appl	233	37	1.3	42571	4	US-09-810-347-3	Sequence 3, Appl
c 161	37	1.3	421	1	US-08-480-784-24	Sequence 24, Appl	c 234	37	1.3	43950	4	US-09-735-934A-3	Sequence 3, Appl
c 162	37	1.3	421	1	US-08-484-553-24	Sequence 24, Appl	c 235	37	1.3	43950	4	US-09-735-934A-3	Sequence 3, Appl
c 163	37	1.3	421	1	US-08-487-002-24	Sequence 24, Appl	236	37	1.3	50000	4	US-09-146-053-3	Sequence 3, Appl
c 164	37	1.3	421	1	US-08-484-554B-24	Sequence 24, Appl	c 237	37	1.3	50000	4	US-09-146-053-3	Sequence 3, Appl
c 165	37	1.3	421	1	US-08-488-011B-24	Sequence 24, Appl	238	37	1.3	70000	4	US-09-851-896-3	Sequence 3, Appl
c 166	37	1.3	421	4	US-08-850-727-24	Sequence 24, Appl	c 239	37	1.3	84495	4	US-09-797-906-3	Sequence 3, Appl
c 167	37	1.3	421	5	PCT-US95-10202-24	Sequence 24, Appl	c 240	36	1.2	685	4	US-09-227-357-100	Sequence 100, App
c 168	37	1.3	421	5	PCT-US95-10203-24	Sequence 24, App:	241	36	1.2	951	4	US-09-605-785-570	Sequence 570, App
c 169	37	1.3	421	5	PCT-US95-10204-24	Sequence 24, App:	c 242	36	1.2	1001	4	US-09-641-638-464	Sequence 464, App
c 170	37	1.3	562	4	US-09-385-962-442	Sequence 442, App	c 243	36	1.2	1373	4	US-09-227-357-13	Sequence 13, Appl
c 171	37	1.3	606	4	US-09-185-982-414	Sequence 414, App	c 244	36	1.2	1459	4	US-09-020-956-174	Sequence 174, App
c 172	37	1.3	632	4	US-09-385-982-177	Sequence 177, App	c 245	36	1.2	1459	4	US-09-030-607-174	Sequence 174, App
c 173	37	1.3	653	4	US-09-385-982-124	Sequence 124, App	c 246	36	1.2	1459	4	US-09-605-785-174	Sequence 174, App

c 247	1.2	1459	4	US-09-435-313-174	Sequence 174, App	c 320	35	1.2	22481	5	PCT-US95-07201-43	Sequence 43, Appl
c 248	1.2	1459	4	US-09-452-616A-174	Sequence 174, App	c 321	35	1.2	22484	4	US-09-875-223-2	Sequence 2, Appl
c 249	1.2	1459	4	US-09-232-145A-174	Sequence 174, App	c 322	35	1.2	26764	1	US-08-370-975B-1	Sequence 1, Appl
c 250	1.2	2099	4	US-08-638-669A-5	Sequence 5, Appl	c 323	35	1.2	29629	4	US-09-729-995-3	Sequence 3, Appl
c 251	1.2	2921	3	US-08-618-70-4	Sequence 4, Appl	c 324	35	1.2	35060	3	US-08-814-095-7	Sequence 7, Appl
c 252	1.2	3350	3	US-09-110-115-2	Sequence 2, Appl	c 325	35	1.2	35100	1	US-08-306-691B-19	Sequence 19, Appl
c 253	1.2	3609	4	US-09-705-249-1	Sequence 11, Appl	c 326	35	1.2	45100	5	PCT-US93-06251-19	Sequence 19, Appl
c 254	1.2	4326	2	US-08-852-827-12	Sequence 12, Appl	c 327	35	1.2	40000	4	US-09-780-049-18	Sequence 18, Appl
c 255	1.2	4517	4	US-09-140-804-9	Sequence 9, Appl	c 328	35	1.2	40328	3	US-08-742-185-102	Sequence 102, App
c 256	1.2	5220	2	US-08-777-405A-1	Sequence 1, Appl	c 329	35	1.2	43795	3	US-08-742-185-101	Sequence 101, App
c 257	1.2	5220	2	US-08-977-871A-1	Sequence 1, Appl	c 330	35	1.2	45716	4	US-08-965-048-5	Sequence 5, Appl
c 258	1.2	5220	2	US-09-225-561-1	Sequence 1, Appl	c 331	35	1.2	45989	4	US-08-965-048-6	Sequence 6, Appl
c 259	1.2	8133	4	US-09-659-791A-10	Sequence 10, Appl	c 332	35	1.2	59065	4	US-09-813-817-3	Sequence 3, Appl
c 260	1.2	13674	2	US-08-852-807-1	Sequence 1, Appl	c 333	35	1.2	59065	4	US-09-978-197-3	Sequence 3, Appl
c 261	1.2	14636	4	US-09-173-914-6	Sequence 6, Appl	c 334	35	1.2	62804	4	US-09-800-960-3	Sequence 3, Appl
c 262	1.2	15297	4	US-09-817-180-3	Sequence 3, Appl	c 335	35	1.2	72928	3	US-09-009-913-1	Sequence 1, Appl
c 263	1.2	16063	4	US-09-801-052-3	Sequence 3, Appl	c 336	35	1.2	81001	4	US-09-750-580-1	Sequence 1, Appl
c 264	1.2	17949	4	US-09-387-465-3	Sequence 3, Appl	c 337	35	1.2	176373	3	US-09-128-155-17	Sequence 17, Appl
c 265	1.2	38564	4	US-09-734-673-3	Sequence 3, Appl	c 338	34	1.2	547	4	US-08-991-789A-158	Sequence 158, App
c 266	1.2	40328	3	US-08-742-185-102	Sequence 102, App	c 339	34	1.2	547	4	US-09-062-451-158	Sequence 158, App
c 267	1.2	43795	3	US-08-742-185-101	Sequence 101, App	c 340	34	1.2	547	4	US-09-598-326-158	Sequence 158, App
c 268	1.2	45716	4	US-08-965-048-5	Sequence 5, Appl	c 341	34	1.2	685	4	US-09-227-357-100	Sequence 100, App
c 269	1.2	55989	4	US-08-965-048-6	Sequence 6, Appl	c 342	34	1.2	728	4	US-09-404-879A-16	Sequence 16, Appl
c 270	1.2	59000	4	US-09-146-053-4	Sequence 4, Appl	c 343	34	1.2	1057	4	US-09-257-173-16	Sequence 16, Appl
c 271	1.2	59065	4	US-09-813-817-3	Sequence 3, Appl	c 344	34	1.2	1220	4	US-09-227-357-54	Sequence 54, Appl
c 272	1.2	59065	4	US-09-978-197-3	Sequence 3, Appl	c 345	34	1.2	1838	4	US-09-227-357-32	Sequence 32, Appl
c 273	1.2	72604	4	US-09-268-992-7	Sequence 7, Appl	c 346	34	1.2	2076	2	US-08-979-095-3	Sequence 3, Appl
c 274	1.2	72604	4	US-09-657-474-7	Sequence 7, Appl	c 347	34	1.2	2129	2	US-08-979-095-1	Sequence 1, Appl
c 275	1.2	577	4	US-09-328-111-302	Sequence 302, App	c 348	34	1.2	2336	1	US-08-247-946A-1	Sequence 1, Appl
c 276	1.2	729	4	US-09-641-636-116	Sequence 116, App	c 349	34	1.2	2336	5	PCT-US95-06420-1	Sequence 1, Appl
c 277	1.2	776	4	US-09-535-008-37	Sequence 37, App	c 350	34	1.2	2337	3	US-09-156-253-1	Sequence 1, Appl
c 278	1.2	1250	4	US-09-018-584A-36	Sequence 36, Appl	c 351	34	1.2	2357	2	US-08-394-152A-48	Sequence 48, Appl
c 279	1.2	2024	2	US-08-458-970A-1	Sequence 1, Appl	c 352	34	1.2	3017	4	US-08-394-152A-39	Sequence 39, Appl
c 280	1.2	2236	3	US-08-829-625-23	Sequence 23, Appl	c 353	34	1.2	3172	4	US-08-978-289-11	Sequence 11, Appl
c 281	1.2	2236	4	US-08-609-563A-25	Sequence 25, Appl	c 354	34	1.2	3198	4	US-09-601-478-3	Sequence 3, Appl
c 282	1.2	2236	4	US-08-937-495-23	Sequence 23, Appl	c 355	34	1.2	4326	2	US-08-852-807-12	Sequence 12, Appl
c 283	1.2	2236	4	US-09-310-367-23	Sequence 23, Appl	c 356	34	1.2	7210	2	US-08-257-963B-10	Sequence 10, Appl
c 284	1.2	2236	4	US-09-032-337-23	Sequence 23, Appl	c 357	34	1.2	7210	4	US-08-367-841A-10	Sequence 10, Appl
c 285	1.2	3172	4	US-08-978-249-11	Sequence 11, Appl	c 358	34	1.2	7210	5	PCT-US95-07201-10	Sequence 10, Appl
c 286	1.2	3198	4	US-09-602-478-3	Sequence 3, Appl	c 359	34	1.2	8385	3	US-08-884-324-10	Sequence 10, Appl
c 287	1.2	3609	4	US-09-705-249-1	Sequence 11, App	c 360	34	1.2	9388	4	US-08-991-789A-141	Sequence 141, App
c 288	1.2	3663	4	US-09-495-884-11	Sequence 11, App	c 361	34	1.2	9488	4	US-09-062-451-141	Sequence 141, App
c 289	1.2	3748	2	US-08-956-240-1	Sequence 1, App	c 362	34	1.2	9488	4	US-09-598-326-141	Sequence 141, App
c 290	1.2	4084	3	US-08-866-440-1	Sequence 1, Appl	c 363	34	1.2	12394	4	US-09-488-856A-10	Sequence 10, Appl
c 291	1.2	4084	3	US-08-856-430-1	Sequence 1, Appl	c 364	34	1.2	14581	4	US-08-520-373D-4	Sequence 4, Appl
c 292	1.2	4460	4	US-09-138-825-4	Sequence 4, Appl	c 365	34	1.2	14636	4	US-09-173-914-6	Sequence 6, Appl
c 293	1.2	4460	4	US-09-163-875-4	Sequence 4, Appl	c 366	34	1.2	15632	4	US-09-644-634-17	Sequence 17, Appl
c 294	1.2	6769	1	US-08-380-763-26	Sequence 26, App	c 367	34	1.2	18074	4	US-09-078-294-12	Sequence 12, Appl
c 295	1.2	6769	1	US-08-380-763-26	Sequence 26, App	c 368	34	1.2	26924	3	US-08-884-324-14	Sequence 14, Appl
c 296	1.2	6769	1	US-08-380-763-26	Sequence 26, App	c 369	34	1.2	44554	4	US-09-146-053-5	Sequence 5, Appl
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c 298	1.2	6769	1	US-08-418-634B-20	Sequence 20, App	c 371	34	1.2	50000	4	US-09-146-053-4	Sequence 4, Appl
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c 302	1.2	6769	5	PCT-US95-13202-20	Sequence 20, App	c 375	33	1.2	125	5	PCT-US95-09114-17	Sequence 17, Appl
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c 304	1.2	8174	1	US-08-393-246-5	Sequence 5, Appl	c 377	33	1.2	384	2	US-08-967-101-68	Sequence 68, Appl
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c 307	1.2	8174	4	US-09-042-583-5	Sequence 5, Appl	c 380	33	1.2	448	4	US-08-496-841C-68	Sequence 68, Appl
c 308	1.2	8174	5	PCT-US91-00899-3	Sequence 3, Appl	c 381	33	1.2	448	4	US-09-124-523-68	Sequence 68, Appl
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c 317	1.2	18073	4	US-09-378-294-12	Sequence 12, App	c 390	33	1.2	819	4	US-09-427-357-88	Sequence 88, Appl
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Sequence 5, Appli
Sequence 5, Appli
Sequence 20, Appli
Sequence 20, Appli

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685 1 1.1 6769 1 US-08-483-554B-20 Sequence 20, Appl
686 1 1.1 6769 1 US-08-488-011B-20 Sequence 20, Appl
687 1 1.1 6769 4 US-08-850-727-20 Sequence 20, Appl
688 1 1.1 6769 5 PCT-US95-10202-20 Sequence 20, Appl
689 1 1.1 6769 5 PCT-US95-10203-20 Sequence 20, Appl
690 1 1.1 6769 5 PCT-US95-10220-20 Sequence 20, Appl
691 1 1.1 7130 4 US-09-056-105-32 Sequence 20, Appl
692 1 1.1 7152 4 US-09-167-681-29 Sequence 20, Appl
693 1 1.1 7505 4 US-09-078-294-15 Sequence 16, Appl
694 1 1.1 7705 2 US-08-687-080-315 Sequence 115, App
695 1 1.1 7720 4 US-09-318-448-5 Sequence 45, Appl
696 1 1.1 8453 4 US-09-167-681-45 Sequence 1, Appl
697 1 1.1 8517 3 US-08-827-268-1 Sequence 1, Appl
698 1 1.1 8517 4 US-09-500-158-1 Sequence 1, Appl
699 1 1.1 8517 4 US-09-448-809-1 Sequence 1, Appl
700 1 1.1 12047 2 US-09-022-461-1 Sequence 1, Appl
701 1 1.1 12047 4 US-09-033-556-4 Sequence 1, Appl
702 1 1.1 12597 4 US-09-705-299-12 Sequence 12, Appl
703 1 1.1 13953 4 US-09-748-884-3 Sequence 4, Appl
704 1 1.1 14753 4 US-09-821-736-3 Sequence 4, Appl
705 1 1.1 15202 3 US-08-922-635-31 Sequence 21, Appl
706 1 1.1 17410 1 US-07-841-646-3 Sequence 3, Appl
707 1 1.1 17410 1 US-08-147-023-3 Sequence 3, Appl
708 1 1.1 17410 1 US-08-447-570-4 Sequence 3, Appl
709 1 1.1 17410 2 US-08-449-730-3 Sequence 3, Appl
710 1 1.1 17410 2 US-08-449-693A-3 Sequence 3, Appl
711 1 1.1 17415 3 US-08-486-143A-1 Sequence 1, Appl
712 1 1.1 17415 5 PCT-US95-07449-1 Sequence 1, Appl
713 1 1.1 18596 4 US-09-318-448-11 Sequence 1, Appl
714 1 1.1 36741 4 US-09-301-665-3 Sequence 1, Appl
715 1 1.1 45546 4 US-09-146-053-6 Sequence 3, Appl
716 1 1.1 49136 4 US-09-422-869-1 Sequence 6, Appl
717 1 1.1 65042 4 US-09-784-336-3 Sequence 1, Appl
718 1 1.1 111282 4 US-09-754-250-3 Sequence 1, Appl
719 1 1.1 169998 4 US-09-679-610B-24 Sequence 24, Appl
720 1 1.1 84 2 US-08-454-553-91 Sequence 41, Appl
721 1 1.1 84 2 US-08-340-4260-91 Sequence 41, Appl
722 1 1.1 84 2 US-08-450-673-91 Sequence 41, Appl
723 1 1.1 84 5 PCT-US95-17111A-91 Sequence 41, Appl
724 1 1.1 151 2 US-08-454-553-52 Sequence 52, Appl
725 1 1.1 151 2 US-08-340-4260-52 Sequence 52, Appl
726 1 1.1 151 2 US-08-450-673-52 Sequence 52, Appl
727 1 1.1 151 5 PCT-US95-17111A-52 Sequence 9, Appl
728 1 1.1 240 1 US-08-222-177A-9 Sequence 45, App
729 1 1.1 345 4 US-09-585-082-145 Sequence 37, Appl
730 1 1.1 377 2 US-08-454-553-42 Sequence 37, Appl
731 1 1.1 377 2 US-08-340-4260-42 Sequence 37, Appl
732 1 1.1 377 5 PCT-US95-17111A-47 Sequence 47, Appl
733 1 1.1 542 4 US-09-205-637-1 Sequence 5, Appl
734 1 1.1 613 4 US-09-085-082-114 Sequence 114, App
735 1 1.1 651 4 US-09-257-177-12 Sequence 12, Appl
736 1 1.1 690 4 US-09-428-111-74 Sequence 74, Appl
737 1 1.1 700 4 US-08-491-789A-174 Sequence 174, App
738 1 1.1 700 4 US-09-062-451-174 Sequence 174, App
739 1 1.1 1000 4 US-09-598-426-174 Sequence 174, App
740 1 1.1 1000 4 US-09-018-584A-42 Sequence 42, App
741 1 1.1 1052 4 US-09-442-143A-9 Sequence 9, Appl
742 1 1.1 1196 3 US-07-959-369-4 Sequence 4, Appl
743 1 1.1 1237 4 US-09-545-008-15 Sequence 5, Appl
744 1 1.1 1419 4 US-08-943-731-164 Sequence 164, App
745 1 1.1 1480 2 US-08-454-553-68 Sequence 48, App
746 1 1.1 1480 2 US-08-340-4260-48 Sequence 48, App
747 1 1.1 1480 2 US-08-450-673-68 Sequence 48, App
748 1 1.1 1480 5 PCT-US95-17111A-38 Sequence 38, Appl
749 1 1.1 1699 4 US-08-923-165A-6 Sequence 6, Appl
750 1 1.1 1744 4 US-09-511-625B-19 Sequence 19, Appl
751 1 1.1 2061 2 US-08-966-622-11 Sequence 11, Appl
752 1 1.1 2777 4 US-09-413-46-3 Sequence 3, Appl
753 1 1.1 2777 4 US-08-842-248A-3 Sequence 3, Appl
754 1 1.1 2790 3 US-08-985-960-20 Sequence 20, Appl
755 1 1.1 2922 4 US-09-310-46-1 Sequence 1, Appl
756 1 1.1 2922 4 US-08-642-24A-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-08-724-194A-20/1

Sequence 20, Application: US/08724194A

Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.

APPLICANT: Kromaul, Gregory S.

APPLICANT: Lauer, Peter M.

APPLICANT: Roddy, David A.

APPLICANT: Thomas, Winston

APPLICANT: Tsuchihashi, Zenta

APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1

TITLE OF INVENTION: Sequences and Antibodies Thereto

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESSES:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-0844

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,194A

FILING DATE: 01 Oct 1996

CLASSIFICATION: 516

ATTORNEY/AGENT INFORMATION:

```

; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H. CONTIG"
US 08/724-394A-20

Query Match
Best Local Similarity 100.0%; DB 2: Length 246240;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTTGGCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGGCCCTAGC 1244
|||||
DB 14447 CCCACCTTGGCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGGCCCTAGC 14393

RESULT 2
US 08/724-394A-21/c
; Sequence 21, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H. CONTIG"
US 08/724-394A-21
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; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H. CONTIG"
US 08/724-394A-21

Query Match
Best Local Similarity 100.0%; DB 2: Length 246240;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTTGGCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGGCCCTAGC 1244
|||||
DB 14447 CCCACCTTGGCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGGCCCTAGC 14393

RESULT 3
US 08/724-394A-22/c
; Sequence 22, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H. CONTIG"
US 08/724-394A-22

Query Match
Best Local Similarity 100.0%; DB 2: Length 246240;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTTGGCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGGCCCTAGC 1244
|||||
DB 14447 CCCACCTTGGCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGGCCCTAGC 14393
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RESULT 4

US-09-345-882-1
Sequence 1, Application US/09345882
Patent No. 6399373
GENERAL INFORMATION:
APPLICANT: Bouguetel, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOLAST-RA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/345.882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,415
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 162450
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 72794
OTHER INFORMATION: 5-124-273 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 88073
OTHER INFORMATION: 5-127-261 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 90842
OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 91714
OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
FEATURE:
NAME/KEY: allele
LOCATION: 97122
OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 97152
OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
FEATURE:
NAME/KEY: allele
LOCATION: 99098
OTHER INFORMATION: 5-130-257 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 99117
OTHER INFORMATION: 5-130-276 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 103806
OTHER INFORMATION: 5-131-395 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 106940
OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108106
OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108149
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
FEATURE:
NAME/KEY: allele
LOCATION: 97099...97145

LOCATION: 108308
OTHER INFORMATION: 5-135-357 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 108471
OTHER INFORMATION: 5-136-174 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION: 5-140-120 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 144362
OTHER INFORMATION: 5-140-148 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 134374
OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
FEATURE:
NAME/KEY: allele
LOCATION: 146328
OTHER INFORMATION: 5-143-84 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 146345
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 150129
OTHER INFORMATION: 5-145-24 : polymorphic base A or G
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NAME/KEY: allele
LOCATION: 160031
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 72771...72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE:
NAME/KEY: allele
LOCATION: 72771...72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
FEATURE:
NAME/KEY: allele
LOCATION: 88050...88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
FEATURE:
NAME/KEY: allele
LOCATION: 88050...88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
FEATURE:
NAME/KEY: allele
LOCATION: 90819...90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
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NAME/KEY: allele
LOCATION: 90819...90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
FEATURE:
NAME/KEY: allele
LOCATION: 93690...93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
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NAME/KEY: allele
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OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE:
NAME/KEY: allele
LOCATION: 97099...97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97099...97145

EARLIER APPLICATION NUMBER: 60/056,270
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,271
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,247
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,073
EARLIER FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 11
LENGTH: 866
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (22)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (37)
OTHER INFORMATION: n equals a,t,g, or c
US-09-257-179-11

Query Match 1.7% Score 49; DB 4; Length 866;
Best Local Similarity 100.0%; Pred. No. 2.1e-12;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1033 AACCTCGCTCCGGGTTCAAGGATCTCTGGCTACGCTCTGAG 108;
|||||
DB 772 AACCTCGCTCCGGGTTCAAGGATCTCTGGCTACGCTCTGAG 74

RESULT 7

US-09-810-671-3
Sequence 3, Application US/09810671
Patent No. 6455291
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEOTIDE SEQUENCES, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO00758
CURRENT APPLICATION NUMBER: US/09/810,671
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 21254
TYPE: DNA
ORGANISM: human
US-09-810-671-3

Query Match 1.7% Score 49; DB 4; Length 21254;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1033 AACCTCGCTCCGGGTTCAAGGATCTCTGGCTACGCTCTGAG 108;
|||||
DB 12052 AACCTCGCTCCGGGTTCAAGGATCTCTGGCTACGCTCTGAG 12100

RESULT 8

US-09-749-588-3
Sequence 4, Application US/09749588
Patent No. 6423521
GENERAL INFORMATION:
APPLICANT: CHANDRAMOULISWARAN, Ishwat et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEOTIDE SEQUENCES, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01068
CURRENT APPLICATION NUMBER: US/09/749,588

CURRENT FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 36159
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(36159)
OTHER INFORMATION: n = A,T,C or G
US-09-749-588-3

Query Match 1.7% Score 49; DB 4; Length 36159;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1187 CTGCCAGCTTGCCCTCCCAAGTGTGGGATTACAGGATGAGCCACT 1235;
|||||
DB 6516 CTGCCAGCTTGCCCTCCCAAGTGTGGGATTACAGGATGAGCCACT 6564

RESULT 9

US-08-323-443B-1
Sequence 1, Application US/08323443B
Patent No. 5654170
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W.
APPLICANT: LANDES, GREGORY M.
APPLICANT: HURN, TIMOTHY C.
APPLICANT: CONNORS, TIMOTHY D.
APPLICANT: JACKOWSKI, WILLIAM R.
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,443B
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DRAWING NUMBER: 0372/0A462
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3157 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: PKU1-CHNMI
US-08-323-443B-1

NAME/KEY: CDS
LOCATION: 4..447
FEATURE:
NAME/KEY: sig-peptide
LOCATION: 4..147
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.6999980926514
OTHER INFORMATION: seq LLLFFGKILVVGG/VG
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 858..863
FEATURE:
NAME/KEY: polyA_site
LOCATION: 880..891
US-09-247-155-141

Query Match 1.68; Score 45; DB 4; Length 1077
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1043 AACCTCTGCTCCCGGGTTCAGGCGATTCTCTGCTCAGGCTCC 1077
|||||
DB 772 AACCTCTGCTCCCGGGTTCAGGCGATTCTCTGCTCAGGCTCC 726

RESULT 16
US-09-288-143-16/C
Sequence 16, Application US/09288143
Patent No. 6433139
GENERAL INFORMATION:
APPLICANT: Brewer et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: P2018P1
CURRENT APPLICATION NUMBER: US/09/288.143
CURRENT FILING DATE: 1999-04-08
EARLIER APPLICATION NUMBER: PCT/US96/21142
EARLIER FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061.463
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061.529
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/071.498
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061.527
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061.546
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061.542
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 219
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 16
LENGTH: 1040
TYPE: DNA
ORGANISM: Homo sapiens
US-09-288-143-16

Query Match 1.68; Score 45; DB 4; Length 1077
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1043 AACCTCTGCTCCCGGGTTCAGGCGATTCTCTGCTCAGGCTCC 1077
|||||
DB 947 AACCTCTGCTCCCGGGTTCAGGCGATTCTCTGCTCAGGCTCC 943

RESULT 17
US-09-078-294-9
Sequence 9, Application US/09078294
Patent No. 6265211
GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree

APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 9
LENGTH: 1701
TYPE: DNA
ORGANISM: BAC P2 contig 5
US-09-078-294-9

Query Match 1.68; Score 45; DB 4; Length 1701;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1033 AACCTCTGCTCCCGGGTTCAGGCGATTCTCTGCTCAGGCTCC 1077
|||||
DB 1182 AACCTCTGCTCCCGGGTTCAGGCGATTCTCTGCTCAGGCTCC 1226

RESULT 18
US-08-257-963B-12
Sequence 12, Application US/08257963B
Patent No. 5840686
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Becerra, S.
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Tanikawa, Takayuki
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION OF ITS NOVEL
TITLE OF INVENTION: BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,963B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DACKET NUMBER: 202641260S1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3267 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: J1109
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: 3.3 kb PCR product

OTHER INFORMATION: using primers, SEQ ID No. 5849686 15 and 16
US-08-257-463B-12

Query Match: 1.6%; Score 45; DB 2; Length 4267;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTTGGCTCCCAAGTGTGGATTACAGGCATGAGCCAC 1234
|||||
DB 613 CCCACCTTGGCTCCCAAGTGTGGATTACAGGCATGAGCCAC 657

RESULT 19

US 08-467-841A-12
Sequence 12, Application US/08367841A
Patent No. 6319687
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Rodriguez,
APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Lomban-Tink, Joyce
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
NUMBER OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367.841A
FILING DATE: 30-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUIH
REGISTRATION NUMBER: 46434
REFERENCE/DOCKET NUMBER: 20264126US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6840
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3267 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: JT109
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: 3.3 kb PCR product
OTHER INFORMATION: using primers, SEQ ID No. 6319687 15 and 16
US-08-367-841A-12

Query Match: 1.6%; Score 45; DB 4; Length 4267;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTTGGCTCCCAAGTGTGGATTACAGGCATGAGCCAC 1234

DB 613 CCCACCTTGGCTCCCAAGTGTGGATTACAGGCATGAGCCAC 657
|||||

RESULT 20

PCT-US95-07201-12
Sequence 12, Application PC/IUS9507201
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
NUMBER OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07201
FILING DATE: 06 JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUIH
REGISTRATION NUMBER: 46434
REFERENCE/DOCKET NUMBER: 20264126PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6840
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3267 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: JT109
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: 3.3 kb PCR product
OTHER INFORMATION: using primers, SEQ ID No: 15 and 16
PCT-US95-07201-12

Query Match: 1.6%; Score 45; DB 5; Length 3267;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTTGGCTCCCAAGTGTGGATTACAGGCATGAGCCAC 1234
|||||

DB 613 CCCACCTTGGCTCCCAAGTGTGGATTACAGGCATGAGCCAC 657

RESULT 21

US-09-499 884-11/C

```
; Sequence 11, Application US/09499884
; Patent No. 6265172
; GENERAL INFORMATION:
; APPLICANT: St. Clair, Daret
; APPLICANT: Urano, Muneyasu
; APPLICANT: Kasarskis, Edward
; TITLE OF INVENTION: DIAGNOSTIC TEST AND THERAPY FOR MANKINSE SUPEROXIDE DISMUTASE
; TITLE OF INVENTION: ASSOCIATED DISEASES
; FILE REFERENCE: 50229-180
; CURRENT APPLICATION NUMBER: US/09/499,884
; CURRENT FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 3663
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-499-884-11

Query Match      1.6%; Score 45; DB 4; Length 4563;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1033 AACCTGCTCCCTCCCGGTTCAAGCGATTCTCTCCCTCCAGCTCC 1077
      |||||
Db 1970 AACCTGCTCCCTCCCGGTTCAAGCGATTCTCTCCCTCCAGCTCC 1926

RESULT 22
US-09-689-423-1
; Sequence 1, Application US/09689423
; Patent No. 6414131
; GENERAL INFORMATION:
; APPLICANT: Berrettini, Wade H.
; TITLE OF INVENTION: Gene and Methods for Diagnosing Neuropsychiatric
; TITLE OF INVENTION: Disorders and Treating Such Disorders
; FILE REFERENCE: PENN-0731
; CURRENT APPLICATION NUMBER: US/09/689,423
; CURRENT FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/195,620
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/159,354
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3844
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-689-423-1

Query Match      1.6%; Score 45; DB 4; Length 644;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1033 AACCTGCTCCCTCCCGGTTCAAGCGATTCTCTCCCTCCAGCTCC 1077
      |||||
Db 1472 AACCTGCTCCCTCCCGGTTCAAGCGATTCTCTCCCTCCAGCTCC 1516

RESULT 23
US-09-520-3730-5
; Sequence 5, Application US/08520373D
; Patent No. 6451763
; GENERAL INFORMATION:
; APPLICANT: Tombran-Tink, Joyce
; APPLICANT: Steele, Fintan R
; APPLICANT: Chader, Gerald J
; APPLICANT: Becerra, Sofia P
; APPLICANT: Johnson, Lincoln V
; APPLICANT: Rodriguez, Ignacio R
; TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NERVE GROWTH FACTOR
; FILE REFERENCE: 2026-4203US1
```

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; CURRENT APPLICATION NUMBER: US/08/520,373D
; CURRENT FILING DATE: 1995-08-29
; PRIOR APPLICATION NUMBER: 08/377,710
; PRIOR FILING DATE: 1995-01-25
; PRIOR APPLICATION NUMBER: 08/279,979
; PRIOR FILING DATE: 1994-07-25
; PRIOR APPLICATION NUMBER: 07/894,215
; PRIOR FILING DATE: 1992-06-04
; PRIOR APPLICATION NUMBER: 07/952,796
; PRIOR FILING DATE: 1992-09-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 5262
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: EXON 35-161; EXON 1142-1297; EXON 1984-2187;
; OTHER INFORMATION: EXON 5170-5255; INTRON 162-1141; INTRON
; OTHER INFORMATION: 1298-1983; INTRON 2188-5169; CDS 35-161; CDS
; OTHER INFORMATION: 1142-1297; CDS 1984-2187; CDS 5170-5255
; NAME/KEY: exon
; LOCATION: (35)..(160)
; NAME/KEY: exon
; LOCATION: (1142)..(1297)
; NAME/KEY: exon
; LOCATION: (1984)..(2187)
; NAME/KEY: exon
; LOCATION: (5170)..(5256)
; NAME/KEY: intron
; LOCATION: (162)..(1141)
; NAME/KEY: intron
; LOCATION: (1298)..(1983)
; NAME/KEY: intron
; LOCATION: (2188)..(5169)
; OTHER INFORMATION: n = a or g or t or c, any base
; US-08-520-3730-5

Query Match      1.6%; Score 45; DB 4; Length 5262;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1190 CCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCAC 1234
      |||||
Db 2607 CCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCAC 2651

RESULT 24
US-08-973-544-1/c
; Sequence 1, Application US/08973544
; Patent No. 6338950
; GENERAL INFORMATION:
; APPLICANT: WEISS, Elisabeth
; TITLE OF INVENTION: NEW IMMUNOREGULATORY PROTEIN LST-1
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKALDO, MARCELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth St., NW, Suite 300, G St. Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,544
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCI EP 96/02663
```

FILING DATE: 20-JUN-1996
PRIOR APPLICATION DATA: EP 95109511.6
FILING DATE: 20-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112201.9
FILING DATE: 03-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kitts, Monica Chin
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P8341-7073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5069
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5581 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: exon
LOCATION: 48..162
FEATURE:
NAME/KEY: exon
LOCATION: 544..652
FEATURE:
NAME/KEY: exon
LOCATION: 1044..1162
FEATURE:
NAME/KEY: exon
LOCATION: 1475..1567
FEATURE:
NAME/KEY: exon
LOCATION: 1775..1797
FEATURE:
NAME/KEY: exon
LOCATION: 2325..2709

Query Match 1.6% Score 45; DB 4; Length 5581
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1633 AACCTGCTCCCGGTTCAAGCGATTCTCTGCTCAGCCTCC 1077
|||||
DB 4362 AACCTGCTCCCGGTTCAAGCGATTCTCTGCTCAGCCTCC 4418

RESULT 25
US-09-328-174A-1
Sequence 1, Application US/09328174A
Patent No. 6448003
GENERAL INFORMATION:
APPLICANT: Guida, Marco
APPLICANT: Kurth, Janice
TITLE OF INVENTION: Genotyping Human Phenol Sulfotransferase
TITLE OF INVENTION: (STP2)
FILE REFERENCE: 4389-6 (formerly SEQ-16P)
CURRENT APPLICATION NUMBER: US/09/328.174A
CURRENT FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 09/328.174
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 8396
TYPE: DNA
ORGANISM: H. sapiens
US-09-328-174A-1

Query Match 1.6% Score 45; DB 4; Length 8396;

Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1033 AACCTGCTCCCGGTTCAAGCGATTCTCTGCTCAGCCTCC 1077
|||||
DB 701 AACCTGCTCCCGGTTCAAGCGATTCTCTGCTCAGCCTCC 745

RESULT 26
US-09-167-681-37
Sequence 37, Application US/09167681A
Patent No. 6265561
GENERAL INFORMATION:
APPLICANT: Weinshilbaum, M.D., Richard M.
APPLICANT: Rattouanis, Rebecca B.
APPLICANT: Wood, Thomas C.
APPLICANT: Otterness, Diane M.
TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
FILE REFERENCE: 07039/118001
CURRENT APPLICATION NUMBER: US/09/167,681A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 37
LENGTH: 8397
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (3730)...(3879)
NAME/KEY: CDS
LOCATION: (3987)...(4112)
NAME/KEY: CDS
LOCATION: (4198)...(4293)
NAME/KEY: CDS
LOCATION: (6088)...(6213)
NAME/KEY: CDS
LOCATION: (6309)...(6404)
NAME/KEY: CDS
LOCATION: (7214)...(7393)
NAME/KEY: CDS
LOCATION: (7516)...(7629)
US-09-167-681-37

Query Match 1.6% Score 45; DB 4; Length 8409;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1033 AACCTGCTCCCGGTTCAAGCGATTCTCTGCTCAGCCTCC 1077
|||||
DB 701 AACCTGCTCCCGGTTCAAGCGATTCTCTGCTCAGCCTCC 745

RESULT 27
US-08-367-841A-43
Sequence 43, Application US/08367841A
Patent No. 6319687
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Rodriguez,
APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Tombran-Tink, Joyce
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,841A
FILING DATE: 30-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 202641260S2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: PL-147
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: full length genomic
OTHER INFORMATION: sequence for PEDF plus flanking sequences.
US-08-167-841A-43

Query Match 1.6% Score 45; DB 4; Length 22481;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTGGCGCTCCCAAGTGGGATTACAGGCATGAGCCAC 1234
|||||
DB 17174 CCCACCTGGCGCTCCCAAGTGGGATTACAGGCATGAGCCAC 17218

RESULT 28
PCT US95-07201-43
Sequence 43, Application PC/TUS9507201
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Recerra, Sofia
APPLICANT: Patricia Schwartz, Jada P.
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR CHARACTERIZATION OF THE PEDF GENE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07201
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:

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APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: PL-147
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: full length genomic
OTHER INFORMATION: sequence for PEDF plus flanking sequences.
PCT-US95-07201-43

Query Match 1.6% Score 45; DB 5; Length 22481;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTGGCGCTCCCAAGTGGGATTACAGGCATGAGCCAC 1234
|||||
DB 17174 CCCACCTGGCGCTCCCAAGTGGGATTACAGGCATGAGCCAC 17218

RESULT 29
US-09-875-223-2
Sequence 2, Application US/09875223
Patent No. 6391850
GENERAL INFORMATION:
APPLICANT: No. 6391850, Western University
APPLICANT: David Dawson
APPLICANT: Paul Gillis
TITLE OF INVENTION: Methods and Compositions for Inhibiting Angiogenesis
FILE REFERENCE: 0290-2303
CURRENT APPLICATION NUMBER: US/09/875,223
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 09/122,079
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: PCT/US98/15228
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: US 08/899,304
PRIOR FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 22484
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Unsure
LOCATION: 1...22484
OTHER INFORMATION: "n" means either a, c, t, or g
US-09-875-223-2

Query Match 1.6% Score 45; DB 4; Length 22484;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
QY 1190 CCACCTTGCGCTCCCAAGTGGCTGGGATTAACAGGCATGAGCCAA 124
||||| ||||||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 17174 CCACCTTGCGCTCCCAAGTGGCTGGGATTAACAGGCATGAGCCAA 17218

RESULT 30
US 09-797-906-3
? Sequence 3, Application US/09797906
? Patent No. 6329188
? GENERAL INFORMATION:
? APPLICANT: Ziaoghe YAN, Karen A. KETCHUM, Valentina DIFFANTUSCO, Eileen M. BEASLEY
? TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND
? TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
? TITLE OF INVENTION: USES THEREOF
? FILE REFERENCE: CLO01151CIP
? CURRENT APPLICATION NUMBER: US/09/797,906
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 3
? LENGTH: 84495
? TYPE: DNA
? ORGANISM: Human
? FEATURE:
? NAME/KEY: misc-feature
? LOCATION: (1)...(84495)
? OTHER INFORMATION: n = A,T,C or G
US-09-797-906-3

Query Match 1.6% Score 45; DB 4; Length 84495;
Best Local Similarity 100.0%; Pred. No. 1e 10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1192 CACTTGGCTCCCAAGTGGCTGGGATTAACAGGCATGAGCCAA 124
||||| ||||||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 24248 CACTTGGCTCCCAAGTGGCTGGGATTAACAGGCATGAGCCAA 24265

RESULT 31
US-08-724-394A-20
? Sequence 20, Application US/08724394A
? Patent No. 5872237
? GENERAL INFORMATION:
? APPLICANT: Feder, John N.
? APPLICANT: Krommal, Gregory S.
? APPLICANT: Lauer, Peter M.
? APPLICANT: Ruddy, David A.
? APPLICANT: Thomas, Winston
? APPLICANT: Tsuchihashi, Zenta
? APPLICANT: Wolff, Roger K.
? TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
? TITLE OF INVENTION: Sequences and Antibodies Thereof
? NUMBER OF SEQUENCES: 31
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
? STREET: Two Embarcadero Center, 8th Floor
? CITY: San Francisco
? STATE: CA
? COUNTRY: USA
? ZIP: 94111-3834
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/724,394A
? FILING DATE: 01-OCT-1996
? CLASSIFICATION: 536
? ATTORNEY/AGENT INFORMATION:
? NAME: Fitts, Renee A.
? REGISTRATION NUMBER: 35,136
? REFERENCE/INKET NUMBER: 017957-000100
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-576-0200
? TELEFAX: 415-576-0400
? INFORMATION FOR SEQ ID NO: 21:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 246240 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: not relevant
? TOPOLOGY: not relevant
? FEATURE: not relevant
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: misc-feature
```

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? REFERENCE/INKET NUMBER: 017957-000100
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-576-0200
? TELEFAX: 415-576-0400
? INFORMATION FOR SEQ ID NO: 20:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 246240 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: not relevant
? TOPOLOGY: not relevant
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: misc-feature
? LOCATION: 1...246240
? OTHER INFORMATION: /note= "HLA-H CONTIG"
US-08-724-394A-20

Query Match 1.6% Score 45; DB 2; Length 246240;
Best Local Similarity 100.0%; Pred. No. 9.6e-11;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1033 AACCTGCGCTCCCAAGTGGCTGGGATTAACAGGCATGAGCCATCC 1077
||||| ||||||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 242021 AACCTGCGCTCCCAAGTGGCTGGGATTAACAGGCATGAGCCATCC 242065

RESULT 32
US-08-724-394A-21
? Sequence 21, Application US/08724394A
? Patent No. 5872237
? GENERAL INFORMATION:
? APPLICANT: Feder, John N.
? APPLICANT: Krommal, Gregory S.
? APPLICANT: Lauer, Peter M.
? APPLICANT: Ruddy, David A.
? APPLICANT: Thomas, Winston
? APPLICANT: Tsuchihashi, Zenta
? APPLICANT: Wolff, Roger K.
? TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
? TITLE OF INVENTION: Sequences and Antibodies Thereof
? NUMBER OF SEQUENCES: 31
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
? STREET: Two Embarcadero Center, 8th Floor
? CITY: San Francisco
? STATE: CA
? COUNTRY: USA
? ZIP: 94111-3834
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/724,394A
? FILING DATE: 01-OCT-1996
? CLASSIFICATION: 536
? ATTORNEY/AGENT INFORMATION:
? NAME: Fitts, Renee A.
? REGISTRATION NUMBER: 35,136
? REFERENCE/INKET NUMBER: 017957-000100
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-576-0200
? TELEFAX: 415-576-0400
? INFORMATION FOR SEQ ID NO: 21:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 246240 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: not relevant
? TOPOLOGY: not relevant
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: misc-feature
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LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H-CONTIG"
US-08-724-394A-21

Query Match 1.6% Score 45; DB 2; Length 246240;
Best Local Similarity 100.0%; Pred. No. 9.6e-11;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1033 AACCTCTGCTCCCGGTTCAAGCGATTCTCTCTCTAGAGTCTG 1672
|||||
DB 242021 AACCTCTGCTCCCGGTTCAAGCGATTCTCTCTCTAGAGTCTG 242021

RESULT 43

US-08-724-394A-22
Sequence 22, Application US/08724394A
Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237
TITLE OF INVENTION: Sequences and Antibodies Thereof
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS: 31
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724.394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Filts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: C17957

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
SIGNATURE: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H-CONTIG"

US-08-724-394A-22

Query Match 1.6% Score 45; DB 2; Length 246240;
Best Local Similarity 100.0%; Pred. No. 9.6e-11;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1033 AACCTCTGCTCCCGGTTCAAGCGATTCTCTCTCTAGAGTCTG 1672
|||||
DB 242021 AACCTCTGCTCCCGGTTCAAGCGATTCTCTCTCTAGAGTCTG 242021

RESULT 34

US-09-374-454-20/c
Sequence 20, Application US/093744454
Patent No. 6395548

GENERAL INFORMATION:

APPLICANT: Lee, Mu En
APPLICANT: Matsumura, Koji
APPLICANT: Hsieh, Chung-Ming
TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
FILE REFERENCE: 05433/037001
CURRENT APPLICATION NUMBER: US/09/374,454
CURRENT FILING DATE: 1999-08-13
EARLIER APPLICATION NUMBER: US 60/096,515
EARLIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 6792
TYPE: DNA
ORGANISM: Homo sapiens
US-09-374-454-20

Query Match 1.5% Score 44; DB 4; Length 6792;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1198 GGCTCTCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCC 1241
|||||

DB 5397 GGCTCTCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCC 5354

RESULT 35

US-09-741-150-3/c
Sequence 3, Application US/09741150
Patent No. 6436689

GENERAL INFORMATION:

APPLICANT: GUGLIER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS.
FILE REFERENCE: USFS THEREOF
FILE REFERENCE: C1C000968
CURRENT APPLICATION NUMBER: US/09/741,150
CURRENT FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 112132
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(112132)
OTHER INFORMATION: n = A,T,C or G

US-09-741-150-3

Query Match 1.5% Score 44; DB 4; Length 112132;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CTTTGCTCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGTC 1237
|||||

DB 18454 CTTTGCTCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGTC 18411

RESULT 36

US-09-128-155-17/c
Sequence 17, Application US/09128155
Patent No. 6117654

GENERAL INFORMATION:

APPLICANT: Pao, Yung
TITLE OF INVENTION: NEW MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09434/052301

CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 176373
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(176373)
OTHER INFORMATION: n - A,T,C or G
US-09-128-155 17

Query Match 1.5%: Score 44; DB 4; Length 176373;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1194 CTTGGCCTCCCAAGTGTGGGATTACAGGATGAGGACACTG 1237
|||||
DB 45158 CTTGGCCTCCCAAGTGTGGGATTACAGGATGAGGACACTG 15115

RESULT 47
US-08-471-570-9/c
Sequence 9, Application US/08471570
Patent No. 5750371
GENERAL INFORMATION:
APPLICANT: IGARASHI, Koichi
APPLICANT: SENOO, Masaharu
APPLICANT: WATANABE, Tatsuya
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,570
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/149,664
FILING DATE:

APPLICATION NUMBER: US 07/743369
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: LINEK, Ernest V
REGISTRATION NUMBER: 29822
REFERENCE/DOCKET NUMBER: 40897
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2310 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 25..1980
US-08-471-570-9

Query Match 1.5%: Score 43; DB 1; Length 2310;
Best Local Similarity 100.0%; Pred. No. 9.1e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1198 GGCCTCCCAAGTGTGGGATTACAGGATGAGGACACTGCGCC 1240
|||||
DB 2066 GGCCTCCCAAGTGTGGGATTACAGGATGAGGACACTGCGCC 2024

RESULT 38
US-08-471-570-7/c
Sequence 7, Application US/08471570
Patent No. 5750371
GENERAL INFORMATION:
APPLICANT: IGARASHI, Koichi
APPLICANT: SENOO, Masaharu
APPLICANT: WATANABE, Tatsuya
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,570
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/149,664
FILING DATE:

APPLICATION NUMBER: US 07/743369
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: LINEK, Ernest V
REGISTRATION NUMBER: 29822
REFERENCE/DOCKET NUMBER: 40897
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2676 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 25..2331
US-08-471-570-7

Query Match 1.5%: Score 43; DB 1; Length 2676;
Best Local Similarity 100.0%; Pred. No. 9.1e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1198 GGCCTCCCAAGTGTGGGATTACAGGATGAGGACACTGCGCC 1240
|||||

Db 2417 GGCCTCCCAAGTGTGGATTACAGGCAATGAGCACTGGCTC 2375

RESULT 39

US-09-975-080-35
Sequence 35, Application US/08975080
Patent No. 6245523
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975-080
FILING DATE: 20-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,435
FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01 WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 14796 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-975-080-35

Query Match 1.5%: Score 43; DB 4; Length 14796;
Best Local Similarity 100.0%; Pred. No. 8.4e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1035 CCTCTGCTCCGGGTTCAAGCGATTCTCTGCTCAGCCTCC 1077
|||||
Db 2420 CCTCTGCTCCGGGTTCAAGCGATTCTCTGCTCAGCCTCC 2362

RESULT 40

US-09-630-706-10
Sequence 10, Application US/09630706
Patent No. 627640
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION
FILE REFERENCE: RTS-0053
CURRENT APPLICATION NUMBER: US/09/630,706
CURRENT FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 94
SEQ ID NO 10
LENGTH: 14796
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS

LOCATION: (2811)...(2921)
NAME/KEY: CDS
LOCATION: (3174)...(3283)
NAME/KEY: CDS
LOCATION: (5158)...(5275)
NAME/KEY: CDS
LOCATION: (11955)...(12044)
US-09-630-706-10

Query Match 1.5%: Score 43; DB 4; Length 14796;
Best Local Similarity 100.0%; Pred. No. 8.4e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1035 CCTCTGCTCCGGGTTCAAGCGATTCTCTGCTCAGCCTCC 1077
|||||
Db 2320 CCTCTGCTCCGGGTTCAAGCGATTCTCTGCTCAGCCTCC 2362

RESULT 41

US-09-496-694B-3
Sequence 3, Application US/09496694B
Patent No. 6335194
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Eric E. Swayze
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
FILE REFERENCE: ISPH-0439
CURRENT APPLICATION NUMBER: US/09/496,694B
CURRENT FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 09/286,407
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 09/163,162
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 249
SEQ ID NO 3
LENGTH: 14796
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (2811)...(2921)
NAME/KEY: CDS
LOCATION: (3174)...(3283)
NAME/KEY: CDS
LOCATION: (5158)...(5275)
NAME/KEY: CDS
LOCATION: (11955)...(12044)
US-09-496-694B-3

Query Match 1.5%: Score 43; DB 4; Length 14796;
Best Local Similarity 100.0%; Pred. No. 8.4e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1035 CCTCTGCTCCGGGTTCAAGCGATTCTCTGCTCAGCCTCC 1077
|||||
Db 2320 CCTCTGCTCCGGGTTCAAGCGATTCTCTGCTCAGCCTCC 2362

RESULT 42

US-09-341-587-7
Sequence 7, Application US/09341587
Patent No. 634606
GENERAL INFORMATION:
APPLICANT: Moellenhauer, Jan
TITLE OF INVENTION: Protein Containing an SRCR Domain
FILE REFERENCE: 4121-108
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 28720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-341-587-7

Query Match 1.5%; Score 43; DB 4; Length 28720;
Best Local Similarity 100.0%; Pred. No. 8.1e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1033 AACCTGCTCCCGGTTCAAGCGATTCTCGTGGTAGGCT 1075
|||||
DB 19480 AACCTGCTCCCGGTTCAAGCGATTCTCGTGGTAGGCT 19522

RESULT 45
US-09-780-049-18
; Sequence 18, Application US/09780049
; Patent No. 6465250
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT
; FILE REFERENCE: RTS-0134
; CURRENT APPLICATION NUMBER: US/09/780,049
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 18
; LENGTH: 40000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-780-049-18

Query Match 1.5%; Score 43; DB 4; Length 40000;
Best Local Similarity 100.0%; Pred. No. 8e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1194 CTTGCTCCCAAGTGTGGGATTACAGGCATGAGCCACTG 1236
|||||
DB 16933 CTTGCTCCCAAGTGTGGGATTACAGGCATGAGCCACTG 16976

RESULT 44
US-09-851-896-3/C
; Sequence 3, Application US/09851896
; Patent No. 6410325
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Wall
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+)-DEPENDENT
; FILE REFERENCE: RTS-0220
; CURRENT APPLICATION NUMBER: US/09/851,896
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 3
; LENGTH: 70000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-851-896-3

Query Match 1.5%; Score 43; DB 4; Length 70000;
Best Local Similarity 100.0%; Pred. No. 7.8e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1199 GTCCTCCCAAGTGTGGGATTACAGGCATGAGCCACTG 1241
|||||
DB 31602 GTCCTCCCAAGTGTGGGATTACAGGCATGAGCCACTG 31563

RESULT 45
US-09-268-992-7/c
; Sequence 7, Application US/09268992
; Patent No. 6342351
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Freimer, N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/268,992
; PRIOR FILING DATE: 1999-03-16
; EARLIER APPLICATION NUMBER: 09/236,134
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: 60/106,056
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/088,312
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/078,044
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 72604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: all n positions
; OTHER INFORMATION: n-a, c, g, or t
US-09-268-992-7

Query Match 1.5%; Score 43; DB 4; Length 72604;
Best Local Similarity 100.0%; Pred. No. 7.8e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1199 GCCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGCGCC 1241
|||||
DB 63856 GCCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGCGCC 63814

RESULT 46
US-09-657-474-7/c
; Sequence 7, Application US/09657474
; Patent No. 6392762
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Freimer, N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/657,474
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 09/288,992
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/106,056
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/088,312
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/078,044
; PRIOR FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 72604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base

```

; LOCATION: all n positions
; OTHER INFORMATION: n-a, c, g, or t
US-09-557 474-7

Query Match      1.5%: Score 43; DB 4; Length 72604;
Best Local Similarity 100.0%; Pred. No. 7,8e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1199 GCGTCGCAAGTCTGGGATTACAGGCATGCGGCATGCGGC 1241
      |||||
DB 64855 GCGTCGCAAGTCTGGGATTACAGGCATGCGGCATGCGGC 64814

RESULT 47
US-09-750-580-1
; Sequence 1, Application US/09750580
; Patent No. 6455280
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Bihain, Bernard
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Ebbets-Reed, Dana
; APPLICANT: Salter-Cid, Luisa
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
; FILE REFERENCE: 89 US2.CIP
; CURRENT APPLICATION NUMBER: US/09750580
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 09/594,362
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCI/IB00/G101
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCI/IB99/02058
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 49/469/099
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/141,032
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 81001
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10946..12946
; OTHER INFORMATION: 5'regulatory region
; NAME/KEY: exon
; LOCATION: 12947..12958
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 13470..13526
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: 13641..13752
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: 14271..15968
; OTHER INFORMATION: exon 4
; NAME/KEY: misc_feature
; LOCATION: 15969..17969
; OTHER INFORMATION: 3'regulatory region
; NAME/KEY: allele
; LOCATION: 1239
; OTHER INFORMATION: 20-828-311 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 12347
; OTHER INFORMATION: 20-841-149.mis complement

; OTHER INFORMATION: 17-42-319 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 15241
; OTHER INFORMATION: 17-41-250 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 42218
; OTHER INFORMATION: 20-841-149 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 45442
; OTHER INFORMATION: 20-842-115 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 77058
; OTHER INFORMATION: 20-853-415 : polymorphic base C or T
; NAME/KEY: primer_bind
; LOCATION: 929..949
; OTHER INFORMATION: 20-828.pu
; NAME/KEY: primer_bind
; LOCATION: 1357..1377
; OTHER INFORMATION: 20-828.rp complement
; NAME/KEY: primer_bind
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; NAME/KEY: primer_bind
; LOCATION: 12581..12603
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; LOCATION: 14992..15012
; OTHER INFORMATION: 17-41.pu
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; OTHER INFORMATION: 17-41.rp complement
; NAME/KEY: primer_bind
; LOCATION: 42070..42090
; OTHER INFORMATION: 20-841.pu
; NAME/KEY: primer_bind
; LOCATION: 42572..42591
; OTHER INFORMATION: 20-841.rp complement
; NAME/KEY: primer_bind
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; NAME/KEY: primer_bind
; LOCATION: 45863..45883
; OTHER INFORMATION: 20-842.rp complement
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; LOCATION: 76644..76664
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; NAME/KEY: primer_bind
; LOCATION: 77166..77185
; OTHER INFORMATION: 20-853.rp complement
; NAME/KEY: primer_bind
; LOCATION: 1220..1238
; OTHER INFORMATION: 20-828-311.mis
; NAME/KEY: primer_bind
; LOCATION: 1240..1258
; OTHER INFORMATION: 20-828-311.mis complement
; NAME/KEY: primer_bind
; LOCATION: 12328..12346
; OTHER INFORMATION: 17-42-319.mis
; NAME/KEY: primer_bind
; LOCATION: 12348..12366
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; NAME/KEY: primer_bind
; LOCATION: 15222..15240
; OTHER INFORMATION: 17-41-250.mis
; NAME/KEY: primer_bind
; LOCATION: 15242..15260
; OTHER INFORMATION: 17-41-250.mis complement
; NAME/KEY: primer_bind
; LOCATION: 42199..42217
; OTHER INFORMATION: 20-841-149.mis
; NAME/KEY: primer_bind
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; OTHER INFORMATION: 20-841-149.mis complement
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NAME/KEY: primer_bind
LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer_bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer_bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc_binding
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc_binding
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc_binding
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc_binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc_binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc_binding
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1

Query Match 1.5%; Score 43; DB 4; Length 8001;
Best Local Similarity 100.0%; Pred. No. 7.7e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1198 GGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCC 1240
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DB 59318 GGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCC 59360

RESULT 48
US-09-791-211-10/C
Sequence 10, Application US/09791211
Patent No. 6448080
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
TITLE OF INVENTION: ANTISENSE MODULATION OF WGN EXPRESSION
FILE REFERENCE: RTS-0205
CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 10
LENGTH: 98844
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: 24962
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 64383
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65468
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65469
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65470
OTHER INFORMATION: unknown

NAME/KEY: unsure
LOCATION: 65471
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 87130
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 89049
OTHER INFORMATION: unknown
US-09-791-211-10

Query Match 1.5%; Score 43; DB 4; Length 98844;
Best Local Similarity 100.0%; Pred. No. 7.7e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1189 GGCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGC 1231
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DB 55998 GGCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGC 55956

RESULT 49
US-09-798-096-10/C
Sequence 10, Application US/09798096
Patent No. 6399178
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXPRESSION
FILE REFERENCE: RTS-0207
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 10
LENGTH: 99500
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-798-096-10

Query Match 1.5%; Score 43; DB 4; Length 93500;
Best Local Similarity 100.0%; Pred. No. 7.7e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1198 GGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCC 1240
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DB 79008 GGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCC 78966

RESULT 50
US-08-812-204-1
Sequence 1, Application US/08812204
Patent No. 5965790
GENERAL INFORMATION:
APPLICANT: Acton, Susan L.
TITLE OF INVENTION: SR-BI REGULATORY SEQUENCES AND
TITLE OF INVENTION: THERAPEUTIC METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,204
FILING DATE: 06-MAR-1997

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CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MIA-014.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1613 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-812-204-1

Query Match      1.5%   Score 42;   DB 2;   Length 1613;
Best Local Similarity 100.0%;   Pred. NO. 2.5e-09;
Matches 42;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY  1040 GCCTCCCGGGTTCAGCGATTCTCTGCTCAGGCTCTGAG 1681
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DB  447 GCCTCCCGGGTTCAGCGATTCTCTGCTCAGGCTCTGAG 486

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Search completed: May 10, 2003, 04:39:45
Job time : 4287.72 secs

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CM nucleic - nucleic search, using sw model

Run on: May 10, 2003, 01:55:23 ; Search time 1947 seconds
(without alignments)
2376.534 Million cell updates/sec

Title: US-09-846-456-5
Perfect score: 159
Sequence: 1 ttaatgaccagccacagggc.....ctttcaagagacacacacata t59

Scoring table:
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Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues
Word size : 0

Total number of hits satisfying chosen parameters: 4112260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post processing: Listing first 45 summaries

Database : GenBank:
1: gb_ba:*
2: gb_htg:*
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10: gb_ro:*
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14: gb_vl:*
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16: em_in:*
17: em_hum:*
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24: em_ph:*
25: em_pl:*
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29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pin:*
35: em_htg_rnd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Prod. No. is the number of results predicted by chosen database

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	159	100.0	159	6	AX351033	AX351033 Sequence
2	159	100.0	357	6	AX351030	AX351030 Sequence
3	77	48.4	10442	6	AX060713	AX060713 Sequence
4	77	48.4	10442	6	AX060892	AX060892 Sequence
5	77	48.4	10442	9	AF285167	AF285167 Homo sapi
6	77	48.4	10474	6	AX060719	AX060719 Sequence
7	77	48.4	10474	6	AX060721	AX060721 Sequence
8	77	48.4	10474	6	AX060898	AX060898 Sequence
9	77	48.4	10474	6	AX060900	AX060900 Sequence
10	77	48.4	149034	9	AF275948	AF275948 Homo sapi
11	60	37.7	200	9	AF258623S2	AF258623S2 Homo sapi
12	60	37.7	298	9	AB037924	AB037924 Homo sapi
13	60	37.7	446	6	AX127764	AX127764 Sequence
14	60	37.7	446	6	AX139751	AX139751 Sequence
15	60	37.7	480	9	HS252277	HS252277 Homo sapi
16	60	37.7	697	9	AF258627	AF258627 Homo sapi
17	60	37.7	6786	9	AB055982	AB055982 Homo sapi
18	60	37.7	7260	6	AX253452	AX253452 Sequence
19	60	37.7	7860	6	AX092594	AX092594 Sequence
20	60	37.7	7862	6	AX135712	AX135712 Sequence
21	60	37.7	9741	6	AX127830	AX127830 Sequence
22	60	37.7	9741	6	AX139817	AX139817 Sequence
23	60	37.7	9741	6	AX351038	AX351038 Sequence
24	60	37.7	9854	6	AX127831	AX127831 Sequence
25	60	37.7	9854	6	AX139818	AX139818 Sequence
26	60	37.7	129608	9	AL353685	AL353685 Human DNA
27	60	37.7	175064	2	AC012230	AC012230 Homo sapi
28	60	37.7	183999	6	AX092589	AX092589 Sequence
29	60	37.7	201144	9	AF287262	AF287262 Homo sapi
30	51	32.1	1556	9	AK024328	AK024328 Homo sapi
31	44	27.7	90698	2	AC021345	AC021345 Homo sapi
32	35	22.0	37	6	AX092843	AX092843 Sequence
33	21	13.2	21	6	AX092705	AX092705 Sequence
34	21	13.2	21	6	AX092707	AX092707 Sequence
35	21	13.2	14809	4	AC091506	AC091506 Suis scro
36	20	12.6	152155	9	AC037388	AC037388 Homo sapi
37	19	11.9	470	6	AX389385	AX389385 Sequence
38	19	11.9	624	6	AR066487	AR066487 Sequence
39	19	11.9	624	6	AR074100	AR074100 Sequence
40	19	11.9	624	6	AR143612	AR143612 Sequence
41	19	11.9	624	6	BD005648	BD005648 Materials
42	19	11.9	684	6	AR074116	AR074116 Sequence
43	19	11.9	684	6	BD005644	BD005644 Materials
44	19	11.9	6842	9	AB014524	AB014524 Homo sapi
45	19	11.9	6855	9	AY099459	AY099459 Homo sapi

ALIGNMENTS

RESULT 1
AX351033
LOCUS AX351033
DEFINITION Sequence 5 : from Patent WO0183746.
ACCESSION AX351033
VERSION AX351033.1 GI:14616389
KEYWORDS
SOURCE Human
ORGANISM Homo Sapiens
REFERENCE 1
Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Kosler, Montu, M.F., Prades, C., Lemoine, C., Naudin, L., Benetle, P.,
Breuer, H., Duvet, N., Kemaley, A. and Santamarina-Farota, S.
TITLE Regulatory elements of the abcl gene

RESULT 5
AF285167 10442 bp mRNA linear PRI 09-AUG-2000
LOCUS Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA,
complete cds.
ACCESSION AF285167
VERSION AF285167.1 GI:9755156
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10442)
AUTHORS Schwartz,K., Lawn,R.M. and Wade,D.P.
TITLE ABCA1 gene expression and apoA1-mediated cholesterol efflux are
regulated by LXR
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 10442)
AUTHORS Lawn,R.M., Wade,D.P., Garvin,M.K., Mont,X., Schwartz,K.,
Porter,J.G., Seilheimer,J.J., Vauthier,A.M. and Garvin,M.P.
Direct Submission
Submitted (06-JUL-2000) Discovery Research, CV Technologies Inc.,
3172 Porter Drive, Palo Alto, CA 94304, USA
FEATURES
Location/Qualifiers
1..10442 /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/map="9q31"
/cell_type="fibroblast"
/tissue_type="skin"
1..10442 /gene="ABCA1"
291..7076 /gene="ABCA1"
/codon_start=1
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/protein_id="AAF98175.1"
/translation="MACWPQRLLIKMLNKKRSGTQCHLVAVWMLPEFLILSVRL
SYPPQHECHFPNKAMPAGILPWGGLICNNANRCPYEDGCAKGVGNFNKSYV
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NLSLPKSTVDKMLKAQVILIKVILQYQVHETSLONGSKSEEMIGLQDAFVSELGLP
KELAAERVLNRNMIDILKPLIKLNTSTSPFSSKELAFALKLHLSLGLAELFSRK
SWSDMRQEVLRNVNNSSTQYCAVSRVWGHPEQGTIKRSIMYEDNNIKALF
GNGLTEEDATFYINSTIPYCNQNMKNLSSPLRTIWEALKPELAKLYETDTLAF
RQVMAENVKTFQELAVFHLEGWHELSRKLKIPMENSLEILVRLLEISKI NHTWE
QQLQGLDWTADIVAFIAKHFEVWSSNGSVYTPFAKLEINAKRTLSREMEVNLK
KLPLEATEVLINJSSMELLERKKAHLYVETLIPQSLFELAKYKIRMDLNVKSK
NKIKGHWDRGPRADPEPRRYVWGHAYLQVYVQALTPVIGLEKKLYVWQWQY
PCYVDDILFVWMSRMPLEKTLATYSVAVLTNGTVYKTAARKETSRIMELNLSK
FSWFISSLIPULYSAGLLVILKLNLEPYSDH SWVEVTSFAVVTIQCEGLSTLF
SRMLAAACGLIYFTLYDPIVAVAGLYVETLKILASTLSVAPRQPTFALPE
EOGIGVQWDLNLFSPVEINGNITTSIMMLIEFTFLVGVWVWLEAVEPQYGIPEW
YFPTCKSYNFGESDEKSSGNKNSLQNFEPLEKALWSTONLVAVYRQWV
AVDLGLNFTVGGTISFLNGACKLIMSLISGLFPPLSTAYLEKTIKSEMSITK
QNLGCPVHNVHFMULTVEEDIPYAREKGLSEHKVKADEKALWGLPSSKLKSL
SOLSCGQKRLSVALAEFGGSKVLEPPTATVLYSKTLELLIKYRQCFLEIST
HMDDEAVLIGRTAITSRLGKLVWSSLEFKNGDTGYVLEVKRWESSLSKRNKS
STVSLYKEDSVSSQSDAGLSHESITLITVSALENLPRHVSARLAVEDIGHIL
TYVLPYAAKGEARVELEFHEIDUKLSGLISSVGLSSELPFLKVALESQVLAETS
DGLTPARKNRKFGKSCIRPTERADINDSDIDEFSPEDLSLSPKSKGSGYVK
GWLTKQOQFVALMKRLLIARSKKGFAGVLPVAVFVWALVESTLVPFGKTPSL
LOPMNYNEQYTFVSNADPEITGLLELNLIKHPECPQWMEINFIPDPCVAGEEEM
TTAPVPTIMDLFONGWIMQNPFAQCSSKCKKMLQVTPCAGGLPFPKQNTA
DILQDLTGRNLSYLVKTYGLIAKSLKNIKNNEFRVPLSLGVSNLGAIPRSDVN
DAIKOMKHLKAKDSADAPLNSLGRMFGLLIRNNKATNNKNGHIAISSFLNVLN
NAILLRNQLQENRSPHYGTFATNHLNITKQVSEVALETSVDVYSTVIFAMSPV
PASVWFLIQENRSKAKHAFISGVKPTVYWSNFWWMPNYYVPALELVITTECPQ
KSYVSNLPLVLLNLILLYKQSTLPLMYPASVFKLPSZAVVLSVNLNITLWNSVA
TEVLELPTDKNLNINILKSVLELIDPCELRCLIRKNAAMADALEETENKPSV
PLSNDILVGRNLFAMARQVVEFLITVLLQYKFFLEPPIASGLISGLNIEHVPKQ

BASE COUNT 2896 a 2297 c 2408 g 2835 t 4 others
ORIGIN
Query Match 48.4% Score 77: DB 9: Length 10442;
Best Local Similarity 99.2% Pred. No. 4.3e-32;
Matches 127: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 32 AGCTCTGAGGCTTGGCTTCAGGCTCCCGACGACACAGCTGGCGTGGCTGAGGGA 91
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DB 229 AGCTCTGAGGCTTGGCTTCAGGCTCCCGACGACACAGCTGGCGTGGCTGAGGGA 288
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QY 92 ACATGGATGCTGGCTTCAGCTGACCTGAGGTGCTGTGGAGAAAGCTCAGCTTCAAGAA 151
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DB 289 ACAAGGTGCTGGCTTCAGCTGAGGTGCTGTGGAGAAAGCTCAGCTTCAAGAA 348
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QY 152 GACAAACA 159
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DB 349 GACAAACA 456
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RESULT 6
AX060719 10474 bp DNA linear PAT 22-JAN-2001
LOCUS AX060719
DEFINITION Sequence 7 from Patent W00078972.
ACCESSION AX060719
VERSION AX060719.1 GI:12406108
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn,R.M., Wade,D. and Garvin,M.
TITLE Regulation with binding cassette transporter protein abcl
JOURNAL Patent: W0 0078972-A 7 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
Location/Qualifiers
1..10474 /organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2906 a 2305 c 2416 g 2843 t 4 others
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Best Local Similarity 99.2% Pred. No. 4.3e-32;
Matches 127: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 32 AGCTCTGAGGCTTGGCTTCAGGCTCCCGACGACACAGCTGGCGTGGCTGAGGGA 91
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DB 261 AGCTCTGAGGCTTGGCTTCAGGCTCCCGACGACACAGCTGGCGTGGCTGAGGGA 320
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QY 92 ACATGGATGCTGGCTTCAGCTGACCTGAGGTGCTGTGGAGAAAGCTCAGCTTCAAGAA 151
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DB 321 ACATGGATGCTGGCTTCAGCTGAGGTGCTGTGGAGAAAGCTCAGCTTCAAGAA 380
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DB 381 GACAAACA 488
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RESULT 7
AX060721 10474 bp DNA linear PAT 22-JAN-2001
LOCUS AX060721
DEFINITION Sequence 9 from Patent W00078972.
ACCESSION AX060721
VERSION AX060721.1 GI:12406109


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RESULT 9
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LOCUS
DEFINITION Sequence 9 from Patent W00078971.
ACCESSION AX060900
VERSION AX060900.1 GI:12406276
KEYWORDS
SOURCE human.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Lawo,R.M., Wade,D., Oram,J.F. and Garvin,M.
TITLE Atp binding cassette transporter protein abcl polypeptides
JOURNAL Patent: WO 0078971-A 9 28-DEC-2000;
CV THERAPEUTICS, INC..(US)
FEATURES
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         ..10474
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BASE COUNT 2507 a 2304 c 2415 g 2844 t          4 others
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Query Match      48.4% Score 77; DB 6; Length 10474;
Best Local Similarity 99.2%; Pred.No. 4.3e-32;
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 AGCTCGGGGCTGCCTTCAGGCTCCGAGGCACACAGCTGGCGTGTGGCTGAGGGA 91
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DB 261 AGCTCGGGGCTGCCTTCAGGCTCCGAGGCACACAGCTGGCGTGTGGCTGAGGGA 320
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QY 92 ACATGGCATGTTCGCTCAGTCAGTTGCTGTGTGGAAGAACCTCACTTCAGAAGAA 151
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DB 321 ACATGGCTGTGTGGCTCAGTCAGTTGCTGTGTGGAAGAACCTCACTTCAGAAGAA 380
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QY 152 GACAACAA 159
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DB 381 GACAACAA 388

RESULT 10
AF275948
LOCUS
DEFINITION Homo Sapiens ABCA1 (ABCA1) gene, complete cds.
ACCESSION AF275948
VERSION AF275948.1 GI:9247085
KEYWORDS
SOURCE Homo sapiens.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Santamaria-Fojo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L.,
Cheng,J.F., Osorio,J., Remaley,A., Yang,X.P., Haudenschild,C.,
Prades,G., Chinini,G., Blackmon,E., Francois,T., Duverger,N.,
Rubin,E.M., Kosier,M., Deneffe,P., Fredrickson,D.S. and Brewer,H.B. Jr.
Complete genomic sequence of the human ABCA1 gene: analysis of the
human and mouse Atp binding cassette A promoter
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
MEDLINE 20345099
PUBMED 10884428
REFERENCE
AUTHORS Santamaria-Fojo,S., Peterson,K.M., Knapper,C.L., Freeman,L.A.,
Remaley,A.T., Yang,X.-P., Haudenschild,C.C., Blackmon,E.E.,
Francois,T.I. and Brewer,H.B. Jr.
Direct Submission
Submitted (08-JUN-2000) Molecular Disease Branch, National
Institutes of Health, National Heart, Lung and Blood Institute,
Bethesda, MD 20892, USA
FEATURES
     location/Qualifiers
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DEFINITION Sequence 3 from Patent WO0130848.
ACCESSION AX127764
VERSION AX127764.1 GI:1413441

KEYWORDS Synthetic construct,
synthetic construct,
artificial sequences.

ORGANISM

REFERENCE 1 (bases 1 to 446)

AUTHORS Benefield, P., Rosier-Montus, M.F., Arnold Requejones, J., Prades, C.,
Naudin, L., Lemoine, C., Duverget, N., Jaye, M., Schreiss, G.B.,
Remaley, A., Brewer, H.B., and Dean, M.

TITLE Nucleic acids of the human abc1 gene and their therapeutic and

diagnostic application

JOURNAL Patent: WO 0130848-A 3 03-MAY-2001

Aventis Pharma S.A. (FR)

FEATURES

Location/Qualifiers
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Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 191 TGTGGGCTCAGCTGAGTTGCTGCTGGAGAAACCTTTCAGAGAAACA 250

RESULT 14

AX149751

LOCUS AX149751

DEFINITION Sequence 3 from Patent EP1094512

ACCESSION AX149751

VERSION AX149751.1 GI:14275338

KEYWORDS Synthetic construct,
artificial sequences.

ORGANISM

REFERENCE 1 (bases 1 to 446)

AUTHORS Benefield, P., Rosier-Montus, M.F., Arnold Requejones, J., Prades, C.,
Naudin, L., Lemoine, C., Duverget, N., Jaye, M., Schreiss, G.B.,
Remaley, A., Brewer, H.B., and Dean, M.

TITLE Nucleic acids of the human abc1 gene and their therapeutic and

diagnostic application

JOURNAL Patent: EP 1096012-A 4 02-MAY-2001

Aventis Pharma S.A. (FR)

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RESULT 15

HSA252277

LOCUS HSA252277

DEFINITION Homo sapiens partial ABC-1 gene for ATP-binding cassette

transporter-1, exon 2.

ACCESSION AJ252277

VERSION AJ252277.1 GI:12140344
KEYWORDS ABC-1 gene; ATP-binding cassette transporter-1.
SOURCE human.

ORGANISM

REFERENCE 1 (bases 1 to 480)

AUTHORS Porsch-Oezcuernomez, M., Langmann, T. and Schmitz, G.
TITLE Cloning and Characterization of the human ATP-binding Cassette
Transporter-1 (ABC-1) Promoter

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 480)

AUTHORS Porsch-Oezcuernomez, M.K.

TITLE Direct Submission

JOURNAL Submitted (07-JAN-2000) Porsch-Oezcuernomez M.K., Institute for

Clinical Chemistry, University of Regensburg,

Franz-Josef-Strauss-Allee 11, 93042 Regensburg, GERMANY

FEATURES

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Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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SUMMARIES

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2	159	100.0	357	24	Human ABC1 transcr
3	77	48.4	10442	22	Nucleotide sequenc
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9	60	37.7	446	22	Partial human ABC1

10	60	37.7	7086	22	ABA09200	Human ABCA1 homolo
11	60	37.7	7086	22	AAK52667	Human polynucleoti
12	60	37.7	7260	22	AAK21326	Human ATP binding
13	60	37.7	7260	22	AAI70315	Human ATP binding
14	60	37.7	7281	22	AAK51683	Human polynucleoti
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27	60	37.7	18399	22	AAAF92831	Human ABC1 genomic
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29	51	32.1	1556	22	AAH18606	Human ABC1 clone (
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34	21	13.2	21	22	AAAF92948	Polymorphic sequen
35	19	11.9	470	24	ABN64546	Human cancer relat
36	19	11.9	577	21	AAA68004	Pinus radiata PAL
37	19	11.9	624	19	AAV23916	Plant PAL enzyme D
38	19	11.9	624	20	AAZ06895	Pinus phenylalanine
39	19	11.9	624	21	AAAF67916	Pinus radiata PAL
40	19	11.9	684	19	AAV23865	Plant PAL enzyme D
41	19	11.9	684	20	AAZ06898	Pinus phenylalanine
42	19	11.9	684	21	AAA69586	Pinus radiata phen
43	19	11.9	684	21	AAA67952	Pinus radiata PAL
44	19	11.9	5286	23	AAAF73156	DNA encoding novel
45	19	11.9	5954	23	AAAS0591	DNA encoding novel

ALIGNMENTS

RESULT 1

ID AAD37269 standard: DNA: 159 BP.

XX AAD37269:

XX 21-AUG-2002 (first entry)

XX Human ABC1 gene exon 1B DNA.

DE Human ABC1 gene exon 1B DNA.

XX Human: ATP-binding cassette 1; ABC1 gene regulation: atherosclerosis;

KW cholesterol metabolism; hypercholesterolaemia; antisense therapy;

KW exon 1B; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 94..159

FT /product: "Protein encoded by human ABC1 gene exon 1B"

FT /note: "CDS does not include stop codon."

FT /partial

XX W0200183746 A2.

XX 08-NOV-2001.

XX 02-MAY-2001: 2001W0-EP05488.

XX 02-MAY-2000: 2000US-201280P.

XX (AVET) AVENTIS PHARMA SA.


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26: AGCTCTGGCGGCTGCTTCCAGAGCTCCGAGCCACACACCTGGGTGTGCTTGAGGGA 420
QY 92 ACATGGATGTTGGCTCAGCTCAGGTTCTGCTGGAGAGAACATCACTTACAGAA 151
DB 1111111111111111111111111111111111111111111111111111111
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QY 152 GACAAACA 159
DB 1111111111111111111111111111111111111111111111111111111
381 GACAAACA 388

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ID AAS44655 standard; cDNA: 446 BP.
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AC AAS44655:
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DE 12 SEP 2001 (first entry)
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KW cardiovascular; neurological; Tangier disease; LCAT deficiency;
KW lecithin:cholesterol acetyltransferase; malaria; diabetes; ss.
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DE 01-MAY-2000: 2000US-0186260.
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DE Denelle P, Rosier-Montus M, Arnold-Reichling L, Evans C, Naudin L,
DE Lemoine G, Duvetier N, Jaye M, Searles SM, Seale A, Brown H,
DE Dean M;
XX
DE W2001:416327/33.
DE P PS06: A0002176.
XX
DE New human ABC1 nucleic acids and polypeptides for treating
XX atherosclerosis, malaria and diabetes.
XX
DE Example 2: Page 167: 368pp: English.
XX
CC The sequence represents the partial reading sequence of human ABC1,
XX which encodes amino acids 1-60 of the human ABC1 protein. The nucleic
XX acid sequence, primers and probes derived from the ABC1 sequence, and
XX polypeptides and vectors are useful for the prevention of
XX atherosclerosis, in a subject affected by a dysfunction of the reverse
XX transport of cholesterol. The polypeptide encoded by the ABC1 gene is
XX useful for screening for an active ingredient for the prevention or
XX treatment of a disease resulting from dysfunction of the reverse
XX transport of cholesterol. The nucleic acids and polypeptides are also
XX useful for treating and preventing cardiovascular and neurological
XX pathologies, and other diseases e.g. Tangier disease, lecithin:
XX cholesterol (LCAT) deficiency, malaria and diabetes.
XX
SQ Sequence 446 BP: 96 A; 123 C; 122 G; 135 T; 6 other.
XX
Query Match 37.7% Score 40.00 E=22.0 Length 446
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Best Local Similarity 100.0%; Pred. No. 2.1e-20;
Matches 60: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 TGTGGCCCTCACTGAGGTTCTGCTGTGGAGAACCTCAGCTTCAGAGAGAGACAAACA 159
DB 1111111111111111111111111111111111111111111111111111111
191 TGTGGCCCTCACTGAGGTTCTGCTGTGGAGAACCTCAGCTTCAGAGAGAGACAAACA 250

RESULT 10
ID AHA09200 standard; cDNA: 7086 BP.
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AC AHA09200:
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DE 11-JAN-2002 (first entry)
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DE Human: ABC1 homologous encoding cDNA, SEQ ID NO:976.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW hematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW cytostatic; antiarthritis; haemostatic; antiarteriosclerotic;
KW osteoporosis; osteopathy; vasotropic; caidiant; virucide; antibacterial;
KW antifungal; vulvectomy; antitumor; ss.
XX
OS Homo sapiens.
XX
DB W2001:57188 A2.
XX
DE 09-AUG-2001.
XX
DE 05-FEB-2001: 2001W0-0504830.
XX
DE 03-FEB-2000: 2000US-0496914.
DE 27-APR-2000: 2000US-0560875.
XX
PA (HYSE-) HYSEQ INC.
XX
DE Tanq YT, Liu C, Lermanac RT;
XX WPI: 2001-457746/49.
DE P-PSUB: A0611966.
XX
DE Human proteins and DNA encoding sequences useful for preventing,
XX treating or ameliorating a medical condition in a mammalian subject
XX e.g. arthritis and cancer.
XX
PS Claim 1: Page 833-835; 1963pp: English.
XX
CC Sequences ABR10981-ABR12340 represent 1350 novel human polypeptides, and
XX sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
XX invention also relates to vectors and recombinant host cells comprising a
XX nucleotide of the invention, methods of producing the novel polypeptides,
XX antibodies against the polypeptides, methods of detecting the nucleotides
XX or polypeptides in a sample, and methods of identifying compounds which
XX bind to polypeptides of the invention. Although novel, many of the
XX polypeptides of the invention have homology to known proteins, thereby
XX giving an insight into their probable biological activities, and hence
XX potential therapeutic applications. The polypeptides of the invention may
XX have various activities, including cytokine, cell proliferation or cell
XX differentiation activities; stem cell growth factor activity;
XX hematopoiesis regulatory activity; tissue growth activity;
XX immunomodulatory activity; activin- or inhibin-related activities;
XX chemotactic or chemokinetic activities; haemostatic, thrombotic or
XX thrombolytic activities; receptor or ligand activities; or may be
XX involved in cell adhesion; cancer cell proliferation or metastasis.
```

depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroectodermal cells that can be used to augment or replace cells damaged by diabetes, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 37.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy - Claim 1; Page 4558-4560; 622lpp; English. The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAH80302) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 4656 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.

Sequence 7086 BP: 1773 A; 1739 G; 1859 G; 1715 T; 0 other;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 47.7%; Score 60; DB 22; Length 786; Best Local Similarity 100.0%; Pred. No. 2,1e-20; Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX The invention relates to four common polymorphisms in the gene encoding
CC ATP-binding cassette transporter-1 (ABCI). ABCI is associated with
CC decreased ApoA-I mediated efflux of cholesterol. The polymorphisms in
CC ABCI directly affects cellular lipid homeostasis, which is a key factor
CC in the athero-genetic processes. The ABCI polymorphisms are useful for
CC diagnosing and treating lipid disorders, cardiovascular diseases
CC (coronary heart disease, atherosclerosis) and inflammatory diseases
CC (psoriasis, lupus erythematosus). The identification of ABCI as a
CC transporter for interleukin-beta (IL-beta) identifies this gene as
CC a candidate for treatment of inflammatory diseases including rheumatoid
CC arthritis and septic shock. The present sequence is human ABCI gene.
XX
SU Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;

Query Match 37.7%; Score 60; DB 22; Length 7260;
Best Local Similarity 100.0%; Pred. No. 2.1e-20;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 TGTGGCTCAGCTGAGTTGCTGCTGTGGAAGAACCTCAGCTTCAGAGAACACAAACA 159
|||||
DB 327 TGTGGCTCAGCTGAGTTGCTGCTGTGGAAGAACCTCAGCTTCAGAGAACACAAACA 385

RESULT 13
AAI70315
ID AAI70315 standard; CDNA: 7260 BP.
AC AAI70315;
XX 07-JAN-2002 (first entry)
DE Human ATP binding cassette transporter 1 (ABCI) cDNA.

KW ATP binding cassette transporter 1; ABCI; human; lipid disorder;
KW cholesterol; cardiovascular disease; inflammatory disease;
KW antiinflammatory; antilipemic; antipsoriasis; dermatological;
KW Tanager disease; coronary heart disease; diagnosis; gene therapy;
KW polymorphism; ss.
XX Homo sapiens.

XX Key Location/Qualifiers
FI CDS 321..7106
FI /*tag- a
FI CDS 501..7106
FI /*tag- b
FI /*note= "alternative open reading frame of AAI70315"
FI variation replace(976,A)
FI /*tag- c
FI variation replace(1516,C)
FI /*tag- d
FI variation replace(2969,G)
FI /*tag- e
FI variation replace(3036,C)
FI /*tag- f

XX EPI136554-AJ.
XX
XX 26-SEP-2001.
XX 24 MAR-2000; 2000EP-0106401.
XX 24-MAR-2000; 2000EP-0106401.
XX (FARB) BAYER AG.
XX Schmitz G, Bodzioch M;
XX WPI: 2001-640389/74.
XX P-PSDB: AAM50228.
XX New adenosine triphosphate binding cassette transporter gene

PT polymorphisms, useful for diagnosing and treating lipid disorders,
PT cardiovascular diseases and inflammatory diseases
XX
PS Disclosure: Page 25-28; 4lpp: English.

XX The present sequence is that of cDNA encoding the human adenosine
CC triphosphate (ATP) binding cassette transporter 1 (ABCI) protein
CC (see AAM50227). The sequence includes an extended open reading
CC frame (ORF) to that provided by the sequence in AAI70314, using
CC an alternative ATG codon as initiation codon and thereby adding an
CC extra 40 N-terminal amino acids to the encoded ABCI protein (see
CC AAM50228). The invention provides 4 common polymorphisms in the
CC ABCI gene. These were identified by sequencing the ABCI gene in
CC different Tanager kindreds. In the variant genes (numbering as in
CC AAI70314), G is changed to A at position 596, T is changed to C at
CC position 1136, A is changed to G at position 2389 or G is changed
CC to C at position 3456, or any combination of these. All of these
CC polymorphisms alter the amino acid sequence of ABCI and therefore
CC may affect its function. The 2 most common polymorphisms (G596A)
CC and A2589G) are both associated with a decreased in vitro ApoA-I
CC mediated efflux of cholesterol from mononuclear phagocytes, a
CC feature typical of Tangier disease. 3 Of the variants (G596A,
CC A2589G and G3456C) are significantly increased in a population of
CC men having low high density lipoprotein-cholesterol levels and
CC established coronary heart disease (CHD) relative to CHD-free
CC control subjects. The use of the provided ABCI polymorphisms for
CC the diagnosis and treatment of lipid disorders, cardiovascular
CC diseases, and inflammatory diseases (e.g. psoriasis, lupus
CC erythematosus) is claimed. Modulation of ABCI transcripts or
CC proteins by antisense or ribozyme technology or RNA decoys is also
CC claimed.

XX
SU Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;

Query Match 37.7%; Score 60; DB 22; Length 7260;
Best Local Similarity 100.0%; Pred. No. 2.1e-20;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 TGTGGCTCAGCTGAGTTGCTGCTGTGGAAGAACCTCAGCTTCAGAGAACACAAACA 159
|||||
DB 327 TGTGGCTCAGCTGAGTTGCTGCTGTGGAAGAACCTCAGCTTCAGAGAACACAAACA 386

RESULT 14
AAK51683
ID AAK51683 standard; cDNA: 7281 BP.
XX
AC AAK51683;
XX 05-NOV-2001 (first entry)
XX Human polyphosphate binding cassette transporter 1 (ABCI) cDNA

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.

XX Homo sapiens.
XX
XX W0200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WJ-US04098.
XX
XX 03-FEB-2000; 2000US-0496914.
XX 27-APR-2000; 2000US-0560875.
XX 20-JUN-2000; 2000US-0598075.
XX 19-JUL-2000; 2000US-0620325.
XX 01-SEP-2000; 2000US-0654936.
XX 15-SEP-2000; 2000US-0663561.
XX 20-OCT-2000; 2000US-0693325.

```
PR 30-NOV-2000: 2060US-0728422.
XX (HYSE-) HYSEO INC.
XX
XX Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wehrman T, Goodrich R;
XX WPI: 2001-476283/51.
DR P-PSDB; AAM78550.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PI useful in diagnosis and gene therapy
XX
XX Claim 1: Page 1086-1096; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK5145A, AAK5145B) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations, the
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC
CC Note: Records for SEQ ID NO.2110 (AAK52581), 2111 (AAK52582) and 1666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
XX Sequence 7281 BP; 1831 A; 1773 C; 1915 G; 1762 T; 1 other;
SQ
Query Match 37.7%; Score 60; DB 22; Length 7857;
Best Local Similarity 100.0%; Pred. No. 2 1e-20;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 100 TGTGGCCCTCAGCTGAGGTTCCTGCTGCGAAGAACCTTCTTCAAGAGAACAAACA 159
Db 349 TGTGGCCCTCAGCTGAGGTTCCTGCTGCGAAGAACCTTCTTCAAGAGAACAAACA 407
RESULT 15
AAC69488
ID AAC69488 standard; CUNA; 7857 BP.
XX
XX AAC69498;
XX
XX 29-JAN-2001 (first entry)
XX
XX Human ABC1 cholesterol transporter FHA-4 mutant cDNA (U014575.2)
XX
XX Human ABC1 cholesterol transporter; chromosome 9q31;
KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
KW cardiovascular disease; coronary artery disease; coronary stenosis;
KW cerebrovascular disease; peripheral vascular disease;
KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KW prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
XX
XX Homo sapiens.
XX
XX W02000055318-A2.
XX
XX 21 SEP-2000.
XX
XX 15-MAR-2000; 2000WO-1800532.
XX
XX 15-MAR-1999; 99US-0124702.
XX 08 JUN-1999; 99US-0138048.
XX 17-JUN-1999; 99US-0139600.
XX 01-SEP-1999; 99US-0151977.
```

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XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (XENO-) XENON BIORESEARCH INC.
XX
XX Hayden MR, Wilson AK, Pimstone SN;
XX
XX WPI: 2000-587528/55.
DR P-PSDB; AAB38107.
XX
XX New ABC1 polypeptide is useful for treating diseases associated with
PI ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
PI disease and cancer
XX
XX Examples: Page 1: 229pp; English.
XX
XX The invention relates to the human ABC1 cholesterol transporter protein
CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
CC a member of the ATP-binding cassette (ABC transporter) superfamily of
CC proteins, and plays a crucial role in cholesterol transport, particularly
CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC located on chromosome 9q31, and mutations in this gene are associated
CC with two genetic HDL (high density lipoprotein) deficiency disorders,
CC Tangier disease (TD) and familial HDL deficiency (FHD). These diseases
CC are distinguishable in that TD is an autosomal recessive disorder, while
CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC cholesterol") in the blood correlate with a high risk of cardiovascular
CC disease, particularly coronary artery disease, but also cerebrovascular
CC disease, coronary stenosis, and peripheral vascular disease.
CC Conversely, a high level of HDL has protective effects against
CC cardiovascular disease. The invention provides genetic constructs and
CC transgenic cells and non-human animals comprising human ABC1 nucleic
CC acids, and methods of gene therapy for the treatment or prevention of
CC cardiovascular disease comprising the administration of an expression
CC vector encoding ABC1 or an active fragment thereof. The invention also
CC encompasses compounds which mimic ABC1 activity, compounds which
CC stimulate ABC1 expression and methods of screening for such compounds.
CC It further relates to methods for determining whether a patient has an
CC increased risk for cardiovascular disease due to polymorphisms in the
CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
CC or prevent cardiovascular disease, especially coronary artery disease,
CC cerebrovascular disease, coronary stenosis or peripheral vascular
CC disease. They may also be used in the treatment of diseases associated
CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC The invention specifically excludes proteins with the exact amino acid
CC sequences of Genbank Accession No: CAA10005.1 and X75926, and the nucleic
CC acid with the exact sequence as Genbank Accession No: AJ012476.1. The
CC present sequence represents cDNA encoding a mutant human ABC1 cholesterol
CC transporter associated with an altered cholesterol level and therefore an
CC altered risk of cardiovascular disease.
CC Note: The present sequence is not shown in the specification, but is
CC derived from the native human ABC1 cDNA shown on pages 157-160.
XX
XX Sequence 7857 BP; 2011 A; 1860 C; 2008 G; 1977 T; 1 other;
```

```
Query Match 37.7%; Score 60; DB 21; Length 7857;
Best Local Similarity 100.0%; Pred. No. 2 2e-20;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 100 TGTGGCCCTCAGCTGAGGTTCCTGCTGCGAAGAACCTTCTTCAAGAGAACAAACA 159
Db 81 TGTGGCCCTCAGCTGAGGTTCCTGCTGCGAAGAACCTTCTTCAAGAGAACAAACA 140
```

Search completed: May 10, 2003, 02:15:55
Job time : 242 secs

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2003, 02:16:03 : Search time 1580 seconds
(without alignment)
1623.79% Million cell updates/sec

Title: US-09-846-456-5
Perfect score: 159
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Scoring table:
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Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1243172

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post processing: Listing first 45 summaries

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1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chain to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	48.4	547	9 AL698654	AL698654 DKFZp686N12109
2	51	32.1	736	9 AU135588	AL698654 AU135588
3	49	24.5	535	12 BG384217	AL698654 BG384217
4	24	15.1	292	14 Z44377	AL698654 Z44377
5	20	12.6	661	13 BI391126	AL698654 BI391126
6	19	11.9	216	12 BF756949	AL698654 BF756949

19	11.9	454	17	AQ369174	AQ369174 HS_5032_A
19	11.9	470	9	AI353952	AI353952 zeh1204.s
19	11.9	493	17	AQ709464	AQ709464 HS_5459_A
19	11.9	546	10	AV953274	AV953274 AV953274
19	11.9	568	14	BQ259614	BQ259614 fca02b03.
19	11.9	618	9	AA495487	AA495487 fca09112.r
19	11.9	643	9	AI497295	AI497295 fca13904.y
19	11.9	694	10	AV997283	AV997283 AV997283
19	11.9	705	13	BI160520	BI160520 602864591
19	11.9	730	10	AW116004	AW116004 f106a11.x
16	11.9	703	12	BF898523	BF898523 CM1-MT018
17	18	231	12	BF898523	BF898523 CM1-MT018
18	11.3	275	17	BH402163	BH402163 AG-ND-102
18	11.3	299	9	AA098714	AA098714 T4026.MVA
18	11.3	303	12	BF903506	BF903506 IL2-MT017
18	11.3	340	17	BH859759	BH859759 SS_X070D2
22	18	346	17	BH859242	BH859242 SS_X070D2
23	18	375	17	BH127062	BH127062 G-10q13.r
24	18	397	12	BF911983	BF911983 IL2-UT007
25	18	461	14	BQ751693	BQ751693 EST632256
26	18	492	14	BQ752118	BQ752118 EST632681
27	18	512	14	BQ751545	BQ751545 EST632108
28	18	529	17	BH396354	BH396354 AG-ND-161
29	18	532	17	AQ776697	AQ776697 HS_2148_B
30	18	532	17	AQ779444	AQ779444 HS_2001_A
31	18	544	10	AV974535	AV974535 AV974535
32	18	548	14	BQ752139	BQ752139 EST632102
33	18	554	17	AZ236353	AZ236353 RNC1-23-7
34	18	558	17	AZ510640	AZ510640 IM0355G15
35	18	566	17	AZ510673	AZ510673 IM0355M15
36	18	597	14	BP010466	BP010466 BP010466
37	18	599	9	AA720413	AA720413 ET2347.Tr
38	18	627	11	AY067297	AY067297 Schmidtea
39	18	631	9	AL652524	AL652524 AL652524
40	18	645	10	BB614720	BB614720 BB614720
41	18	645	13	BI996668	BI996668 t031041B0
42	18	647	17	CNS03C31	AL237303 Tetraodon
43	18	652	14	BQ751274	BQ751274 EST631837
44	18	654	12	BG308188	BG308188 tm58c10.Y
45	18	668	14	BQ751485	BQ751485 EST632048

ALIGNMENTS

AL698654 547 bp mRNA linear EST 21-MAR-2002
DKFZp686N12109.t: 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686N12109.5: mRNA sequence.

AL698654
EST:
AL698654.1 CL:19619194

human.

Homo Sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 547)

Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and Wicmann

S.

EST (Duesterhoeft, et al.)

Unpublished (1999)

Contact: Duesterhoeft A

MIPS

Am Klopsterspitz 18a D-82152 Martinsried, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

consortium of Qiagen (Hilden/Germany) within the cDNA sequencing

No sl sequence available.

This clone (DKFZp686N12109) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin Charlottenburg, GERMANY; Email: clone@rzpd.de.

Small: A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.

BASE COUNT 48 a 39 c 49 g 80 t

ORIGIN

Query Match 11.9%; Score 19; DB 12; Length 454
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 TTTCAGAGAACACAAACA 159
 DB 160 TTTCAGAGAACACAAACA 142

RESULT 7

AQ369174

LOCUS

DEFINITION HS_5032_A2_F04.SP6E RPC111 Human Male BAC Library Homo sapiens genomic clone Plate-608 Col-8 Row-K, DNA sequence.

ACCESSION AQ369174

VERSION AQ369174.1

KEYWORDS GI:4338653

SOURCE GSS.

ORGANISM human.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 454)

Author(s) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,J., Adams,M.D., and

Bach,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (12), 9769-9773 (1999)

MEETING 99R08-89

COMMENT Contact: Mahairas GG, Wallace JC, Broad L

High Throughput Sequencing Center

University of Washington

491 Queen Anne Avenue North, Seattle, WA 98195, USA

TEL: (206) 616-3618

FAX: (206) 616-3887

Email: jwallace@u.washington.edu

Clones may be purchased from Kestrel Clones (KestrelSeq.com).

BAC end Web Server: http://www.hirst.washington.edu

Plate: 608 row: K column: 9

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 454.

Location/Qualifiers

1..454

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone.lib="Plate-608 Col-8 Row-K"

/clone.lib="RPC111 Human Male BAC Library"

/sex="Male"

/cell.type="Lymphocytes"

/note="vector: pBAC3.6; Kest111 Human Male BAC Library"

BASE COUNT 144 a 82 c 90 g 136 t

ORIGIN 2 others

Query Match

Best Local Similarity 11.9%; Score 19; DB 17; Length 454
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 CAGCTGCGGCTGGCTGGCT 85

DB 286 CAGCTGCGGCTGGCTGGCT 303

RESULT 8

AJ354952/c

LOCUS

DEFINITION

zebr204.seq.f Zebratfish Embryonic Heart cDNA Library Danio rerio

cdna 5' mRNA sequence.

ACCESSION AJ354952

VERSION AJ354952.1

KEYWORDS GI:4894105

SOURCE EST.

ORGANISM zebrafish.

Danio rerio

Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes

; Cyprinidae; Danio.

1 (bases 1 to 470)

Author(s) Ton,C., Mably,J.D., Dempsey,A.A., Hwang,D.M., Fishman,M.C. and Liew

C.C.

TITLE Identification and Characterization of Expressed Sequence Tags from

an Embryonic Zebrafish Heart cDNA Library

JOURNAL Unpublished (1999)

COMMENT Contact: Drew CC

Brigham and Women's Hospital

Harvard Medical School

75 Francis St. Boston, MA 02115, USA

Tel: 6177328915

Fax: 6179750995

Email: cliew@rics.bwh.harvard.edu

PCR Primers

FORWARD: 5' GGTAGTTCGAAATTAACCTTCACATAAGGG 3'

BACKWARD: 5' GCACTGAAATGTAATACGACCTACCTATAGGCG 3'

Seq primer: 5' GAATTAACCTTCATTAAGGG 3'

Location/Qualifiers

1..470

/organism="Danio rerio"

/db_xref="taxon:7955"

/clone.lib="Zebratfish Embryonic Heart cDNA Library"

/clone.stage="embryonic day 3 post-fertilization"

/lab.host="E-coli XL1-blue mrf"

/note="organ: heart; Vector: lambda ZAP Express; Site.1:

ECORI; Site.2: XhoI; mRNA was purified from embryonic

zebratfish hearts (3 day post-fertilization). cDNA was

synthesized using a XhoI-Oligo dT adaptor-primer. EORI

adaptors were ligated, followed by digestion with XhoI,

for directional cloning into pre-digested lambda ZAP

Express vector."

BASE COUNT 123 a 112 c 130 g 105 t

ORIGIN

Query Match 11.9%; Score 19; DB 9; Length 470;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 TGGCTCAGCTGAGGTTGC 121

DB 395 TGGCTCAGCTGAGGTTGC 377

RESULT 9

AQ709464/c

LOCUS

DEFINITION

HS_5459_A2_F04_17A RPC1-11 Human Male BAC Library Homo sapiens

genomic clone Plate-1035 Col-8 Row-K, DNA sequence.

ACCESSION AQ709464

VERSION AQ709464.1

KEYWORDS GI:5418890

SOURCE GSS.

ORGANISM human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 493)

Author(s) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,J., Adams,M.D., and

Bach,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

JOURNAL
MEDLINE
COMMENT

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
59380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human HAC library (F011). For HAC
library availability, please contact Peter de Jong
(peter.dejong@med.buffalo.edu). Clones may be purchased from
HAC-PAC Resources (<http://bacpac.med.buffalo.edu/~bacpac.htm>)
or from Research Genetics (<http://inforesgen.com>). HAC and Web Server:
<http://www.htsc.washington.edu>
Plate: 1035 Row: K Column: B
Seq primer: T7
Class: HAC ends
High quality sequence stop: 493.
Location/Qualifiers
1..493
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="RPC1-11 Human Male HAC library"
/sex="male"
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBAC3.6 vector at EcoRI sites"
171 a 94 c 69 g 152 t 7 others

FEATURES

SOURCE

BASE COUNT
ORIGIN

Query Match 11.9% Score 19; 68 17; Length 157
Best local Similarity 100.0% Pred. No. 51
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 139 ACTTCAGAGAGAGACAAA 157
DB 478 ACTTCAGAGAGACAAA 460

RESULT 11

AV954274 546 bp mRNA linear EST 14-MAR-2002
DEFINITION AV954274 Nori Satoh unpublished cDNA library: cleavage stage embryo
Clona intestinalis cDNA clone c102109.1; mRNA sequence.
ACCESSION AV954274
KEYWORDS EST.
SOURCE Clona intestinalis.
ORGANISM Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Platybranchia; Clonidae; Clona.
1 (bases 1 to 546)
Satch,N., Satou,Y., Kohara,Y. and Shimizu
Expressed genes in Clona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satohe@scid.ian.zool.kyoto-u.ac.jp
Location/Qualifiers
1..546
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone="c102109"
/clone_lib="Nori Satoh unpublished cDNA library: cleavage
stage embryo"

FEATURES

SOURCE

/tissue_type="whole animal"
/dev_stage="cleavage stage embryo"
/note="Vector: pBluescript SK"
BASE COUNT 160 a 117 c 86 g 183 t
ORIGIN

Query Match 11.9% Score 19; Length 546;
Best local Similarity 100.0% Pred. No. 52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 145 CCCTACTTTAGAGAGAGA 153
DB 145 CCCTACTTTAGAGAGAGA 163

RESULT 11

BQ259614 568 bp mRNA linear EST 06-MAY-2002
DEFINITION fao02b03.y: zebrafish fin day1 regeneration Danio rerio cDNA clone
5908564.5; similar to SW-UCR2_BOVIN P23004 UB1QINOL-CYCLOHOME C
REDUCTASE COMPLEX CORE PROTEIN 2 PRECURSOR; mRNA sequence.
ACCESSION BQ259614
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danio rerio

REFERENCE

AUTHORS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
Kohn,S., Shan,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
and Wilson,R.
WashU Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1870
Email: zbrfish@watson.wustl.edu
CDNA Library Preparation: Raymond Lee, cDNA Library Arrayed by:
Matthew Clark, DNA Sequencing by: Washington University Genome
Sequencing Center, Clona Distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
kessouren@zeilumprimatdatenbank.berlin.de
zebrafish identity (p-value greater than 1e-99) found to:
g112224979|db,AA45487|AA45487 fa09h12.r1 zebrafish ICRFzfls Danio
rerio cDNA
Seq primer: T3 Et from Amersham
High quality sequence stop: 411.
Location/Qualifiers
1..568
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone="5908564"
/clone_lib="zebrafish fin day1 regeneration"
/sex="mixed male and female"
/tissue_type="1 day fin regenerates"
/db_host="E. coli XL0LR"
/note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XbaI; 1st
strand cDNA primed with (CA)10ACTAGTCTCGAG(T)18, followed
by second strand synthesis, and ligated to 5' adapter (5'
) attccgacacga 3', 3'-gccgctc-5'. cDNA was cloned
directionally (EcoRI/XbaI) into Stratagene Zap express
lambda phage arms. Mass in vivo excision done to obtain
inserts in pBK-CMV phagemid."

FEATURES

SOURCE

Institut fuer Molekulare Genetik Berlin: cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (24 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters of single clones were sequenced additional times to assess quality control."

BASE COUNT 164 a 158 c 170 q 159 t 1 others

Query Match 11.9% Score 19; DB 9; Length 544
Best Local Similarity 100.0%; Pred. No. 54;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 TGGCTCAGCTGAGGTGTC 121
TTTTTTTTTTTTTTTT

DB 395 TGGCTCAGCTGAGGTGTC 377

RESULT 14

AV997283/c

LOCUS

DEFINITION

AV997283

ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

QY 135

DB 604

RESULT 15

B1160520

LOCUS

DEFINITION

B1160520.1

ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

QY 110

DB 682

Search completed: May 16, 2004, 03:17:25

Job time: 1585 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	Count				
1	19	11.9	577	4	US-09-615-192A-97	Sequence 97, Appl	
2	19	11.9	624	2	US-08-713-009-9	Sequence 9, Appl	
3	19	11.9	624	2	US-08-975-315-9	Sequence 9, Appl	
4	19	11.9	624	4	US-09-211-710-9	Sequence 9, Appl	
5	19	11.9	624	4	US-09-615-192A-9	Sequence 95, Appl	
6	19	11.9	684	2	US-08-975-316-45	Sequence 45, Appl	
7	19	11.9	684	4	US-09-615-192A-45	Sequence 45, Appl	
8	16	10.1	39	1	US-08-519-777-63	Sequence 63, Appl	
9	16	10.1	39	1	US-08-742-035-63	Sequence 63, Appl	
10	16	10.1	39	1	US-08-777-019-63	Sequence 63, Appl	
11	16	10.1	39	2	US-08-777-143-63	Sequence 63, Appl	
12	16	10.1	39	3	US-08-775-414-63	Sequence 63, Appl	
13	16	10.1	39	4	US-08-931-858E-63	Sequence 63, Appl	
14	16	10.1	39	4	US-08-981-739-63	Sequence 63, Appl	
15	16	10.1	39	4	US-09-128-026-63	Sequence 63, Appl	
16	16	10.1	57	1	US-08-519-777-18	Sequence 18, Appl	
17	16	10.1	57	1	US-08-742-035-18	Sequence 18, Appl	
18	16	10.1	57	2	US-08-777-019-18	Sequence 18, Appl	
19	16	10.1	57	2	US-08-777-143-18	Sequence 18, Appl	
20	16	10.1	57	3	US-08-775-414-18	Sequence 18, Appl	
21	16	10.1	57	4	US-08-931-858E-18	Sequence 18, Appl	
22	16	10.1	57	4	US-08-981-739-18	Sequence 18, Appl	
23	16	10.1	57	4	US-09-128-026-18	Sequence 18, Appl	
24	16	10.1	169	1	US-08-519-777-29	Sequence 29, Appl	
25	16	10.1	169	1	US-08-742-035-29	Sequence 29, Appl	
26	16	10.1	169	1	US-08-777-019-29	Sequence 29, Appl	
27	16	10.1	169	2	US-08-777-143-29	Sequence 29, Appl	

STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,000
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000,1000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 624 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US 08-713-050-9

Query Match
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 GCTGGGCTGCTGGCTGAG 88
DB 261 GCTGGGCTGCTGGCTGAG 279

RESULT 3
US-08-975-316-9
Sequence 9, Application US/08975316
Patent No. 5952486
GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4125
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
FILING DATE:
CLASSIFICATION: B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000/100001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 624 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-975-316-9

Query Match
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 GCTGGGCTGCTGGCTGAG 88
DB 261 GCTGGGCTGCTGGCTGAG 279

RESULT 4
US-09-211-710-9
Sequence 9, Application US/09211710A
Patent No. 6204434
GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N.
APPLICANT: HAVUKKALA, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000,100003
CURRENT APPLICATION NUMBER: US/09/211,710A
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 624
TYPE: DNA
ORGANISM: Pinus radiata
US-09-211-710-9

Query Match
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 GCTGGGCTGCTGGCTGAG 88
DB 261 GCTGGGCTGCTGGCTGAG 279

RESULT 5
US-09-615-192A-9
Sequence 9, Application US/09615192A
Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N.
APPLICANT: HAVUKKALA, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000,1000040
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 624
TYPE: DNA
ORGANISM: Pinus radiata
US 09-615,192A-9

Query Match 11.9% Score 19; DB 4; Length 684;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 GCTGGGGCTGCTGGCTGAG 88
|||||
Db 261 GCTGGGGCTGCTGGCTGAG 279

RESULT 6
US-09 975 316-45
Sequence 45, Application US/08/975316
Patent No. 5952486
GENERAL INFORMATION:
APPLICANT: BLOKBERG, Leonard N., HAWKKAIA, Ilkka
APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT GROWTH IN NUTR
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
FILING DATE:
CLASSIFICATION: 800
PARENT APPLICATION DATA:
APPLICATION NUMBER: 08/714,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 110067/00301
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09 975 316-45
Query Match 11.9% Score 19; DB 2; Length 684;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 GCTGGGGCTGCTGGCTGAG 88
|||||
Db 261 GCTGGGGCTGCTGGCTGAG 279

RESULT 7
US-09 615 192A-45
Sequence 45, Application US/09/615,192A
Patent No. 6416718
GENERAL INFORMATION:
APPLICANT: BLOKBERG, Leonard N.
APPLICANT: BLOKBERG, Leonard N., HAWKKAIA, Ilkka
TITLE OF INVENTION: Materials and Methods for Pla
TITLE OF INVENTION: Modification of Plant Growth in Nut
FILE REFERENCE: 11000,100340

US-09 615 192A-45
Query Match 11.9% Score 19; DB 2; Length 684;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 GCTGGGGCTGCTGGCTGAG 88
|||||
Db 261 GCTGGGGCTGCTGGCTGAG 279

RESULT 8
US-09 519-777-637C
Sequence 63, Application US/08/519777
Patent No. 5739307
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: TAMPEL, PATRICIA A.
TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROGERS, HEWELL & HAFERKAMP, L.C.
STREET: 7733 PARSYBH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105, 1817
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Edition in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/519,777
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BELLAND, DONALD R.
REGISTRATION NUMBER: 65,197
REFERENCE/DOCKET NUMBER: 954095
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6392
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MEDIUM TYPE: DNA
US-09 519-777 63

US-09 519-777 637C
Query Match 11.9% Score 19; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 GCTGGGGCTGCTGGCTGAG 88
|||||
Db 261 GCTGGGGCTGCTGGCTGAG 279

RESULT 9
US-09 615-192A 45
Sequence 45, Application US/09/615,192A
Patent No. 6416718
GENERAL INFORMATION:
APPLICANT: BLOKBERG, Leonard N.
APPLICANT: BLOKBERG, Leonard N., HAWKKAIA, Ilkka
TITLE OF INVENTION: Materials and Methods for Pla
TITLE OF INVENTION: Modification of Plant Growth in Nut
FILE REFERENCE: 11000,100340

US-09 615-192A 45
Query Match 11.9% Score 19; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 GCTGGGGCTGCTGGCTGAG 88
|||||
Db 261 GCTGGGGCTGCTGGCTGAG 279

US-09 615-192A 45
Sequence 45, Application US/09/615,192A
Patent No. 6416718
GENERAL INFORMATION:
APPLICANT: BLOKBERG, Leonard N., HAWKKAIA, Ilkka
APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT GROWTH IN NUTR
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 3.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
FILING DATE:
CLASSIFICATION: 800
PARENT APPLICATION DATA:
APPLICATION NUMBER: 08/714,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 110067/00301
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MEDIUM TYPE: DNA
US-09 975 316-45

US-09 975 316-45
Query Match 11.9% Score 19; DB 4; Length 684;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 GCTGGGGCTGCTGGCTGAG 88
|||||
Db 261 GCTGGGGCTGCTGGCTGAG 279

RESULT 8
US-09 519-777-637C
Sequence 63, Application US/08/519777
Patent No. 5739307
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: TAMPEL, PATRICIA A.
TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROGERS, HEWELL & HAFERKAMP, L.C.
STREET: 7733 PARSYBH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105, 1817
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Edition in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/519,777
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BELLAND, DONALD R.
REGISTRATION NUMBER: 65,197
REFERENCE/DOCKET NUMBER: 954095
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6392
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MEDIUM TYPE: DNA
US-09 519-777 63

US-09 519-777 637C
Query Match 11.9% Score 19; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 GCTGGGGCTGCTGGCTGAG 88
|||||
Db 261 GCTGGGGCTGCTGGCTGAG 279

RESULT 9
US-09 615-192A 45
Sequence 45, Application US/09/615,192A
Patent No. 6416718
GENERAL INFORMATION:
APPLICANT: BLOKBERG, Leonard N.
APPLICANT: BLOKBERG, Leonard N., HAWKKAIA, Ilkka
TITLE OF INVENTION: Materials and Methods for Pla
TITLE OF INVENTION: Modification of Plant Growth in Nut
FILE REFERENCE: 11000,100340

US-09 615-192A 45
Query Match 11.9% Score 19; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 GCTGGGGCTGCTGGCTGAG 88
|||||
Db 261 GCTGGGGCTGCTGGCTGAG 279

RESULT 10
US-09 615-192A 45
Sequence 45, Application US/09/615,192A
Patent No. 6416718
GENERAL INFORMATION:
APPLICANT: BLOKBERG, Leonard N.
APPLICANT: BLOKBERG, Leonard N., HAWKKAIA, Ilkka
TITLE OF INVENTION: Materials and Methods for Pla
TITLE OF INVENTION: Modification of Plant Growth in Nut
FILE REFERENCE: 11000,100340

US-09 615-192A 45
Query Match 11.9% Score 19; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044

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1 RESULT 7
2 US-08-742 045-63/c
3 ? Sequence 54, Application US/08742015
4 ? Patent No. 5747655
5 ?
6 ? GENERAL INFORMATION:
7 ?
8 ? APPLICANT: JOHNSON JR., EUGENE M.
9 ? APPLICANT: MILBRANDT, JEFFREY D.
10 ? APPLICANT: KOTZBAUER, PAUL T.
11 ? APPLICANT: LAMPE, PATRICIA A.
12 ?
13 ? TITLE OF INVENTION: NEUTROTIN AND RELATED GROWTH FACTORS
14 ? NUMBER OF SEQUENCES: 78

```

1 CORRESPONDENCE ADDRESS:
 2 ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, S.C.
 3 STREET: 7734 FORSYTH BOULEVARD, SUITE 1400
 4 CITY: ST. LOUIS
 5 STATE: MISSOURI
 6 COUNTRY: US
 7 ZIP: 63105-1817
 8
 9 COMPUTER READABLE FORM:
 10 MEDIUM TYPE: Floppy disk
 11 COMPUTER: IBM PC Compatible
 12 OPERATING SYSTEM: PC-DOS/MS-DOS
 13 SOFTWARE: PatentIn Release #1.0, Version #1.25
 14
 15 CURRENT APPLICATION DATA:
 16 APPLICATION NUMBER: US/08/742,035
 17 FILING DATE: 01-NOV-1996
 18 CLASSIFICATION: 435
 19 PRIOR APPLICATION DATA:
 20 APPLICATION NUMBER: 08/519,777
 21 FILING DATE: 28-AUG-1995
 22 ATTORNEY/AGENT INFORMATION:
 23 NAME: HOLLAND, DONALD R.
 24 REGISTRATION NUMBER: 35,197
 25 REFERENCE/DOCKET NUMBER: 953095
 26 TELECOMMUNICATION INFORMATION:
 27 TELEPHONE: (314) 727-5188
 28 TELEFAX: (314) 727-6092
 29 INFORMATION FOR SEQ. ID NO.: 63:
 30 SEQUENCE CHARACTERISTICS:
 31 LENGTH: 39 base pairs
 32 TYPE: nucleic acid
 33 STRANDEDNESS: single
 34 TOPOLOGY: linear
 35 MOLECULE TYPE: cDNA
 36
 37 US 08-742,035-B4

Query Match	10.18	Score 16	18	Length 59
Best Local Similarity	100.00	Pred. No. 22		
Matches 16	Conservative 0	Mismatches 0		Identity 100.00

RESULT 10
 ES: 08 777 917-63/c
 : Sequence 63, Application US/08777019
 : Patent No. 5817622
 : GENERAL INFORMATION:
 : APPLICANT: JOHNSON JR., EUGENE M.
 : APPLICANT: MILBRANDT, JEFFREY D.
 : APPLICANT: KOTZBAUER, PAUL T.
 : APPLICANT: LAMPE, PATRICIA A.
 : TITLE OF INVENTION: NEURTURIN AND RELATED OR WITH THEREOF
 : NUMBER OF SEQUENCES: 78
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: ROGERS, HOWELL & BAKERKAMP, L.P.C.
 : STREET: 7743 FOURSUTH BOULEVARD, SUITE 1400

CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105 1817
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,019
FILING DATE: 30-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/519,777
FILING DATE: 28 AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 953095
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
OS-08-777-019-63

Query Match 10.1%; Score 16; DB 1; Length 39;
Best Local Similarity 100.0%; pred.No. 22;
Matches 16; Conservative 0; Mismatches 0; Indels

RESULT 11
US-08-777-143-63/c
Sequence 63, Application US/08777143
Patent No. 5843914
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANT, JEFFREY D.
APPLICANT: KOIZHAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
TITLE OF INVENTION: NEUTURIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777.143
FILING DATE: 30-05-1996
CLASSIFICATION: G14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 58/519,777
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: HOWLAND, DONALD R.

REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 953095
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-777-143-63

Query Match 10.1%; Score 16; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GCGCGCTGCTTCAG 53
IIIIIIIIIIIIIIIIIIII

DB 36 GCGCGCTGCTTCAG 21

RESULT 12
US-08-775-414-63/c
Sequence 63, Application US/08775414
Patent No. 6090779
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775,414
FILING DATE: 31-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197

REFERENCE/DOCKET NUMBER: 955805
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-775-414-63

Query Match 10.1%; Score 16; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 GCGCGCTGCTTCAG 53
IIIIIIIIIIIIIIIIIIII

DB 36 GCGCGCTGCTTCAG 21

RESULT 13

US-08-931-858E-63/c
Sequence 63, Application US/08931858E
Patent No. 6220222
GENERAL INFORMATION:
APPLICANT: JOHNSON, EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
APPLICANT: KLEIN, ROBERT
APPLICANT: DESAUVAGE, FRED
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858E
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-931-858E-63

Query Match 10.1%; Score 16; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GCGCGCTGCTTCAG 53
IIIIIIIIIIIIIIIIIIII

DB 36 GCGCGCTGCTTCAG 21

RESULT 14

US-08-981-739-61/c
Sequence 63, Application US/08981739
Patent No. 6232449
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US

ZIP: 63105-1817
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/981,739
 FILING DATE: 31-Aug-1998
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US97/03441
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 976144
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314) 727-5188
 TELEFAX: (314) 727-6092
 INFORMATION FOR SEQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 39 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 63:
 TSCAGCGAGTCTGCTCCAG 53

Query Match 10.1%; Score 16; DB 4; Length 43;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 58 GCGCCGTCCTCCAG 53
 Db 36 GCGCCGTCCTCCAG 21

US 09-128-026-63
 Sequence 63, Application US/09128025
 Patent No. 640335
 GENERAL INFORMATION:
 APPLICANT: JOHNSON JR., EUGENE M.
 APPLICANT: MIRKIN, JEFFREY D.
 APPLICANT: KOCZKAUER, PAUL T.
 APPLICANT: LAMPE, PATRICIA A.
 TITLE OF INVENTION: PERSEPHIN AND RELATED DEWETTING AGENTS
 NUMBER OF SEQUENCES: 176
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAFERKAMP, L.L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MISSOURI
 COUNTRY: US
 ZIP: 63195-1817
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/128,026
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 976144
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314) 727-5188
 TELEFAX: (314) 727-6092

INFORMATION FOR SEQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 39 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US 09-128-026-63
 Query Match 10.1%; Score 16; DB 4; Length 39;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 48 GCGCCGTCCTCCAG 53
 Db 36 GCGCCGTCCTCCAG 21

Search completed: May 10, 2003, 03:18:23
 Job time : 48 secs

Db 121 CTGCTGTGGAGAACCTCCTCCTTCAGGAGAACAAACA 159
|||||

RESULT 2

US-09-984-827-4

: Sequence 4: Application US/09984827

: Publication No. US20030056234A1

: GENERAL INFORMATION:

: APPLICANT: DENEFELE, PATRICE

: APPLICANT: ROSIER-MONTIUS, MARIE-FRANCOISE

: APPLICANT: ARNOULD-REGUIGNE, ISABELLE

: APPLICANT: DUVERGER, NICOLAS

: APPLICANT: CAMBIEN, FRANCOIS

: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ARA1 GENE, THEIR USES, AND
DETECTION METHODS AND KITS THEREFOR

: FILE REFERENCE: 03806.0522-00000

: CURRENT APPLICATION NUMBER: US/09/984.827

: PRIOR FILING DATE: 2002-04-01

: PRIOR APPLICATION NUMBER: 60/254,108

: PRIOR FILING DATE: 2000-12-11

: PRIOR APPLICATION NUMBER: FR 00/14037

: NUMBER OF SEQ ID NOS: 161

: SOFTWARE: Patent In Ver. 2.1

: SEQ ID NO 4

: LENGTH: 357

: TYPE: DNA

: ORGANISM: Homo sapiens

: US-09-984-827-4

Query Match 100.0% Score 159; DB 9; Length 457;

Best Local Similarity 100.0%; Pred. No. 7.9e-79;

Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAATGATGACCCAGCGGCGCTGCTGTCAGCTCTGGGAGATGTTTAAAGGCTGGG 63

|||||

Db 100 TTAATGATGACCCAGCGGCGGCTGCTGTCAGCTCTGGGAGATGTTTAAAGGCTGGG 159

QY 61 GAGCCACACAGCTGGCGGCTGCTGTCAGGAGACATGGATGTTGCTGTTGAGGTTG 120

|||||

Db 169 GAGCCACACAGCTGGCGGCTGCTGTCAGGAGACATGGATGTTGCTGTTGAGGTTG 219

QY 121 TGTGTGTGAGAACTCCTCCTTTCAGAGAGAAACA 159

|||||

Db 220 CTGCTGTGAGAACCTCCTCCTTTCAGAGAGAAACA 258

RESULT 3

US-09-846-456-2

: Sequence 4: Application US/09846456

: Patent No. US20020146792A1

: GENERAL INFORMATION:

: APPLICANT: Rosier, Marie

: APPLICANT: Prades, Catherine

: APPLICANT: Lemoine, Cendrine

: APPLICANT: Naudin, Laurent

: APPLICANT: Deneffe, Patrice

: APPLICANT: Duverger, Nicolas

: APPLICANT: Brewer, Bryan

: APPLICANT: Remaley, Alan

: APPLICANT: Foto, Silvia

: TITLE OF INVENTION: Regulatory Nucleic Acid for the ARA1 Gene, Molecules Modifying its

Activity and Therapeutic Uses

: FILE REFERENCE: 3806.0505

: CURRENT APPLICATION NUMBER: US/09/846.456

: CURRENT FILING DATE: 2001-05-02

: PRIOR APPLICATION NUMBER: US 60/261,289

: PRIOR FILING DATE: 2000-05-02

: NUMBER OF SEQ ID NOS: 20

: SOFTWARE: Patent In version 3.0

: SEQ ID NO 2

: LENGTH: 357

: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-846-456-2

Query Match

100.0% Score 159; DB 10; Length 357;

Best Local Similarity 100.0%; Pred. No. 7.9e-79;

Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAATGATGACCCAGCGGCGGCTGCTGTCAGCTCTGGGAGATGTTTAAAGGCTGGG 60

|||||

Db 100 TTAATGATGACCCAGCGGCGGCTGCTGTCAGCTCTGGGAGATGTTTAAAGGCTGGG 159

QY 61 GAGCCACACAGCTGGCGGCTGCTGTCAGGAGACATGGCATGTTGCCCTCAGCTGAGTTG 120

|||||

Db 160 GAGCCACACAGCTGGCGGCTGCTGTCAGGAGACATGGCATGTTGCCCTCAGCTGAGTTG 219

QY 121 CTGCTGTGGAAGAACTCCTCCTTTCAGAGAGAAACA 159

|||||

Db 220 CTGCTGTGGAAGAACTCCTCCTTTCAGAGAGAAACA 258

RESULT 4

US-09-984-827-25

: Sequence 25: Application US/09984827

: Publication No. US20030056234A1

: GENERAL INFORMATION:

: APPLICANT: DENEFELE, PATRICE

: APPLICANT: ROSIER-MONTIUS, MARIE-FRANCOISE

: APPLICANT: ARNOULD-REGUIGNE, ISABELLE

: APPLICANT: DUVERGER, NICOLAS

: APPLICANT: CAMBIEN, FRANCOIS

: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ARA1 GENE, THEIR USES,
DETECTION METHODS AND KITS THEREFOR

: FILE REFERENCE: 03806.0522-00000

: CURRENT APPLICATION NUMBER: US/09/984.827

: PRIOR FILING DATE: 2002-04-01

: PRIOR APPLICATION NUMBER: 60/254,108

: PRIOR FILING DATE: 2000-12-11

: PRIOR APPLICATION NUMBER: FR 00/14037

: PRIOR FILING DATE: 2000-10-31

: NUMBER OF SEQ ID NOS: 161

: SOFTWARE: Patent In Ver. 2.1

: SEQ ID NO 25

: LENGTH: 158

: TYPE: DNA

: ORGANISM: Homo sapiens

US-09-984-827-25

Query Match

89.9% Score 143; DB 9; Length 158;

Best Local Similarity 100.0%; Pred. No. 6.5e-70;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GGCGTCCCTGCTGTCAGCTCTGGCGGCTGCTGTCAGGCTCCCGAGGCTCCCGAGGCTGGG 76

|||||

Db 16 GGCGTCCCTGCTGTCAGCTCTGGCGGCTGCTGTCAGGCTCCCGAGGCTCCCGAGGCTGGG 75

QY 77 GGTCTGCTGAGGAGAACATGGATGTTGCTCAGCTCAGCTGAGGTTGCTGTGGAGAGACC 136

|||||

Db 76 GTCCTGCTGAGGAGAACATGGATGTTGCTCAGCTCAGCTGAGGTTGCTGTGGAGAGACC 135

QY 137 TCACCTTCAGAGAGAGAAACA 159

|||||

Db 136 TCACCTTCAGAGAGAGAAACA 158

RESULT 5

US-09-984-827-26

: Sequence 26: Application US/09984827

: Publication No. US20030056234A1

: GENERAL INFORMATION:

: APPLICANT: DENEFELE, PATRICE

: APPLICANT: ROSIER-MONTIUS, MARIE-FRANCOISE

: APPLICANT: ARNOULD-REGUIGNE, ISABELLE

APPLICANT: DIVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ALFA-1 GENE, THEIR USES, AND METHODS FOR DETECTING POLYMORPHIC SEQUENCES AND KITS THEREFOR
FILE REFERENCE: 03806.0522-00500
CURRENT APPLICATION NUMBER: US/09/984,827
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: FR 09/14037
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 25
LENGTH: 159
TYPE: DNA
ORGANISM: Homo sapiens
US-09-984 627-26

Query Match 67.9%; Score 108; DB 9; Length 159;
Best Local Similarity 99.9%; Pred. No. 20-50; Indels 0; Gaps 0;
Matches 158; Conservative 0; Mismatches 0

QY 1 TTAATGACACACCCAGCGGCGTGTGCTGAGGAGCAATGATGTTGGTCTCAATGAGCTG 159
DB 1 TTAATGACACACCCAGCGGCGTGTGCTGAGGAGCAATGATGTTGGTCTCAATGAGCTG 159
QY 61 GAGGACACACCTGGCGGCTGTGCTGAGGAGCAATGATGTTGGTCTCAATGAGCTG 159
DB 61 GAGGACACACCTGGCGGCTGTGCTGAGGAGCAATGATGTTGGTCTCAATGAGCTG 159
QY 121 CTGTGTGGGAAGAACCTCACTTTTCAGAGAAGAAACA 159
DB 121 CTGTGTGGGAAGAACCTCACTTTTCAGAGAAGAAACA 159

RESULT 6
US-09-924 440-101
Sequence 101, Application US/09/924 440
Publication No. US20030027248A1
GENERAL INFORMATION:
APPLICANT: Bejani, Stephanie
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CUNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91/052,REG
CURRENT APPLICATION NUMBER: US/09/924,440
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/294,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
SEQ ID NO 101
LENGTH: 1062
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: 5'UTR
LOCALIZATION: 1...153
FEATURE:
NAME/KEY: CDS
LOCATION: 154...649
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 649...1062
FEATURE:
NAME/KEY: polyA signal
LOCATION: 1023...1028
FEATURE:
NAME/KEY: polyA site
LOCATION: 1047...1062
US-09-924 440-101

Query Match 37.7%; Score 60; DB 9; Length 1062;
Best Local Similarity 100.0%; Pred. No. 9-6e-24; Indels 0; Gaps 0;
Matches 60; Conservative 0; Mismatches 0

QY 100 TGTGGGCTTCACTTCACTTGTGTGCTGGAAGAACCTCACTTTTCAGAGAAGAAACA 159
DB 100 TGTGGGCTTCACTTCACTTGTGTGCTGGAAGAACCTCACTTTTCAGAGAAGAAACA 159
RESULT 8
US-09-984 627-26
Sequence 1, Application US/09/984 627
Publication No. US2003002726A1
GENERAL INFORMATION:
APPLICANT: Bejani, Stephanie
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CUNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91/054, DIV
CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/294,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 114
SOFTWARE: JPatent
SEQ ID NO 101
LENGTH: 1062
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: 5'UTR
LOCALIZATION: 1...153
FEATURE:
NAME/KEY: CDS
LOCATION: 154...649
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 649...1062
FEATURE:
NAME/KEY: polyA signal
LOCATION: 1023...1028
FEATURE:
NAME/KEY: polyA site
LOCATION: 1047...1062
US-09-924 440-101

Query Match 37.7%; Score 60; DB 9; Length 1062;
Best Local Similarity 100.0%; Pred. No. 9-6e-24; Indels 0; Gaps 0;
Matches 60; Conservative 0; Mismatches 0

QY 100 TGTGGGCTTCACTTCACTTGTGTGCTGGAAGAACCTCACTTTTCAGAGAAGAAACA 159
DB 100 TGTGGGCTTCACTTCACTTGTGTGCTGGAAGAACCTCACTTTTCAGAGAAGAAACA 159

RESULT 7
US-09-924 600A-101
Sequence 101, Application US/09/924600A
Publication No. US2003002726A1
GENERAL INFORMATION:
APPLICANT: Bejani, Stephanie
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CUNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91/054, DIV
CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/294,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 114
SOFTWARE: JPatent
SEQ ID NO 101
LENGTH: 1062
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: 5'UTR
LOCALIZATION: 1...153
FEATURE:
NAME/KEY: CDS
LOCATION: 154...649
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 649...1062
FEATURE:
NAME/KEY: polyA signal
LOCATION: 1023...1028
FEATURE:
NAME/KEY: polyA site
LOCATION: 1047...1062
US-09-924 600A-101

Query Match 37.7%; Score 60; DB 9; Length 1062;
Best Local Similarity 100.0%; Pred. No. 9-6e-24; Indels 0; Gaps 0;
Matches 60; Conservative 0; Mismatches 0

QY 100 TGTGGGCTTCACTTCACTTGTGTGCTGGAAGAACCTCACTTTTCAGAGAAGAAACA 159
DB 100 TGTGGGCTTCACTTCACTTGTGTGCTGGAAGAACCTCACTTTTCAGAGAAGAAACA 159

RESULT 8
US-09-984 627-26
Sequence 1, Application US/09/984 627
Publication No. US2003002726A1
GENERAL INFORMATION:
APPLICANT: Bejani, Stephanie
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CUNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91/054, DIV
CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/294,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 114
SOFTWARE: JPatent
SEQ ID NO 101
LENGTH: 1062
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: 5'UTR
LOCALIZATION: 1...153
FEATURE:
NAME/KEY: CDS
LOCATION: 154...649
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 649...1062
FEATURE:
NAME/KEY: polyA signal
LOCATION: 1023...1028
FEATURE:
NAME/KEY: polyA site
LOCATION: 1047...1062
US-09-924 440-101

```

: APPLICANT: DUVERGER, NICOLAS
: APPLICANT: CAMBIEN, FRANCOIS
: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
: TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
: FILE REFERENCE: 03806.0522-00000
: CURRENT APPLICATION NUMBER: US/09/984,827
: PRIOR FILING DATE: 2002-04-01
: PRIOR APPLICATION NUMBER: 60/254,108
: PRIOR FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: FR 00/14037
: PRIOR FILING DATE: 2000-10-31
: NUMBER OF SEQ ID NOS: 161
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 9741
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: modified_base
: LOCATION: (7009)
: OTHER INFORMATION: a, t, c or g
US-09-846-827-1

```

```

Query Match          37.7%; Score 60; DB 9; Length 9741
Best Local Similarity 100.0%; Pred. No. 90-24;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 100 TGTGGCTCAGCTGAGGTGCTGCTGGAGAACTCATTTCAGAAAGACAAACA 159
      |||||||
DB 191 TGTGGCTCAGCTGAGGTGCTGCTGGAGAACTCATTTCAGAAAGACAAACA 250

```

RESULT 9

```

US-09-846-456-10
: Sequence 10, Application US/09846456
: Patent No. US20020146792A1
: GENERAL INFORMATION:
: APPLICANT: ROSIER, MARIE
: APPLICANT: PRADES, CATHERINE
: APPLICANT: LEMOINE, CENDRINE
: APPLICANT: KAUDIN, LAURENT
: APPLICANT: BENEFFIE, PATRICE
: APPLICANT: DUVERGER, NICOLAS
: APPLICANT: BREWER, BRYAN
: APPLICANT: KEMALEY, ALAN
: APPLICANT: FOJO, SILVIA
: TITLE OF INVENTION: Regulatory Nucleic Acid for the ABCA1 Gene, Polymorphies Modifying Its
: TITLE OF INVENTION: Activity and Therapeutic Uses
: FILE REFERENCE: 3806.0505
: CURRENT APPLICATION NUMBER: US/09/846,456
: PRIOR FILING DATE: 2001-05-02
: PRIOR APPLICATION NUMBER: US 60/201,280
: PRIOR FILING DATE: 2000-05-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 10
: LENGTH: 9741
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: "n" is chosen from q, a, t and c
US-09-846-456-10

```

```

Query Match          37.7%; Score 60; DB 10; Length 9741
Best Local Similarity 100.0%; Pred. No. 90-24;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 100 TGTGGCTCAGCTGAGGTGCTGCTGGAGAACTCATTTCAGAAAGACAAACA 159
      |||||||
DB 191 TGTGGCTCAGCTGAGGTGCTGCTGGAGAACTCATTTCAGAAAGACAAACA 250

```

```

RESULT 10
US-09-984-827-92
: Sequence 92, Application US/09984827
: Publication No. US20030056234A1
: GENERAL INFORMATION:
: APPLICANT: DENEFFIE, PATRICE
: APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
: APPLICANT: ARNOULD-REGUIGNE, ISABELLE
: APPLICANT: DUVERGER, NICOLAS
: APPLICANT: CAMBIEN, FRANCOIS
: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,
: TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
: FILE REFERENCE: 03806.0522-00000
: CURRENT APPLICATION NUMBER: US/09/984,827
: CURRENT FILING DATE: 2002-04-01
: PRIOR APPLICATION NUMBER: 60/254,108
: PRIOR FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: FR 00/14037
: PRIOR FILING DATE: 2000-10-31
: NUMBER OF SEQ ID NOS: 161
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 92
: LENGTH: 9870
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: modified_base
: LOCATION: (7138)
: OTHER INFORMATION: a, t, c or q
US-09-984-827-92

```

```

Query Match          47.7%; Score 60; DB 9; Length 9870;
Best Local Similarity 100.0%; Pred. No. 90-24;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 100 TGTGGCTCAGCTGAGGTGCTGCTGGAGAACTCATTTCAGAAAGACAAACA 159
      |||||||
DB 320 TGTGGCTCAGCTGAGGTGCTGCTGGAGAACTCATTTCAGAAAGACAAACA 379

```

RESULT 11

```

US-09-984-827-93
: Sequence 93, Application US/09984827
: Publication No. US20030056234A1
: GENERAL INFORMATION:
: APPLICANT: DENEFFIE, PATRICE
: APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
: APPLICANT: ARNOULD-REGUIGNE, ISABELLE
: APPLICANT: DUVERGER, NICOLAS
: APPLICANT: CAMBIEN, FRANCOIS
: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,
: TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
: FILE REFERENCE: 03806.0522-00000
: CURRENT APPLICATION NUMBER: US/09/984,827
: CURRENT FILING DATE: 2002-04-01
: PRIOR APPLICATION NUMBER: 60/254,108
: PRIOR FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: FR 00/14037
: PRIOR FILING DATE: 2000-10-31
: NUMBER OF SEQ ID NOS: 161
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 93
: LENGTH: 9870
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: modified_base
: LOCATION: (7138)
: OTHER INFORMATION: a, t, c or q
US-09-984-827-93

```

```

Query Match          47.7%; Score 60; DB 9; Length 9870;
Best Local Similarity 100.0%; Pred. No. 90-24;

```

Matches 60: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 100 TGTGGCTCAGCTGAGTTGCTGCTGGGAAGACCTCATTTCAGAAAGAAACAAACA 159
|||||
Db 320 TGTGGCTCAGCTGAGTTGCTGCTGGGAAGACCTCATTTCAGAAAGAAACAAACA 379

RESULT 12

US-09-984-827-94

? Sequence 94, Application US/09984827

? Publication No. US20030056234A1

? GENERAL INFORMATION:

? APPLICANT: DENEFELE, PATRICE

? APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE

? APPLICANT: ARNOULD-REGUIGNE, ISABELLE

? APPLICANT: DUVERGER, NICOLAS

? APPLICANT: CAMBIEN, FRANCOIS

? TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND

? FILE REFERENCE: 03806.0522-00000

? CURRENT APPLICATION NUMBER: US/09/984.827

? PRIOR FILING DATE: 2002-04-01

? PRIOR APPLICATION NUMBER: 60/254,108

? PRIOR FILING DATE: 2000-12-11

? PRIOR APPLICATION NUMBER: FR 00/14037

? NUMBER OF SEQ ID NOS: 161

? SOFTWARE: PatentIn Ver. 2.1

? SEQ ID NO 94

? LENGTH: 9870

? TYPE: DNA

? ORGANISM: Homo sapiens

? NAME/KEY: modified_base

? LOCATION: (7138)

? OTHER INFORMATION: a, t, c or g

US-09-984-827-94

Query Match

Best Local Similarity 37.78; Score 60; DB 9; Length 9870;

Matches 60: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 100 TGTGGCTCAGCTGAGTTGCTGCTGGGAAGACCTCATTTCAGAAAGAAACAAACA 159
|||||
Db 320 TGTGGCTCAGCTGAGTTGCTGCTGGGAAGACCTCATTTCAGAAAGAAACAAACA 379

RESULT 13

US-09-984-827-95

? Sequence 95, Application US/09984827

? Publication No. US20030056234A1

? GENERAL INFORMATION:

? APPLICANT: DENEFELE, PATRICE

? APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE

? APPLICANT: ARNOULD-REGUIGNE, ISABELLE

? APPLICANT: DUVERGER, NICOLAS

? APPLICANT: CAMBIEN, FRANCOIS

? TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND

? FILE REFERENCE: 03806.0522-00000

? CURRENT APPLICATION NUMBER: US/09/984.827

? PRIOR FILING DATE: 2002-04-01

? PRIOR APPLICATION NUMBER: 60/254,108

? PRIOR FILING DATE: 2000-12-11

? PRIOR APPLICATION NUMBER: FR 00/14037

? NUMBER OF SEQ ID NOS: 161

? SOFTWARE: PatentIn Ver. 2.1

? SEQ ID NO 95

? LENGTH: 9870

? TYPE: DNA

? ORGANISM: Homo sapiens

? NAME/KEY: modified_base

? LOCATION: (7138)

? OTHER INFORMATION: a, t, c or g

US-09-984-827-95

? NAME/KEY: modified_base

? LOCATION: (7138)

? OTHER INFORMATION: a, t, c or g

US-09-984-827-95

Query Match

Best Local Similarity 37.78; Score 60; DB 9; Length 9870;

Matches 60: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 100 TGTGGCTCAGCTGAGTTGCTGCTGGGAAGACCTCATTTCAGAAAGAAACAAACA 159
|||||
Db 320 TGTGGCTCAGCTGAGTTGCTGCTGGGAAGACCTCATTTCAGAAAGAAACAAACA 379

RESULT 14

US-09-984-827-96

? Sequence 96, Application US/09984827

? Publication No. US20030056234A1

? GENERAL INFORMATION:

? APPLICANT: DENEFELE, PATRICE

? APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE

? APPLICANT: ARNOULD-REGUIGNE, ISABELLE

? APPLICANT: DUVERGER, NICOLAS

? APPLICANT: CAMBIEN, FRANCOIS

? TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND

? FILE REFERENCE: 03806.0522-00000

? CURRENT APPLICATION NUMBER: US/09/984.827

? PRIOR FILING DATE: 2002-04-01

? PRIOR APPLICATION NUMBER: 60/254,108

? PRIOR FILING DATE: 2000-12-11

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? NUMBER OF SEQ ID NOS: 161

? SOFTWARE: PatentIn Ver. 2.1

? SEQ ID NO 96

? LENGTH: 9870

? TYPE: DNA

? ORGANISM: Homo sapiens

? NAME/KEY: modified_base

? LOCATION: (7138)

? OTHER INFORMATION: a, t, c or g

US-09-984-827-96

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? Sequence 97, Application US/09984827

? Publication No. US20030056234A1

? GENERAL INFORMATION:

? APPLICANT: DENEFELE, PATRICE

? APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE

? APPLICANT: ARNOULD-REGUIGNE, ISABELLE

? APPLICANT: DUVERGER, NICOLAS

? APPLICANT: CAMBIEN, FRANCOIS

? TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND

? FILE REFERENCE: 03806.0522-00000

? CURRENT APPLICATION NUMBER: US/09/984.827

? PRIOR FILING DATE: 2002-04-01

? PRIOR APPLICATION NUMBER: 60/254,108

? PRIOR FILING DATE: 2000-12-11

? PRIOR APPLICATION NUMBER: FR 00/14037

? SOFTWARE: PatentIn Ver. 2.1

? SEQ ID NO 97

? LENGTH: 9870

? TYPE: DNA

? ORGANISM: Homo sapiens

? NAME/KEY: modified_base

? LOCATION: (7138)

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US-09-984-827-97

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1  NUMBER OF SEQ IDS: 161
2  SOFTWARE: PatentIn Ver. 2.1
3  SEQ ID NO: 97
4  LENGTH: 9870
5  TYPE: DNA
6  ORGANISM: Homo sapiens
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c 205	44	1.5	15266	10	US-09-764-877-3797	Sequence 3797, App	c 478	43	1.5	11754	9	US-09-984-827-5	Sequence 5, Appl
c 206	44	1.5	15271	10	US-09-764-877-3798	Sequence 3798, App	c 479	43	1.5	12045	9	US-09-764-891-9754	Sequence 1579, App
c 207	44	1.5	17216	10	US-09-764-877-3565	Sequence 3565, App	c 480	43	1.5	12822	10	US-10-092-154-1579	Sequence 1579, App
c 208	44	1.5	17217	10	US-09-764-877-3566	Sequence 3566, App	c 481	43	1.5	12822	10	US-09-764-847-1579	Sequence 1579, App
c 209	44	1.5	17450	9	US-09-764-891-8641	Sequence 8641, App	c 482	43	1.5	14176	10	US-09-764-864-1644	Sequence 1644, App
c 210	44	1.5	20869	9	US-10-091-504-2427	Sequence 2427, App	c 483	43	1.5	14796	10	US-09-954-456-973	Sequence 973, App
c 211	44	1.5	20869	10	US-09-764-869-2427	Sequence 2427, App	c 484	43	1.5	14796	10	US-09-954-456-1636	Sequence 1636, App
c 212	44	1.5	20966	10	US-09-776-976-7	Sequence 7, Appl	c 485	43	1.5	14796	10	US-09-918-186A-3	Sequence 3, Appl
c 213	44	1.5	20966	10	US-09-758-055-7	Sequence 7, Appl	c 486	43	1.5	14796	10	US-09-880-107-3421	Sequence 3421, App
c 214	44	1.5	20966	10	US-09-909-547-7	Sequence 7, Appl	c 487	43	1.5	15275	10	US-10-091-504-1475	Sequence 1475, App
c 215	44	1.5	21423	10	US-09-764-877-2845	Sequence 2845, App	c 488	43	1.5	15275	10	US-09-764-869-1475	Sequence 1475, App
c 216	44	1.5	24132	9	US-10-074-095-606	Sequence 606, App	c 489	43	1.5	20966	10	US-09-776-976-7	Sequence 7, Appl
c 217	44	1.5	24132	10	US-09-764-860-661	Sequence 661, App	c 490	43	1.5	20966	10	US-09-758-055-7	Sequence 7, Appl
c 218	44	1.5	31168	9	US-09-764-868-1561	Sequence 1561, App	c 491	43	1.5	20966	10	US-09-909-547-7	Sequence 7, Appl
c 219	44	1.5	31168	9	US-09-764-891-9556	Sequence 9556, App	c 492	43	1.5	32013	10	US-09-764-877-3297	Sequence 3297, App
c 220	44	1.5	32134	9	US-09-764-891-6763	Sequence 6763, App	c 493	43	1.5	32013	10	US-09-764-891-9679	Sequence 9679, App
c 221	44	1.5	32184	9	US-09-764-891-7300	Sequence 7300, App	c 494	43	1.5	32134	9	US-10-092-154-1057	Sequence 1057, App
c 222	44	1.5	32188	9	US-10-074-095-799	Sequence 799, App	c 495	43	1.5	32134	9	US-09-764-891-6357	Sequence 6357, App
c 223	44	1.5	32188	9	US-09-764-860-799	Sequence 799, App	c 496	43	1.5	32134	10	US-09-764-847-1057	Sequence 1057, App
c 224	44	1.5	46218	9	US-10-274-873-3	Sequence 3, Appl	c 497	43	1.5	32134	10	US-09-764-877-3535	Sequence 3535, App
c 225	44	1.5	46218	10	US-09-616-093-3	Sequence 3, Appl	c 498	43	1.5	32190	9	US-10-079-854-201	Sequence 201, App
c 226	44	1.5	66804	10	US-09-740-041-3	Sequence 3, Appl	c 499	43	1.5	32190	9	US-09-764-878-201	Sequence 201, App
c 227	44	1.5	84539	10	US-09-962-436-46	Sequence 46, Appl	c 500	43	1.5	32190	9	US-10-079-854-200	Sequence 200, App
c 228	44	1.5	176373	9	US-10-095-407-17	Sequence 17, Appl	c 501	43	1.5	32193	10	US-09-764-878-200	Sequence 200, App
c 229	43	1.5	105	9	US-10-125-542-606	Sequence 606, App	c 502	43	1.5	32207	10	US-09-764-891-6966	Sequence 6966, App
c 230	43	1.5	105	9	US-10-074-095-606	Sequence 606, App	c 503	43	1.5	32207	10	US-09-764-877-3250	Sequence 3250, App
c 231	43	1.5	105	10	US-09-764-870-104	Sequence 104, App	c 504	43	1.5	32249	9	US-10-079-854-202	Sequence 202, App
c 232	43	1.5	105	10	US-09-764-860-575	Sequence 575, App	c 505	43	1.5	32249	9	US-09-764-891-8024	Sequence 8024, App
c 233	43	1.5	304	10	US-09-867-701-949	Sequence 949, App	c 506	43	1.5	32249	10	US-09-764-878-202	Sequence 202, App
c 234	43	1.5	309	9	US-10-092-154-1475	Sequence 1475, App	c 507	43	1.5	38374	10	US-09-880-107-3463	Sequence 3463, App
c 235	43	1.5	309	10	US-09-764-847-1475	Sequence 1475, App	c 508	43	1.5	49744	10	US-09-927-091-4	Sequence 4, Appl
c 236	43	1.5	309	10	US-09-764-847-1475	Sequence 1475, App	c 509	43	1.5	60153	9	US-10-222-334-7	Sequence 7, Appl
c 237	43	1.5	309	10	US-09-764-847-1475	Sequence 1475, App	c 510	43	1.5	60153	9	US-09-842-364-1	Sequence 1, Appl
c 238	43	1.5	324	9	US-09-764-891-6913	Sequence 6913, App	c 511	43	1.5	81001	10	US-09-751-877-1	Sequence 1, Appl
c 239	43	1.5	324	9	US-09-764-891-6915	Sequence 6915, App	c 512	43	1.5	81001	10	US-09-954-556-17	Sequence 17, Appl
c 240	43	1.5	324	9	US-09-764-891-6917	Sequence 6917, App	c 513	43	1.5	132762	9	US-10-161-510-1	Sequence 1, Appl
c 241	43	1.5	361	10	US-09-867-701-6452	Sequence 6452, App	c 514	43	1.5	133893	9	US-10-238-709-3	Sequence 3, Appl
c 242	43	1.5	391	10	US-09-867-701-7901	Sequence 7901, App	c 515	43	1.5	174493	10	US-09-804-471A-3	Sequence 3, Appl
c 243	43	1.5	412	9	US-09-918-995-7919	Sequence 7919, App	c 516	43	1.5	174493	10	US-09-804-471A-3	Sequence 3, Appl
c 244	43	1.5	418	9	US-09-918-995-34993	Sequence 34993, App	c 517	42	1.5	402850	9	US-09-844-653-5	Sequence 5, Appl
c 245	43	1.5	443	9	US-09-918-995-12842	Sequence 12842, App	c 518	42	1.5	147	9	US-09-764-891-10229	Sequence 10229, App
c 246	43	1.5	462	9	US-09-918-995-5458	Sequence 5458, App	c 519	42	1.5	171	10	US-10-074-095-660	Sequence 660, App
c 247	43	1.5	462	9	US-09-918-995-6488	Sequence 6488, App	c 520	42	1.5	171	10	US-09-764-860-660	Sequence 660, App
c 248	43	1.5	474	9	US-09-918-995-6607	Sequence 6607, App	c 521	42	1.5	253	10	US-09-867-701-5005	Sequence 5005, App
c 249	43	1.5	487	10	US-09-867-701-6728	Sequence 6728, App	c 522	42	1.5	292	9	US-09-764-891-6009	Sequence 6009, App
c 250	43	1.5	504	9	US-09-918-995-1203	Sequence 1203, App	c 523	42	1.5	310	9	US-09-796-692-5928	Sequence 5928, App
c 251	43	1.5	506	9	US-09-918-995-2444H	Sequence 2444H, App	c 524	42	1.5	310	9	US-10-040-862-5928	Sequence 5928, App
c 252	43	1.5	646	9	US-10-091-504-1882	Sequence 1882, App	c 525	42	1.5	360	10	US-09-867-701-6979	Sequence 6979, App
c 253	43	1.5	646	10	US-09-764-869-1882	Sequence 1882, App	c 526	42	1.5	396	9	US-09-918-995-5901	Sequence 5901, App
c 254	43	1.5	670	9	US-09-764-891-9054	Sequence 9054, App	c 527	42	1.5	445	10	US-09-764-877-2736	Sequence 2736, App
c 255	43	1.5	1100	9	US-10-108-677-2	Sequence 2, Appl	c 528	42	1.5	468	9	US-09-918-995-14394	Sequence 14394, App
c 256	43	1.5	1635	10	US-09-822-840A-242	Sequence 242, App	c 529	42	1.5	496	9	US-09-918-995-13721	Sequence 13721, App
c 257	43	1.5	2104	9	US-09-954-131-1	Sequence 1, Appl	c 530	42	1.5	503	10	US-09-764-877-3646	Sequence 3646, App

541	42	1.5	554	10	US-09-764-877-3776	Sequence 3776, Ap	604	42	1.5	32192	9	US-09-764-891-8319	Sequence 8319, Ap
542	42	1.5	747	10	US-09-828-644-51	Sequence 51, Appl	605	42	1.5	32192	10	US-09-764-847-1416	Sequence 1416, Ap
543	42	1.5	1101	10	US-09-721-872-54	Sequence 54, Appl	606	42	1.5	32193	10	US-09-764-877-2623	Sequence 2623, Ap
544	42	1.5	1450	10	US-09-822-840A-251	Sequence 251, Appl	607	42	1.5	41907	10	US-09-967-013-5	Sequence 5, Appl
545	42	1.5	3064	9	US-10-042-154-1289	Sequence 1289, Ap	608	42	1.5	58817	10	US-09-982-091A-5	Sequence 3, Appl
546	42	1.5	3064	9	US-10-042-154-1290	Sequence 1290, Ap	609	42	1.5	62804	12	US-10-096-960-3	Sequence 3, Appl
547	42	1.5	3064	10	US-09-764-847-1289	Sequence 1289, Ap	610	42	1.5	92139	10	US-09-918-686-1	Sequence 1, Appl
548	42	1.5	3138	10	US-09-764-847-1290	Sequence 1290, Ap	611	42	1.5	92139	10	US-09-918-686-1	Sequence 1, Appl
549	42	1.5	3305	9	US-09-764-891-7823	Sequence 7823, Ap	612	42	1.5	113604	9	US-10-227-195A-1	Sequence 2, Appl
550	42	1.5	3305	9	US-09-764-891-7823	Sequence 7823, Ap	613	42	1.5	113604	9	US-10-227-195A-2	Sequence 2, Appl
551	42	1.5	3828	9	US-09-764-891-7518	Sequence 7518, Ap	614	42	1.5	132762	9	US-09-954-556-17	Sequence 17, Appl
552	42	1.5	3961	9	US-09-764-891-6205	Sequence 6205, Ap	615	42	1.5	378351	9	US-09-901-136-3	Sequence 3, Appl
553	42	1.5	3961	9	US-09-764-891-6206	Sequence 6206, Ap	616	41	1.4	114	9	US-10-092-154-1868	Sequence 1868, Ap
554	42	1.5	4431	9	US-10-091-572-665	Sequence 665, Ap	617	41	1.4	114	10	US-09-764-847-1868	Sequence 1868, Ap
555	42	1.5	4433	9	US-09-764-891-6827	Sequence 6827, Ap	618	41	1.4	254	10	US-09-867-701-1718	Sequence 1718, Ap
556	42	1.5	4433	9	US-10-091-572-668	Sequence 668, Ap	619	41	1.4	280	10	US-09-867-701-1718	Sequence 1718, Ap
557	42	1.5	4433	9	US-09-764-891-6827	Sequence 6827, Ap	620	41	1.4	299	10	US-09-867-701-1718	Sequence 1718, Ap
558	42	1.5	4857	9	US-10-092-154-1329	Sequence 1329, Ap	621	41	1.4	329	9	US-10-073-961-53	Sequence 53, Appl
559	42	1.5	4857	9	US-09-764-847-1329	Sequence 1329, Ap	622	41	1.4	332	10	US-09-764-887-53	Sequence 53, Appl
560	42	1.5	5559	10	US-09-959-347-1709	Sequence 1709, Ap	623	41	1.4	332	12	US-09-920-300A-1154	Sequence 1154, Ap
561	42	1.5	5559	10	US-09-959-347-1709	Sequence 1709, Ap	624	41	1.4	332	12	US-10-033-528-1154	Sequence 1154, Ap
562	42	1.5	6044	9	US-09-764-891-7252	Sequence 7252, Ap	625	41	1.4	356	9	US-09-803-719-48	Sequence 48, Appl
563	42	1.5	6053	9	US-09-764-891-7252	Sequence 7252, Ap	626	41	1.4	356	10	US-09-925-300-361	Sequence 361, Appl
564	42	1.5	6422	9	US-09-764-891-7252	Sequence 7252, Ap	627	41	1.4	363	12	US-10-033-528-1863	Sequence 1863, Ap
565	42	1.5	7470	9	US-10-073-961-397	Sequence 397, Appl	628	41	1.4	394	9	US-09-803-719-2110	Sequence 2110, Ap
566	42	1.5	7470	9	US-10-073-961-398	Sequence 398, Appl	629	41	1.4	405	10	US-09-867-701-543	Sequence 543, Appl
567	42	1.5	7470	10	US-09-764-887-397	Sequence 397, Appl	630	41	1.4	412	9	US-09-867-701-543	Sequence 543, Appl
568	42	1.5	7927	10	US-09-764-877-2311	Sequence 2311, Ap	631	41	1.4	412	9	US-09-918-995-2846	Sequence 2846, Ap
569	42	1.5	8167	9	US-09-764-891-5554	Sequence 5554, Ap	632	41	1.4	415	9	US-09-764-891-233	Sequence 233, Appl
570	42	1.5	8167	9	US-09-764-891-5554	Sequence 5554, Ap	633	41	1.4	415	9	US-09-764-891-8739	Sequence 8739, Ap
571	42	1.5	8253	9	US-10-091-572-622	Sequence 622, Ap	634	41	1.4	416	9	US-09-803-719-59	Sequence 59, Appl
572	42	1.5	8253	9	US-10-091-572-622	Sequence 622, Ap	635	41	1.4	431	10	US-09-867-701-6659	Sequence 6659, Ap
573	42	1.5	8268	9	US-09-764-891-668	Sequence 668, Ap	636	41	1.4	444	9	US-09-918-995-14690	Sequence 14690, A
574	42	1.5	8268	9	US-10-074-095-668	Sequence 668, Ap	637	41	1.4	455	9	US-09-918-995-2725	Sequence 2725, Ap
575	42	1.5	8272	9	US-09-764-863-868	Sequence 868, Ap	638	41	1.4	463	9	US-09-918-995-23846	Sequence 23846, A
576	42	1.5	8272	9	US-10-074-095-867	Sequence 867, Appl	639	41	1.4	472	9	US-09-918-995-12121	Sequence 12-21, A
577	42	1.5	9558	10	US-09-764-877-3645	Sequence 3645, Ap	640	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, Ap
578	42	1.5	10378	10	US-10-092-154-1448	Sequence 1448, Ap	641	41	1.4	478	10	US-09-867-701-6702	Sequence 6702, Ap
579	42	1.5	10378	10	US-09-764-847-1448	Sequence 1448, Ap	642	41	1.4	512	9	US-09-834-975-14	Sequence 14, Appl
580	42	1.5	12118	9	US-09-764-891-6995	Sequence 6995, Ap	643	41	1.4	512	9	US-09-918-995-9793	Sequence 9793, Ap
581	42	1.5	12503	9	US-10-125-540-549	Sequence 549, Appl	644	41	1.4	513	10	US-09-764-864-1693	Sequence 1693, Ap
582	42	1.5	12503	9	US-10-125-540-549	Sequence 549, Appl	645	41	1.4	513	10	US-09-764-877-3064	Sequence 3064, Ap
583	42	1.5	12503	10	US-09-764-870-549	Sequence 549, Appl	646	41	1.4	531	10	US-09-867-701-650	Sequence 650, Appl
584	42	1.5	13392	9	US-10-091-572-621	Sequence 621, Appl	647	41	1.4	538	10	US-09-867-701-650	Sequence 650, Appl
585	42	1.5	13392	9	US-09-764-891-6724	Sequence 6724, Ap	648	41	1.4	540	10	US-09-867-701-650	Sequence 650, Appl
586	42	1.5	15054	9	US-10-091-572-577	Sequence 577, Appl	649	41	1.4	548	9	US-09-796-692-9275	Sequence 9275, Ap
587	42	1.5	15054	9	US-09-764-891-6724	Sequence 6724, Ap	650	41	1.4	548	9	US-10-040-862-9275	Sequence 9275, Ap
588	42	1.5	15843	9	US-10-091-504-2396	Sequence 2396, Ap	651	41	1.4	644	10	US-09-867-701-2052	Sequence 2052, Ap
589	42	1.5	15843	9	US-09-764-869-2396	Sequence 2396, Ap	652	41	1.4	719	9	US-09-983-802-74	Sequence 74, Appl
590	42	1.5	16423	9	US-09-989-442-165	Sequence 165, Appl	653	41	1.4	756	9	US-09-974-879-94	Sequence 94, Appl
591	42	1.5	16774	9	US-10-091-504-2395	Sequence 2395, Ap	654	41	1.4	1035	9	US-09-764-877-2982	Sequence 2982, Ap
592	42	1.5	16774	9	US-10-091-504-2395	Sequence 2395, Ap	655	41	1.4	1055	9	US-10-092-154-1795	Sequence 1795, Ap
593	42	1.5	16774	10	US-09-764-869-2395	Sequence 2395, Ap	656	41	1.4	1055	10	US-10-092-154-1795	Sequence 1795, Ap
594	42	1.5	16774	10	US-09-764-869-2398	Sequence 2398, Ap	657	41	1.4	1055	10	US-09-764-847-1795	Sequence 1795, Ap
595	42	1.5	17965	9	US-09-764-891-8198	Sequence 8198, Ap	658	41	1.4	1105	9	US-09-974-879-67	Sequence 67, Appl
596	42	1.5	19969	9	US-10-190-593-3	Sequence 3, Appl	659	41	1.4	1229	9	US-09-764-891-6292	Sequence 6292, Ap
597	42	1.5	20522	10	US-09-764-877-3774	Sequence 3774, Ap	660	41	1.4	1403	10	US-09-822-830A-510	Sequence 510, Appl
598	42	1.5	21535	9	US-10-103-313-609	Sequence 609, Appl	661	41	1.4	1420	9	US-10-050-704-89	Sequence 89, Appl
599	42	1.5	21535	9	US-09-820-002-3	Sequence 3, Appl	662	41	1.4	1429	9	US-09-764-891-6291	Sequence 6291, Ap
600	42	1.5	23668	10	US-10-254-577-3	Sequence 3, Appl	663	41	1.4	1456	10	US-09-822-849A-110	Sequence 110, Appl
601	42	1.5	23668	10	US-09-741-148A-3	Sequence 3, Appl	664	41	1.4	1873	10	US-09-834-975-756	Sequence 756, Appl
602	42	1.5	28588	9	US-10-073-961-399	Sequence 399, Appl	665	41	1.4	1873	10	US-09-834-975-757	Sequence 757, Appl
603	42	1.5	28588	9	US-09-764-887-399	Sequence 399, Appl	666	41	1.4	2259	10	US-09-822-849A-491	Sequence 491, Appl
604	42	1.5	31766	10	US-09-765-344-5	Sequence 5, Appl	667	41	1.4	2559	9	US-09-961-253-4	Sequence 4, Appl
605	42	1.5	31766	10	US-09-765-344-5	Sequence 5, Appl	668	41	1.4	2781	9	US-10-092-154-1364	Sequence 1364, Ap
606	42	1.5	32187	9	US-09-764-891-6303	Sequence 6303, Ap	669	41	1.4	2781	10	US-09-984-827-1364	Sequence 1364, Ap
607	42	1.5	32187	9	US-10-102-627-109	Sequence 109, Appl	670	41	1.4	2884	9	US-09-984-827-1364	Sequence 1364, Ap
608	42	1.5	32192	9	US-09-764-891-6304	Sequence 6304, Ap	671	41	1.4	2888	9	US-09-984-827-1364	Sequence 1364, Ap
609	42	1.5	32192	9	US-10-092-154-1476	Sequence 1476, Ap	672	41	1.4	2889	9	US-09-984-827-1364	Sequence 1364, Ap
610	42	1.5	32192	9	US-09-764-891-7945	Sequence 7945, Ap	673	41	1.4	2893	9	US-09-984-827-1364	Sequence 1364, Ap
611	42	1.5	32192	9	US-09-764-891-8220	Sequence 8220, Ap	674	41	1.4	2893	9	US-09-984-827-1364	Sequence 1364, Ap
612	42	1.5	32192	9	US-09-764-891-8220	Sequence 8220, Ap	675	41	1.4	2893	9	US-09-984-827-1364	Sequence 1364, Ap
613	42	1.5	32192	9	US-09-764-891-8220	Sequence 8220, Ap	676	41	1.4	2893	9	US-09-984-827-1364	Sequence 1364, Ap

c 677	41	1.4	2893	9	US-09-984-827-141	Sequence 141, App	750	41	1.4	14962	9	US-10-079-854-244	Sequence 244, App
c 678	41	1.4	2893	9	US-09-984-827-142	Sequence 142, App	751	41	1.4	14962	10	US-09-764-878-244	Sequence 244, App
c 679	41	1.4	2893	9	US-09-984-827-143	Sequence 143, App	c 752	41	1.4	15044	9	US-10-091-504-1790	Sequence 1790, App
c 680	41	1.4	2893	9	US-09-984-827-144	Sequence 144, App	c 753	41	1.4	15044	10	US-09-764-869-1790	Sequence 1790, App
c 681	41	1.4	2893	9	US-09-984-827-145	Sequence 145, App	c 754	41	1.4	15046	9	US-10-091-504-1791	Sequence 1791, App
c 682	41	1.4	2893	9	US-09-984-827-146	Sequence 146, App	c 755	41	1.4	15046	10	US-09-764-869-1791	Sequence 1791, App
c 683	41	1.4	2893	9	US-09-984-827-147	Sequence 147, App	c 756	41	1.4	16181	9	US-10-092-154-1426	Sequence 1426, App
c 684	41	1.4	2893	9	US-09-984-827-148	Sequence 148, App	c 757	41	1.4	16181	10	US-09-764-891-6956	Sequence 6956, App
c 685	41	1.4	2893	9	US-09-984-827-149	Sequence 149, App	c 758	41	1.4	16181	9	US-09-764-847-1426	Sequence 1426, App
c 686	41	1.4	2893	9	US-09-984-827-150	Sequence 150, App	c 759	41	1.4	16181	10	US-09-764-877-3349	Sequence 3349, App
c 687	41	1.4	2893	9	US-09-984-827-151	Sequence 151, App	c 760	41	1.4	16181	9	US-10-091-504-1599	Sequence 1599, App
c 688	41	1.4	2893	9	US-09-984-827-152	Sequence 152, App	c 761	41	1.4	17967	10	US-09-764-869-1599	Sequence 1599, App
c 689	41	1.4	2893	9	US-09-984-827-153	Sequence 153, App	c 762	41	1.4	17967	9	US-10-116-016-50	Sequence 50, App
c 690	41	1.4	2893	9	US-09-984-827-154	Sequence 154, App	c 763	41	1.4	17967	10	US-09-764-848-50	Sequence 50, App
c 691	41	1.4	2893	10	US-09-846-456-3	Sequence 3, App	c 764	41	1.4	17967	9	US-10-103-313-650	Sequence 3, App
c 692	41	1.4	2893	10	US-09-846-456-3	Sequence 3, App	c 765	41	1.4	17967	10	US-09-764-891-7441	Sequence 7441, App
c 693	41	1.4	2893	9	US-09-984-827-147	Sequence 147, App	c 766	41	1.4	18408	9	US-09-764-891-7442	Sequence 7442, App
c 694	41	1.4	2893	9	US-09-984-827-148	Sequence 148, App	c 767	41	1.4	18408	10	US-09-764-864-1698	Sequence 1698, App
c 695	41	1.4	3172	9	US-09-954-531-580	Sequence 580, App	c 768	41	1.4	18408	9	US-10-092-154-1425	Sequence 1425, App
c 696	41	1.4	3231	9	US-09-984-827-141	Sequence 141, App	c 769	41	1.4	18408	10	US-09-764-864-1698	Sequence 1698, App
c 697	41	1.4	3231	10	US-09-969-347-147	Sequence 147, App	c 770	41	1.4	19553	9	US-10-092-154-1425	Sequence 1425, App
c 698	41	1.4	3269	10	US-09-969-347-147	Sequence 147, App	c 771	41	1.4	19553	10	US-09-764-864-1698	Sequence 1698, App
c 699	41	1.4	3651	10	US-09-764-877-3308	Sequence 3308, App	c 772	41	1.4	20261	9	US-10-079-854-325	Sequence 325, App
c 700	41	1.4	3999	9	US-09-999-248-5	Sequence 5, App	c 773	41	1.4	20261	10	US-09-764-878-325	Sequence 325, App
c 701	41	1.4	4150	12	US-10-016-725-15	Sequence 15, App	c 774	41	1.4	20645	9	US-09-764-891-8043	Sequence 8043, App
c 702	41	1.4	4166	9	US-10-125-540-625	Sequence 625, App	c 775	41	1.4	20645	10	US-09-764-872-816	Sequence 816, App
c 703	41	1.4	4166	10	US-09-764-870-625	Sequence 625, App	c 776	41	1.4	21358	9	US-09-764-891-9107	Sequence 9107, App
c 704	41	1.4	5088	9	US-10-091-504-1760	Sequence 1760, App	c 777	41	1.4	21358	10	US-09-764-872-816	Sequence 816, App
c 705	41	1.4	5088	9	US-09-764-891-5823	Sequence 5823, App	c 778	41	1.4	21676	9	US-09-764-891-9106	Sequence 9106, App
c 706	41	1.4	5088	9	US-09-764-891-6384	Sequence 6384, App	c 779	41	1.4	21676	10	US-09-764-891-9106	Sequence 9106, App
c 707	41	1.4	5088	9	US-09-764-891-9497	Sequence 9497, App	c 780	41	1.4	21913	9	US-09-764-891-6066	Sequence 6066, App
c 708	41	1.4	5088	10	US-09-764-891-9497	Sequence 9497, App	c 781	41	1.4	21913	10	US-09-764-891-6066	Sequence 6066, App
c 709	41	1.4	5216	9	US-10-125-540-607	Sequence 607, App	c 782	41	1.4	23431	9	US-09-764-864-1754	Sequence 1754, App
c 710	41	1.4	5216	10	US-10-074-094-605	Sequence 605, App	c 783	41	1.4	23431	10	US-09-764-864-1754	Sequence 1754, App
c 711	41	1.4	5216	10	US-09-764-870-607	Sequence 607, App	c 784	41	1.4	24577	9	US-09-764-868-1349	Sequence 1349, App
c 712	41	1.4	5216	10	US-09-764-866-695	Sequence 695, App	c 785	41	1.4	24577	10	US-09-764-868-1349	Sequence 1349, App
c 713	41	1.4	5426	10	US-09-798-029-7	Sequence 7, App	c 786	41	1.4	24577	9	US-10-061-119-4	Sequence 3, App
c 714	41	1.4	5950	10	US-09-880-107-1446	Sequence 107, App	c 787	41	1.4	25377	10	US-09-764-877-3194	Sequence 3194, App
c 715	41	1.4	6633	12	US-10-044-090-531	Sequence 531, App	c 788	41	1.4	25377	9	US-09-764-877-3194	Sequence 3194, App
c 716	41	1.4	6640	9	US-10-092-154-1277	Sequence 1277, App	c 789	41	1.4	30625	10	US-09-764-891-9479	Sequence 9479, App
c 717	41	1.4	6640	10	US-09-764-847-1077	Sequence 1077, App	c 790	41	1.4	30625	9	US-09-764-891-9479	Sequence 9479, App
c 718	41	1.4	6942	9	US-09-947-949-5	Sequence 947, App	c 791	41	1.4	32012	10	US-09-764-891-9479	Sequence 9479, App
c 719	41	1.4	7023	10	US-09-764-877-802	Sequence 802, App	c 792	41	1.4	32012	9	US-10-103-313-604	Sequence 604, App
c 720	41	1.4	7727	9	US-09-764-891-7885	Sequence 7885, App	c 793	41	1.4	32012	10	US-09-764-891-6303	Sequence 6303, App
c 721	41	1.4	8253	9	US-09-764-891-7885	Sequence 7885, App	c 794	41	1.4	32134	9	US-09-764-891-6303	Sequence 6303, App
c 722	41	1.4	8448	9	US-10-091-512-832	Sequence 832, App	c 795	41	1.4	32134	10	US-09-764-891-6303	Sequence 6303, App
c 723	41	1.4	8448	9	US-09-764-891-7885	Sequence 7885, App	c 796	41	1.4	32169	9	US-10-092-154-1963	Sequence 1963, App
c 724	41	1.4	8974	9	US-10-092-154-1963	Sequence 1963, App	c 797	41	1.4	32169	10	US-09-764-847-1963	Sequence 1963, App
c 725	41	1.4	8974	10	US-09-764-847-1963	Sequence 1963, App	c 798	41	1.4	32169	9	US-09-764-847-1963	Sequence 1963, App
c 726	41	1.4	9339	9	US-09-764-891-5485	Sequence 5485, App	c 799	41	1.4	32248	10	US-09-764-864-1769	Sequence 1769, App
c 727	41	1.4	9474	9	US-10-079-854-325	Sequence 325, App	c 800	41	1.4	32248	10	US-09-764-864-1769	Sequence 1769, App
c 728	41	1.4	9474	10	US-09-764-878-472	Sequence 472, App	c 801	41	1.4	32248	9	US-09-764-877-3487	Sequence 3487, App
c 729	41	1.4	9566	9	US-10-091-572-844	Sequence 844, App	c 802	41	1.4	32248	10	US-09-764-877-3487	Sequence 3487, App
c 730	41	1.4	9566	10	US-09-764-891-9498	Sequence 9498, App	c 803	41	1.4	34641	9	US-09-954-456-1110	Sequence 1110, App
c 731	41	1.4	10093	9	US-09-764-891-9498	Sequence 9498, App	c 804	41	1.4	34641	10	US-09-954-456-1110	Sequence 1110, App
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c 733	41	1.4	10445	10	US-09-764-891-5410	Sequence 5410, App	c 806	41	1.4	4641	10	US-09-820-003A-3	Sequence 3, App
c 734	41	1.4	10680	9	US-09-764-891-8467	Sequence 8467, App	c 807	41	1.4	48351	9	US-09-844-653-32	Sequence 32, App
c 735	41	1.4	10797	10	US-10-092-154-1577	Sequence 1577, App	c 808	41	1.4	48351	10	US-10-060-763-4	Sequence 4, App
c 736	41	1.4	10923	9	US-09-764-847-1577	Sequence 1577, App	c 809	41	1.4	48351	9	US-09-782-378A-17	Sequence 17, App
c 737	41	1.4	10923	10	US-10-092-154-1577	Sequence 1577, App	c 810	41	1.4	48351	10	US-09-782-378A-17	Sequence 17, App
c 738	41	1.4	11304	9	US-09-764-847-1577	Sequence 1577, App	c 811	41	1.4	48351	9	US-09-858-546-3	Sequence 3, App
c 739	41	1.4	11304	10	US-09-764-891-5631	Sequence 5631, App	c 812	41	1.4	48351	10	US-09-858-546-3	Sequence 3, App
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c 742	41	1.4	14221	9	US-10-091-572-844	Sequence 844, App	c 815	41	1.4	48351	9	US-09-858-546-3	Sequence 3, App
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c 744	41	1.4	14417	9	US-09-860-670-251	Sequence 251, App	c 817	41	1.4	48351	9	US-09-858-546-3	Sequence 3, App
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c 746	41	1.4	14426	9	US-09-860-670-251	Sequence 251, App	c 819	41	1.4	48351	9	US-09-858-546-3	Sequence 3, App
c 747	41	1.4	14426	10	US-09-860-670-251	Sequence 251, App	c 820	41	1.4	48351	10	US-09-858-546-3	Sequence 3, App
c 748	41	1.4	14448	9	US-09-860-670-251	Sequence 251, App	c 821	41	1.4	48351	9	US-09-858-546-3	Sequence 3, App
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RESULT 2

US-09-846-456-3
: Sequence 3, Application US/09846456
: Patent No. US20020146792A1
: GENERAL INFORMATION:
: APPLICANT: Rosier, Marie
: APPLICANT: Prades, Catherine
: APPLICANT: Lemoine, Cendrline
: APPLICANT: Naudin, Laurence
: APPLICANT: Benefile, Patrice
: APPLICANT: Duverger, Nicolas
: APPLICANT: Brewer, Bryan
: APPLICANT: Remaley, Alan
: APPLICANT: Fojo, Silvia
: TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying
: FILE REFERENCE: 3806.0505
: CURRENT APPLICATION NUMBER: US/09/846,456
: CURRENT FILING DATE: 2001-05-02
: PRIOR APPLICATION NUMBER: US 60/201,280
: PRIOR FILING DATE: 2000-05-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 3
: LENGTH: 2893
: TYPE: DNA
: ORGANISM: Homo sapiens

US-09-846-456-3

Query Match 100.0%; Score 2893; Db 10; Length 2893;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2893; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Qy	901	GCTGGCGCTGGGCTTTAGAAAGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCT	960						
Db	901	GCTGGCGCTGGGCTTTAGAAAGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCT	960						
Qy	961	TTAATTTCTGACAGGAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1020						
Db	961	TTAATTTCTGACAGGAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1020						

Qy	1021	TCGACTCACTCTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1080						
Db	1021	TCGACTCACTCTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1080						
Qy	1081	GATAAGAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1140						
Db	1081	GATAAGAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1140						
Qy	1141	TCATCATGTTGGTCAAGGTTGGTTCGAACTCTGAACTCTGAACTCTGAACTCTG	1200						
Db	1141	TCATCATGTTGGTCAAGGTTGGTTCGAACTCTGAACTCTGAACTCTGAACTCTG	1200						
Qy	1201	CTCCCAAGTCTGGGATTCAGGATTCAGGATTCAGGATTCAGGATTCAGGATTC	1260						
Db	1201	CTCCCAAGTCTGGGATTCAGGATTCAGGATTCAGGATTCAGGATTCAGGATTC	1260						
Qy	1261	CTAAGGCAAAAGTTCGATGTTGATGAAACCACTGATGTTGATGTTGATGTTG	1320						
Db	1261	CTAAGGCAAAAGTTCGATGTTGATGAAACCACTGATGTTGATGTTGATGTTG	1320						
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Db	1321	GACTCCAGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1380						
Qy	1381	TTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1440						
Db	1381	TTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1440						
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Qy	1801	TGGCAGAAATGAAGTGGATTTAGTTTGTGGCTTGGATGATGATGATGATGATG	1860						
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RESULT 4

US-09-846-456-1
; Sequence 1, Application US/09846456
; Patent No. US20020146792A1
; GENERAL INFORMATION:
; APPLICANT: Rosier, Marie
; APPLICANT: Prades, Catherine


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DB 2881 CGGCAAAACCC 2893
RESULT 5
US-09-984-827-158
: Sequence 158, Application US/9984827
: Publication No. US20030056234A1
: GENERAL INFORMATION:
: APPLICANT: DENEFFLE, PAIRICE
: APPLICANT: RUSIER-MONTUS, MARIE-FRANCOISE
: APPLICANT: ARNOULD-REGUIGNE, ISABELLE
: APPLICANT: DUVERGER, NICOLAS
: APPLICANT: CAMBIEN, FRANCOIS
: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,
: FILE REFERENCE: 03806.0522-00000
: CURRENT APPLICATION NUMBER: US/09/984.827
: CURRENT FILING DATE: 2002-04-01
: PRIOR APPLICATION NUMBER: 60/254,108
: PRIOR FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: FR 00/14037
: PRIOR FILING DATE: 2000-10-31
: NUMBER OF SEQ ID NOS: 161
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 158
: LENGTH: 2893
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-984-827-158
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Best Local Similarity 100.0%; Pctd No. 0;
Matches 2879; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 GCCAGATCTACCAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
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DB 121 AAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
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DB 541 ACCAGTATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
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RESULT 7

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RESOL 1 /
US-09-984-827-139
; Sequence 139, Application US/09984827
; Publication No. US2001005234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGNIENE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984.827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254.108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 2893
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-827-139

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Query Match          98.2%; Score 2842; DB 9; Length 2893;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 9
US-09-984-827-141
; Sequence 141: Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFFLE, PATRICE
; APPLICANT: KOSTER-MONTUS, MARIE FRANCOISE
; APPLICANT: ARNOULD-REQUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,
; FILE REFERENCE: 03805-0522-00000
; CURRENT APPLICATION NUMBER: US/09/984-827
; CURRENT FILING DATE: 2002-04-01
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; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 141
; LENGTH: 2893
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-827-141
Query Match 98.28; Score 2842; DB 9; Length 2893;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 10

US-09-846-827-142
Sequence 142: Application US/09964-27
Publication No. US20030056214A1
GENERAL INFORMATION:
APPLICANT: BENEFL, PATRICE
APPLICANT: ROSE, ER-MONTUS, MARIE-FRANCOISE
APPLICANT: ARNOUD-REGUINE, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN AB 24. GENE, THEIR USES, AND
FILE REFERENCE: 03806.0522-00000
CURRENT APPLICATION NUMBER: US/09/984.827
CURRENT FILING DATE: 2002-04-01
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PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 142
LENGTH: 2893
TYPE: DNA
ORGANISM: Homo sapiens
US-09-846-827-142

Query Match

98.2% Score 2842: DB 9: Length 2893

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 901 CCGGCGCTTGGGCTTTAGAAAGCTCATCTCTGGCTTTCTGAGATCATCTCCCTTTCTTT 960
DB 901 CCGGCGCTTGGGCTTTAGAAAGCTCATCTCTGGCTTTCTGAGATCATCTCCCTTTCTTT 960
QY 961 TTATTTTCTTGAACAGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
DB 961 TTATTTTCTTGAACAGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
QY 1021 TCGATCTATCTGAACTTTCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
DB 1021 TCGATCTATCTGAACTTTCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080

DB 1021 TCGACACGACCTCTGCTCCCGGGTTCAGAGATTC TCTCCCTACACCTCTGCA 1080
QY 1081 GATACAGCGCCGCCACACATCTGGCTAAATTTTGTATTTTATAGTAAGTACTGGCT 1140
DB 1081 GATACAGCGCCGCCACACATCTGGCTAAATTTTGTATTTTATAGTAAGTACTGGCT 1140
QY 1141 CATCACTGTCGCCAGGTGGTTTCGAATCTCGACCTGAGGAGGAGTCTGGAGCTGGG 1200
DB 1141 CATCACTGTCGCCAGGTGGTTTCGAATCTCGACCTGAGGAGGAGTCTGGAGCTGGG 1200
QY 1201 CTGCGAAGTCTGGGATTCAGGATTCAGGATTCAGGATTCAGGATTCAGGATTCAGG 1260
DB 1201 CTGCGAAGTCTGGGATTCAGGATTCAGGATTCAGGATTCAGGATTCAGGATTCAGG 1260
QY 1261 CTAGGCAACAGCTCCATGGTCAAGGGGCCATGACAGAGATTA TACTACTGCG 1320
DB 1261 CTAGGCAACAGCTCCATGGTCAAGGGGCCATGACAGAGATTA TACTACTGCG 1320
QY 1321 GACTCCAGATTCCTTGGCTGGTGGCTCCACATGCACTTCCAGGGGCTGTTTGGGCTTC 1380
DB 1321 GACTCCAGATTCCTTGGCTGGTGGCTCCACATGCACTTCCAGGGGCTGTTTGGGCTTC 1380
QY 1381 TTTATGCTGCTGCTGAGTGTGATAGAACCTGATGAGTACTGCTGAGCTGCTGAGCC 1440
DB 1381 TTTATGCTGCTGCTGAGTGTGATAGAACCTGATGAGTACTGCTGAGCTGCTGAGCC 1440
QY 1441 GTGGCTGGAGATCTGTTGACTGTAGCTAGGAGGCTTGTGCACTGCACTGCTGCA 1500
DB 1441 GTGGCTGGAGATCTGTTGACTGTAGCTAGGAGGCTTGTGCACTGCACTGCTGCA 1500
QY 1501 TGCAGTGTGGGATTCGGAATATGATGGAGCTGAGGTGGTAAGAGAGAGTACTGCT 1560
DB 1501 TGCAGTGTGGGATTCGGAATATGATGGAGCTGAGGTGGTAAGAGAGAGTACTGCT 1560
QY 1561 GGGAGCTCTCTGACCTCATCTGCGCAAACTCAGGTCAGACCTGAGAGTCT 1620
DB 1561 GGGAGCTCTCTGACCTCATCTGCGCAAACTCAGGTCAGACCTGAGAGTCT 1620
QY 1621 AATGTGAATTCGCTTCAAGTGGGTACAAAGTATCTTGTCAAGTGAAGTACTGCT 1680
DB 1621 AATGTGAATTCGCTTCAAGTGGGTACAAAGTATCTTGTCAAGTGAAGTACTGCT 1680
QY 1681 GTGGCTCCAGCTGACCTTCAGGGCTGCTGGGCTGCTTCAAGGCTGAGTCTGAGT 1740
DB 1681 GTGGCTCCAGCTGACCTTCAGGGCTGCTGGGCTGCTTCAAGGCTGAGTCTGAGT 1740
QY 1741 GTTCTAATCTTCAGGCGAGATTCATATTTAATTTAATTTAATTTAATTTAATTTAAT 1800
DB 1741 GTTCTAATCTTCAGGCGAGATTCATATTTAATTTAATTTAATTTAATTTAATTTAAT 1800
QY 1801 TGGGAGAAATAGGTGACATTTAGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1860
DB 1801 TGGGAGAAATAGGTGACATTTAGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1860
QY 1861 TGGTGTGAGGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
DB 1861 TGGTGTGAGGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
QY 1921 AATTTTGTGCTTACAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 1980
DB 1921 AATTTTGTGCTTACAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 1980
QY 1981 AATTTTACAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 2040
DB 1981 AATTTTACAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 2040
QY 2041 GTGCTGTGTTTATACAGGAGGCTGATCAATATATATATATATATATATATATATAT 2100
DB 2041 GTGCTGTGTTTATACAGGAGGCTGATCAATATATATATATATATATATATATATAT 2100
QY 2101 CATATGTCAGTGTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2160
DB 2101 CATATGTCAGTGTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2160

QY 2161 TCTTCTCTCAATTTATGAAGACAGACAGTAAAGTGTCTCTCTCGGTCTCTGAGGGA 2220
DB 2161 TCTTCTCTCAATTTATGAAGACAGACAGTAAAGTGTCTCTCTCGGTCTCTGAGGGA 2220
QY 2221 CCGGGAGCTTGAAGCTGGGAATCTCCAAAGCAGTGTGCTTATCAAAATCAAAAGTC 2280
DB 2221 CCGGGAGCTTGAAGCTGGGAATCTCCAAAGCAGTGTGCTTATCAAAATCAAAAGTC 2280
QY 2281 CAGGTTGTGGGGGAAACAAAGACAGGCTTACCCAGAGGACTTCCGCTTCCGCT 2340
DB 2281 CAGGTTGTGGGGGAAACAAAGACAGGCTTACCCAGAGGACTTCCGCTTCCGCT 2340
QY 2341 CACCCAGCTTGAAGCTTGAAGCAACAAAGACAGGCTTATGGGCTCTGA 2400
DB 2341 CACCCAGCTTGAAGCTTGAAGCAACAAAGACAGGCTTATGGGCTCTGA 2400
QY 2401 GGGAGATTCAGCTAGGCTCTCTCTCCCAATCTCTCCGCTCGGCTGAGGAATTAAC 2460
DB 2401 GGGAGATTCAGCTAGGCTCTCTCTCCCAATCTCTCCGCTCGGCTGAGGAATTAAC 2460
QY 2461 AAGGCAAAATTTGGGAAGCAGGATTTAGAGGAGCAAAATTCCTGCTGCTGCT 2520
DB 2461 AAGGCAAAATTTGGGAAGCAGGATTTAGAGGAGCAAAATTCCTGCTGCTGCT 2520
QY 2521 GGTCTCCGGGAGCTGGACTAGAGTCTGCGGGCAGGCTGCGGAGCCAGCGCTTCCGC 2580
DB 2521 GGTCTCCGGGAGCTGGACTAGAGTCTGCGGGCAGGCTGCGGAGCCAGCGCTTCCGC 2580
QY 2581 GGTCTTAGGCTGCGGGCCGCGGGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
DB 2581 GGTCTTAGGCTGCGGGCCGCGGGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
QY 2641 CTGTGTGAGCTTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCTG 2700
DB 2641 CTGTGTGAGCTTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCTG 2700
QY 2701 TGTGGGGCTGACGCTGCGGCTTTAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 2760
DB 2701 TGTGGGGCTGACGCTGCGGCTTTAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 2760
QY 2761 TCACTGACTGAATACATAAAGAGGCGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 2820
DB 2761 TCACTGACTGAATACATAAAGAGGCGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 2820
QY 2821 GCTTGAAGGATAGTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
DB 2821 GCTTGAAGGATAGTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
QY 2881 GGGCAAAATTT 2893
DB 2881 GGGCAAAATTT 2893

RESULT 11

US-09-984-827-143

: Sequence 143, Application US/09/984827

: Publication No. US2003056234A1

: GENERAL INFORMATION:

: APPLICANT: DENEFE, PATRICE

: APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE

: APPLICANT: ARNOULD-RECUIGNE, ISABELLE

: APPLICANT: DUVERGER, NICOLAS

: APPLICANT: CAMBIEN, FRANCOIS

: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,

: TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR

: FILE REFERENCE: 03806.0522-00000

: CURRENT APPLICATION NUMBER: US/09/984.827

: CURRENT FILING DATE: 2002-04-01

: PRIOR APPLICATION NUMBER: 60/254,108

: PRIOR FILING DATE: 2000-12-11

: PRIOR APPLICATION NUMBER: FR 00/14037

: PRIOR FILING DATE: 2000-10-31

NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 143
LENGTH: 2893
TYPE: DNA
ORGANISM: Homo sapiens
US-09-846-456-3.oli30.rnbp

Query Match 98.28; Score 2842; DB 9; Length 2893;
Best Local Similarity 100.0%; Pred No 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACAGGGCAGTGGCAGGCTGTAAATCTCAGTACTCGGGAGCTGGAGTACCAATGA 60
DB 1 ACAGGGCAGTGGCAGGCTGTAAATCTCAGTACTCGGGAGCTGGAGTACCAATGA 60

QY 61 GCGCAGATCGCAGCAATCGACTCCAGCTGGCAACAAAGGTCAAACTCATCTCAAT 120
DB 61 GCGCAGATCGCAGCAATCGACTCCAGCTGGCAACAAAGGTCAAACTCATCTCAAT 120

QY 121 AAAAAAAGAAATGATTTGGTGGTCCACTTCAAAATAGGTAGGAGAGAGAGAGAGG 180
DB 121 AAAAAAAGAAATGATTTGGTGGTCCACTTCAAAATAGGTAGGAGAGAGAGAGAGG 180

QY 181 AGATGGAGGTCAGGAGATCTAATTAATCTCTAATATCGCTAGGAAGATATAACACT 240
DB 181 AGATGGAGGTCAGGAGATCTAATTAATCTCTAATATCGCTAGGAAGATATAACACT 240

QY 241 TTTAATAACACTCTCTGCTTTTATAACATCAATCTGCCAGAGAGTCAAAATTTCAACA 300
DB 241 TTTAATAACACTCTCTGCTTTTATAACATCAATCTGCCAGAGAGTCAAAATTTCAACA 300

QY 301 AAGTTCACTTTTCAGAAAACCCCTTTGAGGAAGACAGAAATATATATTTTTCATTTTA 360
DB 301 AAGTTCACTTTTCAGAAAACCCCTTTGAGGAAGACAGAAATATATATTTTTCATTTTA 360

QY 361 AAGATGAAGAAACAGGCGGCGGCAATGGCTAATGCCGTGTAATCCAGCAATTTGGGAGG 420
DB 361 AAGATGAAGAAACAGGCGGCGGCAATGGCTAATGCCGTGTAATCCAGCAATTTGGGAGG 420

QY 421 CTGAGGCGAGGATCGGCTTGGCTCCAGAGTTTCAGAGCTGAGCTGATATATATATAT 480
DB 421 CTGAGGCGAGGATCGGCTTGGCTCCAGAGTTTCAGAGCTGAGCTGATATATATATAT 480

QY 481 ACCCTGTCTACAAAAAATAACAAAAATAGATGGTGTGGTGGCAATATATATATATAT 540
DB 481 ACCCTGTCTACAAAAAATAACAAAAATAGATGGTGTGGTGGCAATATATATATATAT 540

QY 541 CCCAGCTACTTTGGGAGGCTAAGGTGGAGATCGCTTCCAGCTGAGCTGATATATATAT 600
DB 541 CCCAGCTACTTTGGGAGGCTAAGGTGGAGATCGCTTCCAGCTGAGCTGATATATATAT 600

QY 601 CTGAGCCATGATTTGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 CTGAGCCATGATTTGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660

QY 661 AAAAAAAGAAATGAAG 720
DB 661 AAAAAAAGAAATGAAG 720

QY 721 GAGGGGGAGGAG 780
DB 721 GAGGGGGAGGAG 780

QY 781 GATGAACAGAGGCGAG 840
DB 781 GATGAACAGAGGCGAG 840

QY 841 CCCCCAACCCCAATTTATTGACCAAGGTTATCTTTTACCTGAGGAGAGAGAGAGAGAG 900
DB 841 CCCCCAACCCCAATTTATTGACCAAGGTTATCTTTTACCTGAGGAGAGAGAGAGAGAG 900

QY 901 CCGGCGGCTGGGCTTTAGAAAGGCTCATCTCTGAGATCAATCTTTTCTGAGATCAAT 960
DB 901 CCGGCGGCTGGGCTTTAGAAAGGCTCATCTCTGAGATCAATCTTTTCTGAGATCAAT 960

DB 901 CCGGCGGCTGGGCTTTAGAAAGGCTCATCTCTGAGATCAATCTTTTCTGAGATCAAT 960
QY 961 TTAATTTCTTGAACAGGAGTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 961 TTAATTTCTTGAACAGGAGTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020

QY 1021 TCGACTCACTGTAATCTCTGCTCCGGGTTCAAGCCGATTCCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 TCGACTCACTGTAATCTCTGCTCCGGGTTCAAGCCGATTCCTGCTGCTGCTGCTGCTGCT 1080

QY 1081 GATAACAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140
DB 1081 GATAACAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140

QY 1141 TCATCATGTTGTCAGGTTGTTTTCGAACCTCTGACCTGAGTGGAGTGGCCACCTTGGC 1200
DB 1141 TCATCATGTTGTTGAGGTTGTTTTCGAACCTCTGACCTGAGTGGAGTGGCCACCTTGGC 1200

QY 1201 CTCCAAAGTCTGGGATTTACAGGCTGAGCCACTGCGCCGAGCTCAGATCCATCCCTTT 1260
DB 1201 CTCCAAAGTCTGGGATTTACAGGCTGAGCCACTGCGCCGAGCTCAGATCCATCCCTTT 1260

QY 1261 CTAAAGGCGAAGCAGTCCATGTTGCAAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1320
DB 1261 CTAAAGGCGAAGCAGTCCATGTTGCAAGGGGCGGCGGCGGCGGCGGCGGCGGCGG 1320

QY 1321 GACTCCAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1321 GACTCCAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380

QY 1381 TTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1381 TTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440

QY 1441 GTGGCTGCGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
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QY 1501 TCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1501 TCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560

QY 1561 GGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
DB 1561 GGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620

QY 1621 AAATGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB 1621 AAATGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680

QY 1681 GTGGCTTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
DB 1681 GTGGCTTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740

QY 1741 CTCTTATGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
DB 1741 CTCTTATGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800

QY 1801 TGCCAGAAATAGGTTGACATTTAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
DB 1801 TGCCAGAAATAGGTTGACATTTAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860

QY 1861 TGGTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
DB 1861 TGGTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920

QY 1921 AGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
DB 1921 AGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980

QY 1981 AATTTTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
DB 1981 AATTTTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040

1981 AATTTTACAGACTGCAATCTCTGCTGCACTTCACAAATGATATACAAATTAATACAA 2040
QY
2041 GTCTCTGTTTATACAGGAGGCTGATCAATATAATGAATTAATGAATGCTGCTGCTG 2100
DB
2041 GTCTCTGTTTATACAGGAGGCTGATCAATATAATGAATTAATGAATGCTGCTGCTG 2100
QY
2101 CATATGTTCTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 2160
DB
2101 CATATGTTCTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 2160
QY
2161 TCTTCTCTCAATTTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
DB
2161 TCTTCTCTCAATTTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
QY
2221 CTGAGGAGCTCAGGCTGGAATCTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
DB
2221 CTGAGGAGCTCAGGCTGGAATCTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
QY
2281 CAGGTTTGTGGGGGAAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
DB
2281 CAGGTTTGTGGGGGAAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
QY
2341 CAGGTTTGTGGGGGAAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
DB
2341 CAGGTTTGTGGGGGAAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
QY
2401 GAGGATTCAGGCTAGAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
DB
2401 GAGGATTCAGGCTAGAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
QY
2461 AAGGAG 2520
DB
2461 AAGGAG 2520
QY
2521 GAGTCTGAGGAG 2580
DB
2521 GAGTCTGAGGAG 2580
QY
2581 GAGTCTGAGGAG 2640
DB
2581 GAGTCTGAGGAG 2640
QY
2641 GAGTCTGAGGAG 2700
DB
2641 GAGTCTGAGGAG 2700
QY
2701 GAGTCTGAGGAG 2760
DB
2701 GAGTCTGAGGAG 2760
QY
2761 GAGTCTGAGGAG 2820
DB
2761 GAGTCTGAGGAG 2820
QY
2821 GAGTCTGAGGAG 2880
DB
2821 GAGTCTGAGGAG 2880
QY
2881 GAGTCTGAGGAG 2940
DB
2881 GAGTCTGAGGAG 2940

RESULT 12
US-09-984-827-144
; Sequence 144, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNIE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS

; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES
; FILE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984.827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254.108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ. ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ. ID NO: 144
; LENGTH: 2893
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-827-144

Query Match 98.2%; Score 2842; DB 9; Length 2893;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACAGGGCATGTCGCAAGTGCCTGTAATCTCAGTTACTCGGAGGTGGAGGTTGCAATCA 60
DB 1 ACAGGGCATGTCGCAAGTGCCTGTAATCTCAGTTACTCGGAGGTGGAGGTTGCAATCA 60
QY 61 GCCCAGATCCACGATTCGACTCCAGCTGGGCAACAAAGGTGAACTCCATCTCAATT 120
DB 61 GCCCAGATCCACGATTCGACTCCAGCTGGGCAACAAAGGTGAACTCCATCTCAATT 120
QY 121 AAAAAAAGAAATGATTTTGGTGGCTGCACTTCAAAATAGTAGGAGAGAGAGAGAGG 180
DB 121 AAAAAAAGAAATGATTTTGGTGGCTGCACTTCAAAATAGTAGGAGAGAGAGAGAGG 180
QY 181 AGATGGAGGTTCAGGAGATCTAATTAATCTCTAATAATCATGCTAGGAGAGATACACCT 240
DB 181 AGATGGAGGTTCAGGAGATCTAATTAATCTCTAATAATCATGCTAGGAGAGATACACCT 240
QY 241 TTTAATAACACTCTCTCTCTTTTAAATCAATCAATCTGCCAGGAGCTCAAGGTTTCAACA 300
DB 241 TTTAATAACACTCTCTCTCTTTTAAATCAATCAATCTGCCAGGAGCTCAAGGTTTCAACA 300
QY 301 AAGTTCACTTTACAAAACCCCTTTGAGGAGAGACAAATATACATCTCTCTCCATTTTA 360
DB 301 AAGTTCACTTTACAAAACCCCTTTGAGGAGAGACAAATATACATCTCTCTCCATTTTA 360
QY 361 AAGATGAAGAAACAGGCGGAGCAATGCTTAATGCTGTATATCCAGCACTTGGAGAGG 420
DB 361 AAGATGAAGAAACAGGCGGAGCAATGCTTAATGCTGTATATCCAGCACTTGGAGAGG 420
QY 421 CTGAGGCAAGAGATCGCTTGAGCTCCAGAGTTTGAGACCAGCTCGGATAAATGCAAAA 480
DB 421 CTGAGGCAAGAGATCGCTTGAGCTCCAGAGTTTGAGACCAGCTCGGATAAATGCAAAA 480
QY 481 ACCCTGTCTTTACAAAAAATACAAAAATAGATGGGTGTGGGATGCGACCTGTGCT 540
DB 481 ACCCTGTCTTTACAAAAAATACAAAAATAGATGGGTGTGGGATGCGACCTGTGCT 540
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DB 541 CCCAGCTACTTGGAGGCTAAGGTGGGAGGATCGCTTGAGCCAGGAGGTCAAGTCTACA 600
QY 601 CTGAGCCATGATTGATCACTGCACTCCAGCTGGGTAGACAGAGAGAGAGAGAGAGAG 660
DB 601 CTGAGCCATGATTGATCACTGCACTCCAGCTGGGTAGACAGAGAGAGAGAGAGAGAG 660
QY 661 AAAAAAGAAATGAAG 720
DB 661 AAAAAAGAAATGAAG 720
QY 721 GAGGGGGGAG 780
DB 721 GAGGGGGGAG 780

781 GATCAACAGAGGAGAGAGACTTTACGTAATTTGCTCATCATGTGGTTGTAAGTTTGA 840
781 GATCAACAGAGGAGAGAGACTTTACGTAATTTGCTCATCATGTGGTTGTAAGTTTGA 840
841 GCGCAAAACCAATTTATTGACCAAGGTATATCTTTGACTGAGGCAAGGCTTCCGCTCT 900
841 GCGCAAAACCAATTTATTGACCAAGGTATATCTTTGACTGAGGCAAGGCTTCCGCTCT 900
901 CCGGCGCTTGGGCTTTAGAAAGCTCATCTGCGCTTTCTGAGATCCATPCTTTGCTTT 960
901 CCGGCGCTTGGGCTTTAGAAAGCTCATCTGCGCTTTCTGAGATCCATPCTTTGCTTT 960
961 TTATTTTCTGACAGGAGTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
961 TTATTTTCTGACAGGAGTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
1021 TCGACTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
1021 TCGACTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
1081 GATAACAGGCGCGCGCCACCATCTGGCTAAATTTTATATTTTATGTAAGATGCGTT 1140
1081 GATAACAGGCGCGCGCCACCATCTGGCTAAATTTTATATTTTATGTAAGATGCGTT 1140
1141 TCATCATCTTGGCAGGTTGGTTTCCGACCTCTGACCTGACCTGACCTGACCTGAC 1200
1141 TCATCATCTTGGCAGGTTGGTTTCCGACCTCTGACCTGACCTGACCTGACCTGAC 1200
1201 CTCGCAAGTCTGGGATTACAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1260
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1261 GTAAAGGTAACAGTCCATGGTGCAGAGGCGGATGCTGACCTGACCTGACCTGAC 1320
1261 GTAAAGGTAACAGTCCATGGTGCAGAGGCGGATGCTGACCTGACCTGACCTGAC 1320
1321 GACTCCAGAAATTCCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
1321 GACTCCAGAAATTCCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
1381 TTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
1381 TTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
1441 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
1441 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
1501 TGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
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1561 GAGCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
1561 GAGCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
1621 AAATGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
1621 AAATGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
1681 GTGGCTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
1681 GTGGCTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
1741 CTCTATGTAATCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
1741 CTCTATGTAATCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
1801 TGGCAGATAAGGTGACATTTAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
1801 TGGCAGATAAGGTGACATTTAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
1861 TGGCAGATAAGGTGACATTTAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
1861 TGGCAGATAAGGTGACATTTAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920

RESULT 13

1861 TGGTGTGTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
1921 AGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
1921 AGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
1981 AATTTTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
1981 AATTTTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
2041 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
2041 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
2101 CATATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
2101 CATATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
2161 TCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
2161 TCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
2221 CTTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
2221 CTTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
2281 CAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340
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RESULT 14
US-09-984-827-146
Sequence 146, Application US/09984827
Publication No. US2004005624A1
GENERAL INFORMATION:
APPLICANT: DENEJEE, PATRICE
APPLICANT: KOSTER-MONTUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-REGUINE, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,
TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
FILE REFERENCE: 03806.0522-00000
CURRENT APPLICATION NUMBER: US/09/984,827
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 146
LENGTH: 2893
TYPE: DNA
ORGANISM: Homo sapiens
US-09-984-827-146
Query Match 98.2% Score 2842; DB 9; Length 2893;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 17

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US-09-984-827-152
: Sequence 152, Application US/09984827
: Publication No. US2003005234A1
: GENERAL INFORMATION:
: APPLICANT: DENFLE, PATRICE
: APPLICANT: KOSIER-MONTUS, MARIE-FRANCOISE
: APPLICANT: ARNOULD-REGUIGNE, ISABELLE
: APPLICANT: DUVERGER, NICOLAS
: APPLICANT: CAMBIEN, FRANCOIS
: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN APOA1 GENE, THEIR USES, AND
: FILE REFERENCE: DETECTION METHODS AND KITS THEREFOR
: CURRENT APPLICATION NUMBER: US/09/984,827
: PRIOR FILING DATE: 2002-04-01
: PRIOR APPLICATION NUMBER: 60/254,108
: PRIOR FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: FR 00/14037
: NUMBER OF SEQ ID NOS: 161
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 152
: LENGTH: 2893
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-984-827-152
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Query Match      98.2%; Score 2842; DB 9; Length 2893;
Best local Similarity 100.0%; Pred. No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Caps 0;
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Qy 241 TTTAATAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
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Qy 301 AAGTTCACTTTTCAGAAACCCCTTTGAGGAAGACAGAAATATACATCTCTCTCTCTCT 360
Db 301 AAGTTCACTTTTCAGAAACCCCTTTGAGGAAGACAGAAATATACATCTCTCTCTCTCT 360
Qy 361 AAGATGAAGAAGCAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
Db 361 AAGATGAAGAAGCAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
Qy 421 CTGAGGCGCAGAGGATCGGTTTGAGCTCCAGAGTTTGACACAGCTTGATAAATGCAAA 480
Db 421 CTGAGGCGCAGAGGATCGGTTTGAGCTCCAGAGTTTGACACAGCTTGATAAATGCAAA 480
Qy 481 ACCCTGTCTCTACAAAAAATACAAAAATAGATGGTGTGGTGGTGGTGGTGGTGGT 540
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Qy 541 CCCAGCTACTTTGGAGGCTAAGGTGGGAGGATCGCTTGAGCCAGGAGTCAAGTCTACA 600
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Db 661 AAAAAAAGCAATGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 720
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Db 721 GAGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
Qy 781 GATGAACAGAGCTAGAAAGCAATTAAGTAAATTCATCATCTGCTGCTCAAGTCTCA 840
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Qy 841 CCCCCAACCCCAATTTATTTGACCAAGGTTATTTTGTGAGTGGAGGGGGTCCGCTCT 900
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DB 2281 CAGGTTGTGGGGGAAACAAAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
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DB 2341 CACCCAGCTTGGGCTTTTGAAGGAAACAAAAGCAGAGAGAGAGAGAGAGAGAGAG 2400
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DB 2641 CCGTCTGTACCTTCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCC 2700
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DB 2821 GCTTTGACCGATAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
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DB 2881 CGGCAAAACCCG 2893

RESULT 18

US-09-984-827-153

; Sequence 153, Application US/09984827

; Publication No. US200300563441

; GENERAL INFORMATION:

; APPLICANT: DENEFLA, PATRICE

; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE

; APPLICANT: ARNOULD-REGUIGNE, ISABELLE

; APPLICANT: DUVERGER, NICOLAS

; APPLICANT: CAMBIEN, FRANCOIS

; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR

; FILE REFERENCE: 03806.0522-00000

; CURRENT FILING DATE: 2002-04-01

; PRIOR FILING DATE: 2000-12-11

; PRIOR FILING DATE: 2000-12-11

; PRIOR FILING DATE: 2000-12-11

; NUMBER OF SEQ ID NOS: 161

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 153

; LENGTH: 2893

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-984-827-153

Query Match

Best Local Similarity 100.0%; Score 2842; DB 9; Length 2893;

QY 2161 TCCTTCCTCAATTTATGAGAGAGAGCAGTAGAAGTTCCTCTCTGGGTCCTCTGAGGGA 2220
DB 2161 TCCTTCCTCAATTTATGAGAGAGAGCAGTAGAAGTTCCTCTCTGGGTCCTCTGAGGGA 2220
QY 2221 CTTGGGAGCTCAGGCTGGCAATCTCCAAAGGAGTAGGTCGCTATCAAAAGATCAAGATC 2280
DB 2221 CTTGGGAGCTCAGGCTGGCAATCTCCAAAGGAGTAGGTCGCTATCAAAAGATCAAGATC 2280
QY 2281 CAGGTTTGTGGGGGAAACAAAAGCAGGCTATTACAGAGAGAGCTGCTGCTGCTGCT 2340
DB 2281 CAGGTTTGTGGGGGAAACAAAAGCAGGCTATTACAGAGAGAGCTGCTGCTGCTGCT 2340
QY 2341 CAGCCAGCTCAGGCTTTGAAAGGAAACAAAAGCAGGCTATTACAGAGAGAGCTGCT 2400
DB 2341 CAGCCAGCTCAGGCTTTGAAAGGAAACAAAAGCAGGCTATTACAGAGAGAGCTGCT 2400
QY 2401 GGGAGATTACGCTAGAGCTCTCTCTCCGCCAATCCCTCCGCTGAGAAATAC 2460
DB 2401 GGGAGATTACGCTAGAGCTCTCTCTCCGCCAATCCCTCCGCTGAGAAATAC 2460
QY 2461 AAGCAAAAAAATTCGGGAAGCAGGATTAGAGAGAGCAATTCACCTCTGCTCT 2520
DB 2461 AAGCAAAAAAATTCGGGAAGCAGGATTAGAGAGAGCAATTCACCTCTGCTCT 2520
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DB 2521 GGTTCGGGGAACCTGGACTAGAGAGTCTGCGCGCAGGCGCCGAGCCGCTCTGCT 2580
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DB 2881 GGGCAAAACCCC 2893

RESULT 19
US-09-846-827-154
Sequence 154, Application US/09984827
Publication No. US20030056234A1
GENERAL INFORMATION:
APPLICANT: DENEUE, PATRICE
APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN APO(A) GENE, THEIR USES, AND
TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
FILE REFERENCE: 03806.0522-00000
CURRENT APPLICATION NUMBER: US/09/984.827
PRIOR FILING DATE: 2002-04-01
PRIOR FILING DATE: 2002-04-108
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 161

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 154
LENGTH: 2893
TYPE: DNA
ORGANISM: Homo sapiens
US-09-984-827-154
Query Match 98.2%; Score 2842; DB 9; Length 2893;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACAGGGCATGCTGCTAGCTGCTCTAATCTCAGTTACTCGGAGGTGCGAGTTGCAATGA 60
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DB 61 GCGCAGATCGCACCATTGCATCCAGCTCGGCAACAAAAGGTGAAACTCCATCTCAAT 120
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DB 181 AGATGGAGGTGAGGAGATCTAATTAATCTCTTAAATCATGCTAGGAAAGATACACCT 240
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DB 361 AAGTGAAGAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
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DB 421 CTGAGGCGAGAGAGAGCTGAGTTCGAGGCTTGAAGAGAGAGAGAGAGAGAGAGAG 480
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DB 541 CCGAGCTACTTGGAGGCTAAGGTGGGAGGATCGCTTGAAGAGAGAGAGAGAGAGAGAG 600
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DB 601 CTGAGGCTGATTGGATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
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DB 721 GAGGGGGGAG 780
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DB 901 CCGGAGCTGCTGCTTAAAG 960

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Qy 1081 GATTAACAGGCGCCGCCACACATCTGGCTAAATTTTGTGATTTTATTAATTAATTAAT 1140
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Db 1321 GATTCAGAAATTCCTTGGCTGGCTCCGACATGCTGAGCTGAGCTTGGC 1380
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Db 1861 TGGTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
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Db 2161 TCT 2220
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Db 2881 CGGCAAAACCCC 2893

RESULT 20
US-09-984-827-155
; Sequence 155, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEPIE, PATRICE
; APPLICANT: ROSTER, MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOLD-RECUIGNE, ISABELLE
; APPLICANT: DUMERGUE, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,


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DB 2401 GGGAGATTGAGCTTAGGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
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QY 2521 GCTTGGCGGAGCTGAGAGTCTGCGGCGGAGCTGCGGCGGAGCTGCGGCGGAGCTGCGG 2580
DB 2521 GCTTGGCGGAGCTGAGAGTCTGCGGCGGAGCTGCGGCGGAGCTGCGGCGGAGCTGCGG 2580
QY 2581 GCGTCTTAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2640
DB 2581 GCGTCTTAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2640
QY 2641 CTTGCTGTACCTTCCACCCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700
DB 2641 CTTGCTGTACCTTCCACCCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700
QY 2701 TGTGTTGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 2760
DB 2701 TGTGTTGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 2760
QY 2761 TGAATGAGTGAATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
DB 2761 TGAATGAGTGAATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
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DB 2821 GCTTTGAGGAGTGAATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
QY 2881 GGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2940
DB 2881 GGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2940
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RESULT 2:

us-09-846-456-3.oli30.rnpb

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; Sequence 157, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEPIE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806-0522-00000
; CURRENT APPLICATION NUMBER: US/09/984.827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 157
; LENGTH: 2893
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-827-157
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Query Match 98.2%; Score 2842; DB 9; Length 2893;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 ACAGGGCATGCTGGCAGGTGCTGTAATCTCAGTTACTCGGAGGTGGAGTTGCAATGA 60
QY 61 GCCAGATCGCACCATTCAGCTCCAGCTGGGCAACAAAGGTGAATCTCCATCTCAAT 120
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QY 181 AGATCGAGGTCAGGAGATGCTAATCTCTCTAAATCATGCTAGGAAAGATACACCT 240
DB 181 AGATCGAGGTCAGGAGATGCTAATCTCTCTAAATCATGCTAGGAAAGATACACCT 240
QY 241 TTTAATAACATCTCTGCTTTTATACATCATTTTGCAGAGAGCTCAAGGTTTCAACA 300
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QY 301 AAGTTTCACTTTTTCAGAAACCCCTTTGAGAGAGAGAGATATACATCTCTCCATTTA 360
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QY 361 AAGATGAAGAAACAGCGCGGCGCAATGGCTAATGCCCTGTAAATCCAGCAGCTTTGGAGG 420
DB 361 AAGATGAAGAAACAGCGCGGCGCAATGGCTAATGCCCTGTAAATCCAGCAGCTTTGGAGG 420
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DB 421 CTGAGGCCAGAGATCGCTTGGCTCCAGAGTTTTCAGACAGCCTGGGATACATCGGCAAA 480
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QY 1621 AAATGTGAATCTGCCCTTCAAGGTGGCTACAAAGGTATCTTTCTCAAGTAAAGACCTT 1680
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QY 1681 GTGGCTCCACGTCCAGCTTCAGGGCCIGCTTGGCCCTCTCTTACGGGTCTGTCCTCAGT 1740
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QY 1801 GGGCAGAAATAGGTGACATTTAGTTGGCTTTAAGATGACATTAATATTAAC- 1859
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QY 1860 -ATGGTGTAGGCTGCATCTCTACTCTTGGCTTTCTTTTGGCCCTGAGTCTTTGG 1918
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QY 1919 GTAGTTTGTCCCTTACAGCAAGGCAACAGAGAGAGTGGAGGTCTGAGTGGCTAC 1978
Db 1921 GTAGTTTGTCCCTTACAGCAAGGCAACAGAGAGAGTGGAGGTCTGAGTGGCTAC 1980
QY 1979 ATAATTATACAGACTCAATCTCTGGCTGCACCTTCACAAATGATACAACTAAATAC 2038
Db 1981 ATAATTATACAGACTCAATCTCTGGCTGCACCTTCACAAATGATACAACTAAATAC 2040
QY 2039 AAGTCTGTGTTTTATCAGAGGAGGCTGATCAATATAAIGAAATAAAGGGGCTG 2098
Db 2041 AAGTCTGTGTTTTATCAGAGGAGGCTGATCAATATAAIGAAATAAAGGGGCTG 2100
QY 2099 TCAATATTGTTCTGTTTTGTTTGTGTTTCTGTTTCTGTTTCTGTTTCTGTTG 2158
Db 2101 TCAATATTGTTCTGTTTTGTTTGTGTTTCTGTTTCTGTTTCTGTTTCTGTTG 2160
QY 2159 GGTCTTCTCTCAATTTATGAGAGAGAGTAAAGTGTCTGTTGAGGAGTCTGTTG 2218
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Db 2641 CACCTGTCTACCTCTCCACCCGCCACCCAGCAGCTCTCTCTCTCTCTCTCTCTCTCTCT 2700
QY 2699 TGTCTGGCGGCTGAACGTGGCGGCTTTAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 2758

Db 2701 TGTCTGGCGGCTGAACGTGGCGGCTTTAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 2760
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Db 2761 GCTGAGTGAATCACTACATAAAGAGAGCGCGGAGGAGGCGGGGAGGAGGAGGAGC 2820
QY 2819 AGGCTTTGACCATATAGTAACTCTGCGTGGTGGAGGCGGATCTATATAAGGAACTAGT 2878
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QY 2879 CCGGCAAAAGCC 2893
Db 2881 CCGGCAAAAGCC 2895
RESULT 23
US-09-846-827-156
; Sequence 156, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFE, PAIRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES,
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984.827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
; LENGTH: 2888
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-846-827-156
Query Match 92.3%, Score 2670, DB 9, Length 2888;
Best Local Similarity 100.0%, Pred. No. 0;
Matches 2670; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGGCGATGTCGAGGAGTGGCTGTAATCTCAGTTACTCGGAGGTGGAGTTGCAATGA 60
Db 1 ACAGGCGATGTCGAGGAGTGGCTGTAATCTCAGTTACTCGGAGGTGGAGTTGCAATGA 60
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Db 181 AGATGAGGAGTCAAGGAGATCTAATTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
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Db 241 TTTAATAACACATCT 300
QY 301 AAGTTTCACTTTTCAAGAAACCCCTTTGAGGAGAGAGATATACATCTCTCTCTCTCTCT 360
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QY 361 AAGATGAAGAAACACACCCCGGGGACCAATGGCTTAATGCCCTGTATCCAGCACTTTGGAGG 420
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DB 1621 AAATGTGAATCGCCCTTCAAGGTGCTACAAAGGTATCTTTGTCAAGGTAAGAGCTCT 1680
QY 1681 GTGGGCTCGACGTGACCTTCCAGGCGCTGCTTGGGCGCTGCTTCTAGGGCTCTTCTAGG 1740
DB 1681 GTGGGCTCGACGTGACCTTCCAGGCGCTGCTTGGGCGCTGCTTCTAGGGCTCTTCTAGG 1740
QY 1741 GTTCTATGAATCGCTTCAAGGCGATTCATATTTAGACCTCTTCAAGGTTTCAATGAGCTT 1800
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QY 1801 TGGGCGAATAAGGTGACATTTAGTCTTGGCTGTAGGATGATTAATTAATTAAGACA 1860
DB 1801 TGGGCGAATAAGGTGACATTTAGTCTTGGCTGTAGGATGATTAATTAATTAAGACA 1860
QY 1861 TGGTGTGAGGCTCGATTCCTACTCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 1920
DB 1861 TGGTGTGAGGCTCGATTCCTACTCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 1920
QY 1921 AGTTTGTCTGCTTACAGGCGAAGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
DB 1921 AGTTTGTCTGCTTACAGGCGAAGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
QY 1981 AATTTACAGGCTGCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
DB 1981 AATTTACAGGCTGCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
QY 2041 GTCCTGTGTTTATCAGGCGAGGCTGATCAATTAATTAATTAATTAATTAATTAATTAAT 2100
DB 2041 GTCCTGTGTTTATCAGGCGAGGCTGATCAATTAATTAATTAATTAATTAATTAATTAAT 2100
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DB 2101 CATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
QY 2161 TCTTCTCTCAATTTATGAGAGAGCAGTAAAGTCTTCTGCGGTCTGCTGAGGGA 2220
DB 2161 TCTTCTCTCAATTTATGAGAGAGCAGTAAAGTCTTCTGCGGTCTGCTGAGGGA 2220
QY 2221 CTTGGGAGCTCAGGCTGGAATCTCGAAGGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
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DB 2281 CAGGTTTGTGGGGGAAACAAAGGAGGCTATTAATTAATTAATTAATTAATTAATTAATTA 2340
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DB 2341 CAGGTTTGTGGGGGAAACAAAGGAGGCTATTAATTAATTAATTAATTAATTAATTAATTA 2400
QY 2401 GAGGATTCAGGCTAGAGCTCTCTCTGCGGCAATTCCTGCTGCTGCTGCTGCTGCTGCTG 2460
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QY 2761 TGAAGTCACTGAACTACATAAAGAGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGG 2820
DB 2757 TGAAGTCACTGAACTACATAAAGAGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGG 2816
QY 2821 GCTTTGACGATAGTAAAGCTCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 2880
DB 2817 GCTTTGACGATAGTAAAGCTCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 2876
QY 2881 CGGCAAAAACGCC 2893
DB 2877 CGGCAAAAACGCC 2889
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US-09-984-827-151
; Sequence 151, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, PATRICE
; APPLICANT: KOSIER-MONTIUS, MARIE-FRANCOISE
; APPLICANT: ARNOLD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBLEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABC1 GENE, THEIR USES,
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.9522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 151
; LENGTH: 2884
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-827-151
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Query Match 78.9%; Score 2284; DB 9; Length 2884;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2884; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

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DB 1 ACAGGCGATGCTGGGAGAGTGGCTGTAATCTCAGTTACTCGGAGGTGGAGGTTCGAATGA 60
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DB 61 GCCAGATCGACCATTTGGCTCCAGCTCCAGCTGGGCAACAAAGGTGAAACTCCATCTCAATT 120
QY 121 AAAAAAAGAAAGTGAATTTGGTGGTGGCTCAATAGTAGGAGAGAGAGAGAGG 180
DB 121 AAAAAAAGAAAGTGAATTTGGTGGTGGCTCAATAGTAGGAGAGAGAGAGAGG 180
QY 181 AGATGGAGGCTCAGGAGATCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
DB 181 AGATGGAGGCTCAGGAGATCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
QY 241 TTTAATAACACTCTCTGCTTTTATAACATCAATTTCTCCAGGAGCTCAAAAGGTTCACACA 300
DB 241 TTTAATAACACTCTCTGCTTTTATAACATCAATTTCTCCAGGAGCTCAAAAGGTTCACACA 300
QY 301 AAGTTCACTTTAGAAAAAGGCTTTGAGGAGAGACAAATACATCTTCTCTCCATTTTA 360
DB 301 AAGTTCACTTTAGAAAAAGGCTTTGAGGAGAGACAAATACATCTTCTCTCCATTTTA 360
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QY	481	ACCTGTCTCTACAAAAAATAACAAAAATATAGATGGGTGTGCTGGCATGTACTGTGGT	540
DB	481	ACCTGTCTCTACAAAAAATAACAAAAATATAGATGGGTGTGCTGGCATGTACTGTGGT	540
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QY	601	CTGAGCCATGATGGATCACTGCATCCAGCGCTGGTAGACAGACCAAGCTGTGTCTCA	660
DB	601	CTGAGCCATGATGGATCACTGCATCCAGCGCTGGTAGACAGACCAAGCTGTGTCTCA	660
QY	661	AAAAAAGAAATGAAGACAAACAAAGAAAGGAGAGGACAGGAGATGAGCGGAGGAGG	720
DB	661	AAAAAAGAAATGAAGACAAACAAAGAAAGGAGAGGACAGGAGATGAGCGGAGGAGG	720
QY	721	GAGGGGGGAGGAGGAGGAAGGAAGGAAGAAAGAAAGATGAATAAAGAAAAACAA	780
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QY	901	CTGGGCGCTTGGGCTTTAGAAAGCTCATCTCTGGGCTTCTGATGATCAATTTTCTTT	960
DB	901	CTGGGCGCTTGGGCTTTAGAAAGCTCATCTCTGGGCTTCTGATGATCAATTTTCTTT	960
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DB	961	TTATTTTCTTGACAGCGAGCTCTGCTCTGTCACATCAATGAGAGTGTAGTATGATCTC	1020
QY	1021	TGAGCTCACTGTAACTCTCGCTCCCGGCTTAAGGAGATCTCTGGCTGAGCTCTCTGA	1080
DB	1021	TGAGCTCACTGTAACTCTCGCTCCCGGCTTAAGGAGATCTCTGGCTGAGCTCTCTGA	1080
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DB	1081	GATAACAGGCGCGCGCCACACATCTGGCTAATTTTGTATTTTAAATAAATGCTGGT	1140
QY	1141	TCATCATGTTGGCCAGGTTGGTTTGAAGTCTGATCTGAAGTGAATGCTATGCTTGGC	1200
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QY	1381	TCTATGCGTCTGCTCGTAGTGTGTATGAACCACTGATGTCAGTATGCTGAGCTTGAAGC	1440
DB	1381	TCTATGCGTCTGCTCGTAGTGTGTATGAACCACTGATGTCAGTATGCTGAGCTTGAAGC	1440
QY	1441	GTGCGCTGGAGATTCCTCTTCACTGTAGCATGGAGGGGCTTGTGACAGTGAATTTGA	1500

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QY 1611 ICAGAGCTTAATGTGAATCTGCCCTTCAGGTGGCTACAAAGGTATCTTCTCAAGGT 1670
Db 1621 TGAAGAGCTTAATGTGAATCTGCCCTTCAGGTGGCTACAAAGGTATCTTCTCAAGGT 1680
QY 1671 AGAGAGCTTGTGGCTCCAGCTGCAGCTTCAGAGCTGCTTGGGCTCTTCTACGGCTC 1730
Db 1681 AGAGAGCTTGTGGCTCCAGCTGCAGCTTCAGAGCTGCTTGGGCTCTTCTACGGCTC 1740
QY 1731 TGTCTGAGTCTTATGAATCTCTCAGGSCAGATTCATATTTAGAGCTCTACAGCTTG 1790
Db 1741 TGTCTGAGTCTTATGAATCTCTCAGGSCAGATTCATATTTAGAGCTCTACAGCTTG 1800
QY 1791 ACCTGAGTTTGGCCAGATTAAGGTGACATTTAGTCTTGTGGCTTGAAGAGTACATAA 1850
Db 1801 ACCTGAGTTTGGCCAGATTAAGGTGACATTTAGTCTTGTGGCTTGAAGAGTACATAA 1860
QY 1851 TATTAGACATGGTGTAGGCTGCATCTCTAGCTCTGCTTTTCTTTTCTGGCTCCAG 1910
Db 1861 TATTAGACATGGTGTAGGCTGCATCTCTAGCTCTGCTTTTCTTTTCTGGCTCCAG 1920
QY 1911 TGTTTTGGGTAGTTTCTCCCTACAGCCAAAGGCAAGTACAGAACTTCAGCTGTGA 1970
Db 1921 TGTTTTGGGTAGTTTCTCCCTACAGCCAAAGGCAAGTACAGAACTTCAGCTGTGA 1980
QY 1971 GTGGCTACATAATTTACAGACTGCAATTCIGGCTGCACTTCACAAATGATACAAA 2030
Db 1981 GTGGCTACATAATTTACAGACTGCAATTCIGGCTGCACTTCACAAATGATACAAA 2040
QY 2031 CTAAATACAACTCTGTTTATACAGAGAGTCTATCAATATATATGAATATTAAG 2090
Db 2041 CTAAATACAACTCTGTTTATACAGAGAGTCTATCAATATATATGAATATTAAG 2100
QY 2091 GGAGCTGTCCATATGCTGTGTTTCTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 2150
Db 2101 GGAGCTGTCCATATGCTGTGTTTCTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 2160
QY 2151 TTTGTGCTCTCTCTCTCTCAATTTATGAAGAGAGTAAAGTCTGCTGGGCT 2210
Db 2161 TTTGTGCTCTCTCTCTCTCAATTTATGAAGAGAGTAAAGTCTGCTGGGCT 2220
QY 2211 CTCTGAGGAGCTGGGAGCTCAGGCTGGGAATCTCAAGSCAGTAGGTGCTATCAAA 2270
Db 2221 CTCTGAGGAGCTGGGAGCTCAGGCTGGGAATCTCAAGSCAGTAGGTGCTATCAAA 2280
QY 2271 AATCAAGTCCAGGTTTGTGGGGGAAACAAAGAGAGCTATACCCAGAGCTGCTC 2330
Db 2281 AATCAAGTCCAGGTTTGTGGGGGAAACAAAGAGAGCTATACCCAGAGCTGCTC 2340
QY 2331 GCTTCTCCCTCAGCCCTAGGCTTGAAGAGAAACAAAGAGAGTAAATGATTT 2390
Db 2341 GCTTCTCCCTCAGCCCTAGGCTTGAAGAGAAACAAAGAGAGTAAATGATTT 2400
QY 2391 GGCGTCTCTGAGGAGATTCAGCTAGAGCTCTCTCTGCTCCCAATCTGCTGCTGCTG 2450
```

```
Db 2401 GCGTCTCTGAGGAGATTCAGCTAGAGCTCTCTCTCCCAATCCCTCCCTCGGCTGA 2460
QY 2451 GGAAGAACTAACAAAGAAAAAAATTCGGAAGCAGAGATTAGAGGAAGCAAAATTCAC 2510
Db 2461 GGAAGAACTAACAAAGAAAAAAATTCGGAAGCAGAGATTAGAGGAAGCAAAATTCAC 2520
QY 2511 TGGTGGCTTGGCTCCCGGAGCTGAGTCTAGAGTCTGCGGCGAGCCCGAGCCAG 2570
Db 2521 TGGTGGCTTGGCTCCCGGAGCTGAGTCTAGAGTCTGCGGCGAGCCCGAGCCAG 2580
QY 2571 CCTTCCCGGCTGCTTAGCGCGGCGCGGCGGGAAGGGAGCGAGACCGCGGA 2630
Db 2581 CCTTCCCGGCTGCTTAGCGCGGCGCGGCGGGAAGGGAGCGAGACCGCGGA 2640
QY 2631 CCTAAGACACCTGCTGTAACCTCCACCCCAACCCCAACCCCAACCTCCCAACTC 2690
Db 2641 CCTAAGACACCTGCTGTAACCTCCACCCCAACCCCAACCCCAACCTCCCAACTC 2700
QY 2691 CCTAGATGTGCTGGGCGGTGAACGTGCGCCGTTTAAAGGGGGGGCGGCTCCAG 2750
Db 2701 CCTAGATGTGCTGGGCGGTGAACGTGCGCCGTTTAAAGGGGGGGCGGCTCCAG 2760
QY 2751 TGTCTTCTGCTGAGTGAACATACATAACAGAGCGCGGAAGGGGGGGGAGGAGG 2810
Db 2761 TGTCTTCTGCTGAGTGAACATACATAACAGAGCGCGGAAGGGGGGGGAGGAGG 2820
QY 2811 GAGAGCAGAGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCGAGCCGAATCTATAAAG 2870
Db 2821 GAGAGCAGAGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCGAGCCGAATCTATAAAG 2880
QY 2871 GAACCTAGTCTCCGCAAAACCC 2893
Db 2881 GAACCTAGTCTCCGCAAAACCC 2903

RESULT 27
US-09-770-689A-3
; Sequence 3, Application US/09770689A
; Patent No. US20020115171A1
; GENERAL INFORMATION:
; APPLICANT: VAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO01079
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 98865
; TYPE: DNA
; ORGANISM: HUMAN
US-09-770-689A-3

Query Match 1.9% Score 54; DB 10; Length 98865;
Best Local Similarity 100.0%; Pred. No. 2.le-17;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1187 CTGCCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGGCC 1240
Db 5881 CTGCCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGGCC 5934
```

```
RESULT 28
US-10-125-540-545/c
; Sequence 545, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: kosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214C1
```


; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 545
; LENGTH: 5451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-125-540-545

Query Match 1.8%; Score 52; DB 9; Length 5451;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1193 ACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 1244
|||||
DB 989 ACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 938

RESULT 24
US-09-764-870-545/c
; Sequence 545, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 545
; LENGTH: 5351
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-870-545

Query Match 1.8%; Score 52; DB 10; Length 5351;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1193 ACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 1244
|||||
DB 989 ACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 938

RESULT 30
US-10-125-540-546/c
; Sequence 546, Application US/10125546
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 546
; LENGTH: 6461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-125-540-546

Query Match 1.8%; Score 52; DB 9; Length 6461;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1193 ACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 1244
|||||

DB 4277 ACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 4226
RESULT 31
US-09-764-870-546/c
; Sequence 546, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 546
; LENGTH: 6461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-870-546

Query Match 1.8%; Score 52; DB 10; Length 6461;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1193 ACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 1244
|||||
DB 4277 ACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 4226

RESULT 32
US-09-764-891-5924
; Sequence 5924, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5924
; LENGTH: 10901
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-5924

Query Match 1.8%; Score 52; DB 9; Length 10901;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1189 GCCACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCC 1240
|||||
DB 3932 GCCACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCC 3983

RESULT 33
US-10-224-562-3/c
; Sequence 3, Application US/10224562
; Publication No. US2003002229A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: C1001098DIV
; CURRENT APPLICATION NUMBER: US/10/224,562
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3
LENGTH: 53332
TYPE: DNA
ORGANISM: Homo sapiens
US-10-224-562-3

Query Match 1.8%; Score 52; DB 9; Length 5332;
Best Local Similarity 100.0%; Pred. No. 2,3e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1190 CCACCTTGGCTCCCAAGTGTGGGATTACAGGCAATGACCTGGGCT 1241
|||||
DB 46511 CCACCTTGGCTCCCAAGTGTGGGATTACAGGCAATGACCTGGGCT 46460

RESULT 34
US-09-801-861-3/C
Sequence 3; Application US/09801861
Patent No. US20020119544A1
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001098
CURRENT APPLICATION NUMBER: US/09/801,861
PRIOR FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 53332
TYPE: DNA
ORGANISM: Human
US-09-801-861-3

Query Match 1.8%; Score 52; DB 10; Length 5332;
Best Local Similarity 100.0%; Pred. No. 2,3e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1190 CCACCTTGGCTCCCAAGTGTGGGATTACAGGCAATGACCTGGGCT 1241
|||||
DB 46511 CCACCTTGGCTCCCAAGTGTGGGATTACAGGCAATGACCTGGGCT 46460

RESULT 35
US-09-764-891-6418/C
Sequence 6418; Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
PRIOR FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6418
LENGTH: 17904
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-6418

Query Match 1.8%; Score 51; DB 9; Length 17904;
Best Local Similarity 100.0%; Pred. No. 7,1e-16;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1190 CCACCTTGGCTCCCAAGTGTGGGATTACAGGCAATGACCTGGGCT 1240
|||||
DB 4415 CCACCTTGGCTCCCAAGTGTGGGATTACAGGCAATGACCTGGGCT 4265

RESULT 36

US-09-764-877-2678/C
Sequence 2678; Application US/09764877
Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
PRIOR FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2678
LENGTH: 26591
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-877-2678

Query Match 1.8%; Score 51; DB 10; Length 26591;
Best Local Similarity 100.0%; Pred. No. 7,3e-16;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTGTGGGATTACAGGCAATGACCTGGGCT 1237
|||||
DB 11281 CTGCCACCTTGGCTCCCAAGTGTGGGATTACAGGCAATGACCTGGGCT 11231

RESULT 37
US-09-563-728A-36
Sequence 36; Application US/09563728A
Publication No. US20030078216A1
GENERAL INFORMATION:
APPLICANT: MacLeod, Alan R
APPLICANT: Li, Zoumei
TITLE OF INVENTION: Inhibition of Histone Deacetylase
FILE REFERENCE: 106101,229
CURRENT APPLICATION NUMBER: US/09/563,728A
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/132,287
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 36
LENGTH: 122186
TYPE: DNA
ORGANISM: Homo sapiens
US-09-563-728A-36

Query Match 1.8%; Score 51; DB 9; Length 122186;
Best Local Similarity 100.0%; Pred. No. 7,9e-16;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CTTGGCTCCCAAGTGTGGGATTACAGGCAATGACCTGGGCTGGCCAGC 1244
|||||
DB 65150 CTTGGCTCCCAAGTGTGGGATTACAGGCAATGACCTGGGCTGGCCAGC 65200

RESULT 38
US-09-880-107-3814
Sequence 3814; Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, David T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Iwe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14

;; PRIOR APPLICATION NUMBER: US 60/237,054
;; PRIOR FILING DATE: 2000-10-02
;; NUMBER OF SEQ ID NOS: 3950
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 3814
;; LENGTH: 198285
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: Genbank Accession No. US20020142581A1 X87344
US-09-880-167-3814

Query Match 1.7% Score 51; DB 10; Length 198285;
Best Local Similarity 100.0%; Pred. No. 8,1e-16;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1190 CCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGACCCACTGCGG 1240
|||||
DB 3571 CCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGACCCACTGCGG 1621

RESULT 39

US-10-091-504-1779
;; Sequence 1779, Application US/10091504
;; Publication No. US20030059908A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PC00701
;; CURRENT APPLICATION NUMBER: US/10/091,504
;; CURRENT FILING DATE: 2002-03-07
;; NUMBER OF SEQ ID NOS: 2442
;; Prior Application removed - See File Wrapper or PAF
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1779
;; LENGTH: 5819
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-091-504-1779

Query Match 1.7% Score 50; DB 9; Length 5819;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1192 CACCTTGGCTCCCAAGTCTGGGATTACAGGCATGACCCACTGCGG 1241
|||||
DB 3669 CACCTTGGCTCCCAAGTCTGGGATTACAGGCATGACCCACTGCGG 1618

RESULT 40

US-09-764-891-9890
;; Sequence 1779, Application US/09764891
;; Publication No. US20030077808A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PC007
;; CURRENT APPLICATION NUMBER: US/09/764,891
;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - refer to PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 2442
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1779
;; LENGTH: 5819
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-764-891-9890

Query Match 1.7% Score 50; DB 10; Length 1621;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1192 CACCTTGGCTCCCAAGTCTGGGATTACAGGCATGACCCACTGCGG 1241

|||||
DB 3669 CACCTTGGCTCCCAAGTCTGGGATTACAGGCATGACCCACTGCGGC 3718
RESULT 41
US-09-764-891-9890
;; Sequence 9890, Application US/09764891
;; Publication No. US20030077808A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PC006
;; CURRENT APPLICATION NUMBER: US/09/764,891
;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 10231
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 9890
;; LENGTH: 11618
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-764-891-9890

Query Match 1.7% Score 50; DB 9; Length 11618;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGACCCACTG 1236
|||||
DB 8181 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGACCCACTG 8243

RESULT 42

US-09-764-891-9810
;; Sequence 7810, Application US/09764891
;; Publication No. US20030077808A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PC006
;; CURRENT APPLICATION NUMBER: US/09/764,891
;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 10231
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 7810
;; LENGTH: 14216
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-764-891-9810

Query Match 1.7% Score 50; DB 9; Length 13216;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGACCCACTG 1236
|||||
DB 12177 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGACCCACTG 12245

RESULT 43

US-09-764-891-9967
;; Sequence 9967, Application US/09764891
;; Publication No. US20030077808A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PC006
;; CURRENT APPLICATION NUMBER: US/09/764,891
;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 10241
;; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 9967
LENGTH: 19929
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-9967

Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1013 AACCTCTGCTCCCGGTTCAAGCGATTCCTGGCTGGCTGACGCTCTGAGA 1082
|||||
DB 6669 AACCTCTGCTCCCGGTTCAAGCGATTCCTGGCTGGCTGACGCTCTGAGA 4716

RESULT 44

US-09-764-891-9966
; Sequence 9966, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9966
; LENGTH: 20907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (44777)
; OTHER INFORMATION: n equals a.t.g. or c
; NAME/KEY: SITE
; LOCATION: (4480)
; OTHER INFORMATION: n equals a.t.g. or c
; NAME/KEY: SITE
; LOCATION: (4483)
; OTHER INFORMATION: n equals a.t.g. or c
US-09-764-891-9966

Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1013 AACCTCTGCTCCCGGTTCAAGCGATTCCTGGCTGGCTGACGCTCTGAGA 1082
|||||
DB 5667 AACCTCTGCTCCCGGTTCAAGCGATTCCTGGCTGGCTGACGCTCTGAGA 4716

RESULT 45

US-09-764-891-8807/c
; Sequence 8807, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8807
; LENGTH: 21936
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8807

Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTG 1236
|||||
DB 4160 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTG 4111

RESULT 46

US-09-764-891-9446
; Sequence 9446, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9446
; LENGTH: 21936
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-9446

Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTG 1236
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DB 17777 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTG 17826

RESULT 47

US-09-764-891-7809
; Sequence 7809, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7809
; LENGTH: 29163
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7809

Query Match
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Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 12174 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTG 12223

RESULT 48

US-10-067-514-1/c
; Sequence 1, Application US/10067514
; Publication No. US20030054531A1
; GENERAL INFORMATION:
; APPLICANT: Grelarsdotter, Solveig
; APPLICANT: Jonsdotter, Sit
; APPLICANT: Reynoldsdotter, Sigridur Th.
; TITLE OF INVENTION: HUMAN STROKE GENE

FILE REFERENCE: 2345.2010-003
CURRENT APPLICATION NUMBER: US/10/067.514
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: US/09/811/352
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1691139
TYPE: DNA
ORGANISM: Human
US-10-067-514-1

Query Match: 1.7%; Score 50; DB 9; Length 1691139;
Best Local Similarity 100.0%; Pred. No. 6e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 644059 GGCTCCCAAGTCTGGGATTACAGGATGAGTACTGGCGCACTCA 644059

RESULT 49

US-09-918-995-2616/c
Sequence 2616, Application US/99/18995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/245,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2616
LENGTH: 448
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1)...(448)
OTHER INFORMATION: n = A,T,C or G
US 09 918 995 2616

Query Match: 1.7%; Score 49; DB 9; Length 448;
Best Local Similarity 100.0%; Pred. No. 6.5e-15;
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DB 426 AACCTCGCTCCCGGTTCAAGCGATTCTCTGGCTCAAGCTCTGAG 426

RESULT 50

US-09-729 835-11/c
Sequence 11, Application US/09/729835
Patent No. US20010016647A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 29 Human Secreted Proteins
FILE REFERENCE: P2015P1
CURRENT APPLICATION NUMBER: US/09/729,835
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 09/257,179
PRIOR FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: 60/056,270
PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 60/056,271
PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 60/056,247

PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 60/056,073
PRIOR FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 866
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (22)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (37)
OTHER INFORMATION: n equals a,t,g, or c
US-09-729-835-11

Query Match: 1.7%; Score 49; DB 10; Length 866;
Best Local Similarity 100.0%; Pred. No. 6.7e-15;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 772 AACCTCGCTCCCGGTTCAAGCGATTCTCTGGCTCAAGCTCTGAG 724

Search completed: May 10, 2003, 02:58:19
Job time : 3143.16 Secs

GenCore version 5.1.5
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OM nucleotide - nucleotide search, using sw model

Run on: May 9, 2003, 13:08:16 : Search time 582.623 seconds
(without alignments)
9544.109 Million cell updates/sec

Title: US-09-846-456-3

Perfect score: 2893

Sequence: 1 acaggcatggtggcaggtg.....ctatcccccgaagaaacccc 2893

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

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Total number of hits satisfying chosen parameters: 14094

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	814	28.1	183999	22	AAF92831	Human ABC1 genomic
4	541	18.7	1643	22	AAF24681	Nucleotide sequence
5	541	18.7	1643	22	AAF24703	Nucleotide sequence
6	420	14.5	1197	24	ABL58400	Human large ATP-bi
7	55	1.9	2890	24	ABK34575	Human cDNA for nov
8	55	1.9	13646	24	AAS20126	Human gene for ret
9	55	1.9	13646	24	AAS20128	Human gene for re

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Hereditary haemoch	1.9	237326	19	AAV57903
Human cancer relat	1.8	475	24	ABN65629
Human ribosomal S1	1.8	1316	22	AAI64613
Human DNA for a no	1.8	5351	22	AAS31466
Human polynucleoti	1.8	5351	24	ABQ66790
Human DNA for a no	1.8	6461	22	AAS31467
Human polynucleoti	1.8	6461	24	ABQ66791
Human immune/haema	1.8	8319	22	AAK65197
Human reproductive	1.8	10901	22	AAI03236
Human nervous syst	1.8	29329	22	ABA18026
Human immune/haema	1.8	29329	22	ABA20511
Human immune/haema	1.8	29329	22	AAK70791
Human immune/haema	1.8	29329	22	AAK78512
Human secreted pro	1.8	149	21	AAC25949
Human prostate exp	1.8	358	23	ABV03782
Human prostate exp	1.8	359	23	ABV13951
Human prostate exp	1.8	366	23	ABV13744
Human prostate exp	1.8	381	23	ABV04575
Human prostate exp	1.8	396	22	AAI81653
Human polynucleoti	1.8	406	23	ABV34857
Human prostate exp	1.8	412	23	ABV34073
Human prostate exp	1.8	412	23	ABV42939
Human polynucleoti	1.8	425	22	AAI87958
Human prostate exp	1.8	438	23	ABV43803
Human prostate exp	1.8	446	23	ABV04619
Human prostate exp	1.8	459	23	ABV02959
Human prostate exp	1.8	512	23	ABV34901
Human prostate exp	1.8	515	23	ABV33273
Human prostate exp	1.8	515	23	ABV43707
Human prostate exp	1.8	521	23	ABV32646
Human prostate exp	1.8	521	23	ABV41571
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Human prostate exp	1.8	521	23	ABV43750
Human prostate exp	1.8	670	23	ABV21487
Human prostate exp	1.8	670	23	ABV21910
Human prostate exp	1.8	670	23	ABV22485
Human prostate exp	1.8	670	23	ABV22952
Human prostate exp	1.8	670	23	ABV27305
Human prostate exp	1.8	670	23	ABV27742
Human prostate exp	1.8	670	23	ABV28300
Human prostate exp	1.8	670	23	ABV28752
Human prostate exp	1.8	670	23	ABV28784
Human prostate exp	1.8	756	23	ABV12128
Human prostate exp	1.8	759	23	ABV11501
Human prostate exp	1.8	788	23	ABV02332
Human prostate exp	1.8	803	23	ABV13788
Human immune/haema	1.8	1856	22	AAK77921
Human polypeptide-	1.8	2046	22	AAI64545
Human immune/haema	1.8	7759	22	AAK77916
Human ovarian and	1.8	17904	22	ABA07913
Human reproductive	1.8	17904	22	AAI03730
Human musculoskele	1.8	26591	22	AAI36313
Human DNA for a no	1.8	32186	22	AAS34422
Human thiorodoxin	1.8	66566	22	AAAS3450
Human histone deac	1.8	122186	22	AAAC89560
Retinoblastoma bin	1.8	162450	21	AAZ86967
Human cDNA differe	1.8	198285	24	ABK84699
Gene #3817 used to	1.8	198285	24	ABN97319
Human polynucleoti	1.7	320	22	AAI91676
Human gene signatu	1.7	327	16	AAAT26600
Novel human polynu	1.7	377	22	AAAF67515
Human prostate exp	1.7	452	23	AAAF57113
Human inflammatory	1.7	700	22	AAH92172
Human transcrip	1.7	1989	24	ABK47950
Chromosome 13q31-q	1.7	3001	21	AAH51743
Human cardiovascular	1.7	5819	22	AAAS36279
Human nervous syst	1.7	8774	22	ABA21246
Human reproductive	1.7	11618	22	AAI07202
Human immune/haema	1.7	11618	22	AAK87088
DNA encoding human	1.7	11618	22	AAK33447
Human reproductive	1.7	13216	22	AAI05122
Human testicular a	1.7	13216	23	ABL98014

83	50	1.7	19929	22	AAL07279	Human reproductive	c 156	49	1.7	31718	22	AAK87442	Human immune/haema
84	50	1.7	19929	23	ABL98825	Human testicular a	c 157	49	1.7	31718	22	AAK87443	Human immune/haema
85	50	1.7	20907	22	AAL07278	Human reproductive	c 158	49	1.7	31718	22	AAK87573	Human immune/haema
86	50	1.7	20907	23	ABL98824	Human testicular a	c 159	49	1.7	31718	22	AAK87592	Human immune/haema
87	50	1.7	21936	22	ABAI5865	Human nervous syst	c 160	49	1.7	31718	22	AAK90359	Human digestive sy
88	50	1.7	21936	22	AAL06115	Human reproductive	c 161	49	1.7	31718	22	AAK90360	Human digestive sy
89	50	1.7	21936	22	AAL06758	Human reproductive	c 162	49	1.7	32190	22	AAK36709	Human cardiovascular
90	50	1.7	21936	22	AAL06264	Human breast, ov	c 163	49	1.7	36159	24	ABN55329	Human kinase gene
91	50	1.7	21936	23	ABL98864	Human testicular a	c 164	49	1.7	46785	22	AAK22208	Human immune/haema
92	50	1.7	21936	23	ABL98867	Human immune/haema	c 165	49	1.7	43069	21	AAK216335	Genomic sequence
93	50	1.7	23815	22	AAK85678	Human immune/haema	c 166	49	1.7	44147	24	ABK84481	Human CDNA differe
94	50	1.7	23815	22	AAK85679	Human immune/haema	c 167	49	1.7	49436	24	AAK89533	Human corneal N-ac
95	50	1.7	29163	22	AAL05121	Human reproductive	c 168	49	1.7	56743	22	AAK68202	Human immune/haema
96	50	1.7	29163	23	ABL98811	Human testicular a	c 169	49	1.7	56743	22	AAK81760	Human immune/haema
97	50	1.7	33513	22	AAK78746	Human immune/haema	c 170	49	1.7	128600	24	ABK83461	Human CDNA differe
98	50	1.7	40267	24	AAK18458	Human cadherin-like	c 171	49	1.7	139389	24	ABK84795	Human CDNA differe
99	50	1.7	162450	21	AAK28697	Human fibroblast bin	c 172	49	1.7	139389	24	ABK84795	Human CDNA differe
100	49	1.7	217	22	AAK76272	Human immune/haema	c 173	49	1.7	160552	22	AAD02697	Human glycosyl sul
101	49	1.7	366	22	AAK93046	Human polynucleoti	c 174	49	1.7	167343	24	ABL64403	Stomach cancer rel
102	49	1.7	393	23	ABV19916	Human prostate exp	c 175	49	1.7	167343	24	ABL67239	Thyroid cancer rel
103	49	1.7	423	21	AAC12571	Human secreted pro	c 176	48	1.7	98	22	AAK85113	Human immune/haema
104	49	1.7	538	24	ABN62419	Human cancer relat	c 177	48	1.7	126	22	AAK66842	Human immune/haema
105	49	1.7	748	22	AAH05601	Human CDNA clone (c 178	48	1.7	141	22	AAK83995	Human immune/haema
106	49	1.7	761	22	AAK195179	Human neuroblastom	c 179	48	1.7	234	24	AAK169091	Activated T-cell d
107	49	1.7	851	21	AAK81129	Human secreted pro	c 180	48	1.7	270	22	AAK73295	Human immune/haema
108	49	1.7	866	20	AAK10145	Human secreted pro	c 181	48	1.7	311	23	AAK41813	CDNA encoding nove
109	49	1.7	1127	22	AAH44727	Human isopentenyl	c 182	48	1.7	378	22	AAK182255	Human polynucleoti
110	49	1.7	2266	22	AAK89548	Human digestive sy	c 183	48	1.7	398	24	ABL83417	Human ovarian canc
111	49	1.7	2315	22	AAH15989	Human CDNA sequenc	c 184	48	1.7	453	22	AAK63500	Human immune/haema
112	49	1.7	2539	22	AAL07149	Human reproductive	c 185	48	1.7	505	24	ABN62093	Human cancer relat
113	49	1.7	3139	22	AAK71190	Human immune/haema	c 186	48	1.7	513	24	ABN63664	Human cancer relat
114	49	1.7	4096	22	AAK163976	Human polynucleoti	c 187	48	1.7	604	24	ABN64817	Human cancer relat
115	49	1.7	4140	22	AAK37255	Human musculoskele	c 188	48	1.7	651	24	ABQ59878	Human colon cancer
116	49	1.7	4602	22	AAK72562	Human immune/haema	c 189	48	1.7	651	24	ABN61582	Human cancer relat
117	49	1.7	4694	22	AAK76970	Human immune/haema	c 190	48	1.7	861	20	AAK222252	Human secreted pro
118	49	1.7	4694	22	AAK85342	Human immune/haema	c 191	48	1.7	980	22	AAK37188	Human musculoskele
119	49	1.7	5076	22	ABAI6694	Human nervous syst	c 192	48	1.7	987	22	AAK85117	Human immune/haema
120	49	1.7	5335	22	AAK69240	Human immune/haema	c 193	48	1.7	988	22	AAK35434	Human musculoskele
121	49	1.7	5742	22	AAK85943	Human immune/haema	c 194	48	1.7	1020	21	AAK49558	Partial DNA sequen
122	49	1.7	5997	22	AAK42580	Human genomic DNA	c 195	48	1.7	1022	22	AAK66790	Human immune/haema
123	49	1.7	6093	22	AAK42581	Human avian-like DNA	c 196	48	1.7	1209	22	AAK82755	Human immune/haema
124	49	1.7	6435	22	ABAI5651	Human nervous syst	c 197	48	1.7	1387	22	AAK87436	Human immune/haema
125	49	1.7	7233	22	AAK36623	Human cardiovascular	c 198	48	1.7	1387	22	AAK87438	Human immune/haema
126	49	1.7	7398	22	AAL07145	Human reproductive	c 199	48	1.7	1668	22	AAK94501	Human toll length
127	49	1.7	7507	22	AAK87178	Human immune/haema	c 200	48	1.7	1696	22	AAK85286	Human immune/haema
128	49	1.7	8658	22	AAK87179	Human immune/haema	c 201	48	1.7	1733	23	AAK42476	Genomic sequence
129	49	1.7	10117	22	AAK87179	Human immune/haema	c 202	48	1.7	2280	22	AAH14649	Human CDNA sequenc
130	49	1.7	11319	22	AAK49642	Genomic sequence	c 203	48	1.7	2291	24	AAL47087	Human regulatory p
131	49	1.7	11319	22	AAK90025	Human digestive sy	c 204	48	1.7	3286	22	AAK85287	Human immune/haema
132	49	1.7	11987	23	AAL07284	Human reproductive	c 205	48	1.7	3417	22	AAH18467	Human CDNA sequenc
133	49	1.7	11987	23	ABL98840	Human testicular a	c 206	48	1.7	4678	22	ABAI6110	Human nervous syst
134	49	1.7	12574	22	AAK05318	Human reproductive	c 207	48	1.7	6306	24	ARA03923	Human NHP protein
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136	49	1.7	13996	22	AAK31523	Human DNA for a no	c 209	48	1.7	8448	22	AAK40680	DNA encoding human
137	49	1.7	13996	22	ABQ66847	Human polynucleoti	c 210	48	1.7	8448	22	AAK06568	Human reproductive
138	49	1.7	14001	22	AAK31522	Human DNA for a no	c 211	48	1.7	9566	22	AAK40682	DNA encoding hu
139	49	1.7	14001	24	ABQ66846	Human polynucleoti	c 212	48	1.7	9566	22	AAL06570	Human reproductive
140	49	1.7	14175	22	AAK27814	DNA encoding novel	c 213	48	1.7	9593	22	ABA20507	Human nervous syst
141	49	1.7	14175	22	AAK78859	Human immune/haema	c 214	48	1.7	10055	22	AAK75286	Human immune/haema
142	49	1.7	14403	22	AAL07146	Human reproductive	c 215	48	1.7	10503	22	ABA05768	Human genomic DNA
143	49	1.7	16891	20	AAK37084	MEV gene sequence	c 216	48	1.7	10503	22	AAK28598	Genomic sequence
144	49	1.7	18860	22	AAK35952	Human musculoskele	c 217	48	1.7	10503	22	AAI63970	Human polynucleoti
145	49	1.7	21234	24	AAK42039	Human kinase prote	c 218	48	1.7	10503	22	AAK31500	Human DNA for a no
146	49	1.7	22927	22	AAL04782	Human reproductive	c 219	48	1.7	10503	22	AAK35054	DNA for a no
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149	49	1.7	24268	22	AAK67462	Human immune/haema	c 222	48	1.7	11231	22	AAK89691	Human digestive sy
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151	49	1.7	31718	22	AAK39515	Genomic sequence	c 224	48	1.7	14221	22	AAK40681	DNA encoding human
152	49	1.7	31718	22	AAK39516	Genomic sequence	c 225	48	1.7	14221	22	AAL06569	Human reproductive
153	49	1.7	31718	22	AAL06415	Human reproductive	c 226	48	1.7	14784	21	AAA64141	Nucleotide sequenc
154	49	1.7	31718	22	AAL06416	Human reproductive	c 227	48	1.7	17185	22	AAH16049	Human nervous syst
155	49	1.7	31718	22	AAK74104	Human immune/haema	c 228	48	1.7	17185	22	AAK75628	Human immune/haema

375	47	1.6	1503900	22	AAK95240	Human neuroendocrine	c 448	46	1.6	5947	22	AAK86768	Human immune/haema
376	47	1.6	1503900	22	AAK96733	Human neuroendocrine	c 449	46	1.6	6319	24	ABK97631	Human prostate spe
377	46	1.6	132	22	AAI83143	Human polynucleotide	c 450	46	1.6	7417	22	AAK70374	Human immune/haema
378	46	1.6	150	21	AAI12976	Human secreted pro	c 451	46	1.6	7742	22	AAK72501	Human immune/haema
379	45	1.6	150	22	AAI05408	Human secreted pro	c 452	46	1.6	7754	22	AAK72498	Human immune/haema
380	45	1.6	258	22	AAK57746	Human immune/haema	c 453	46	1.6	8047	22	AAK81256	Human immune/haema
381	46	1.6	262	22	AAK89113	Human digestive sy	c 454	46	1.6	8047	22	AAK86767	Human immune/haema
382	46	1.6	262	22	AAK31863	Human liver associ	c 455	46	1.6	8577	22	ABAI17047	Human nervous syst
383	46	1.6	262	24	AAK90218	Human liver outlq	c 456	46	1.6	8577	22	AAI06167	Human nervous syst
384	46	1.6	307	22	AAK87671	Human immune/haema	c 457	46	1.6	8577	23	ABI198712	Human testicular a
385	46	1.6	315	21	AAK29578	Human secreted pro	c 458	46	1.6	9039	22	AAK75933	Human immune/haema
386	46	1.6	341	24	ABL84368	Human ovarian can	c 459	46	1.6	9039	22	AAK85246	Human immune/haema
387	46	1.6	394	22	AAI82243	Human polynucleot	c 460	46	1.6	10202	22	AAK86002	Human immune/haema
388	46	1.6	394	24	ABL84358	Human ovarian can	c 461	46	1.6	10587	22	AAK82482	Human immune/haema
389	46	1.6	400	24	ABL61718	Human adenocarcino	c 462	46	1.6	10867	22	AAI37605	Human musculoskele
390	46	1.6	400	24	ABL62279	Human adenocarcino	c 463	46	1.6	10867	22	AAK36613	Human cardiovascu
391	46	1.6	418	22	AAK59421	cDNA encoding nove	c 464	46	1.6	10867	22	AAK66345	Human immune/haema
392	46	1.6	418	22	AAK88273	Human digestive sy	c 465	46	1.6	10894	22	AAK36611	Human cardiovascu
393	46	1.6	418	22	AAK88273	Human prostate exp	c 466	46	1.6	10894	22	AAK66343	Human immune/haema
394	46	1.6	460	24	ABT04066	Human ovary speci	c 467	46	1.6	10907	22	AAI37603	Human musculoskele
395	46	1.6	473	22	AAK359765	Genomic sequence #	c 468	46	1.6	10907	22	AAK36612	Human cardiovascu
396	46	1.6	473	22	AAK90118	Human digestive sy	c 469	46	1.6	10907	22	AAK66344	Human immune/haema
397	46	1.6	505	24	ABN64662	Human cancer relat	c 470	46	1.6	11870	22	AAI07328	Human reproductive
398	46	1.6	518	22	AAK56887	Human immune/haema	c 471	46	1.6	11870	22	AAI07329	Human reproductive
399	46	1.6	520	24	ABO56470	Human colon cancer	c 472	46	1.6	11870	22	AAK82242	Human immune/haema
400	46	1.6	531	22	AAK71044	Human immune/haema	c 473	46	1.6	11870	22	AAK82243	Human immune/haema
401	46	1.6	531	22	AAK71045	Human immune/haema	c 474	46	1.6	11870	22	AAK84792	Human immune/haema
402	46	1.6	531	22	AAH13269	Human cDNA clone (c 475	46	1.6	11870	22	AAK84793	Human immune/haema
403	46	1.6	535	22	AAH12272	Human cDNA clone (c 476	46	1.6	12555	23	AAK78331	Human immune/haema
404	46	1.6	543	24	ABN64981	Human cancer relat	c 477	46	1.6	12555	23	ABK42300	Genomic sequence #
405	46	1.6	552	22	AAK69055	Human immune/haema	c 478	46	1.6	12562	22	AAI36095	Human musculoskele
406	46	1.6	553	24	ABN63320	Human cancer relat	c 479	46	1.6	12562	22	AAK72631	Human immune/haema
407	46	1.6	581	22	AAH13463	Human cDNA clone (c 480	46	1.6	12718	22	AAI37607	Human musculoskele
408	46	1.6	620	24	ABN65477	Human cancer relat	c 481	46	1.6	12718	22	AAK66346	Human immune/haema
409	46	1.6	684	22	AAK90712	Human digestive sy	c 482	46	1.6	13002	22	AAK81377	Human immune/haema
410	46	1.6	695	22	AAI10188	Human breast cancer	c 483	46	1.6	16489	22	AAK27823	DNA encoding novel
411	46	1.6	731	22	AAI19768	Human breast cancer	c 484	46	1.6	16552	22	AAK91416	Human digestive sy
412	46	1.6	762	22	AAI195961	Human neuroblastom	c 485	46	1.6	16552	22	AAK91417	Human digestive sy
413	46	1.6	850	24	ABO89526	Human prostate exp	c 486	46	1.6	16552	22	AAI57784	Human colorectal c
414	46	1.6	903	22	ABAU8242	Human secreted pro	c 487	46	1.6	16552	22	AAI57785	Human colorectal c
415	46	1.6	912	22	AAK68828	Human immune/haema	c 488	46	1.6	17821	22	AAK66003	Human immune/haema
416	46	1.6	917	22	AAK68826	Human immune/haema	c 489	46	1.6	20892	22	ABAI15709	Human nervous syst
417	46	1.6	966	22	AAI88604	Human polynucleot	c 490	46	1.6	27733	22	ABAI19324	Human nervous syst
418	46	1.6	1121	22	AAK82524	Human immune/haema	c 491	46	1.6	29222	24	ABI39412	Human electron-tra
419	46	1.6	1124	22	AAK82525	Human immune/haema	c 492	46	1.6	32189	22	AAI04670	Human reproductive
420	46	1.6	1127	22	AAK82521	Human immune/haema	c 493	46	1.6	42189	23	ABU97577	Human testicular a
421	46	1.6	1127	22	AAK82522	Human immune/haema	c 494	46	1.6	42221	22	AAK39766	Human testicular a
422	46	1.6	1157	22	AAK78477	Human immune/haema	c 495	46	1.6	42221	22	AAK90119	Human digestive sy
423	46	1.6	1205	24	AAK81823	DNA secreted pro	c 496	46	1.6	45414	21	AAAD00147	TR12 related DNA-1
424	46	1.6	1389	21	AAK26374	Human secreted pro	c 497	46	1.6	46221	22	AAK00624	Human death-associ
425	46	1.6	1450	22	AAK82521	Human immune/haema	c 498	46	1.6	39801	24	AAK83462	Human cDNA differe
426	46	1.6	1733	21	AAK59421	Human secreted pro	c 499	46	1.6	51474	22	AAK97846	Human neuroblastom
427	46	1.6	1954	22	AAH18403	Human cDNA sequence	c 500	46	1.6	99014	24	ABN96931	Gene #3429 used to
428	46	1.6	1957	22	AAH14756	Human cDNA sequence	c 501	46	1.6	110096	24	ABN5044	Gene #1542 used to
429	46	1.6	2251	22	AAH17556	Human cDNA sequence	c 502	46	1.6	138169	21	AAA34791	Human adenosine re
430	46	1.6	2756	22	ABAO6812	Human genomic DNA	c 503	46	1.6	141589	21	AAK20913	Human ELAM-1 polyn
431	46	1.6	2756	22	AAK17552	Genomic sequence #	c 504	46	1.6	141589	21	AAK21127	Human low adenosin
432	46	1.6	2835	22	AAH14665	Human cDNA sequence	c 505	46	1.6	141589	21	AAK21152	Human low adenosin
433	46	1.6	2844	22	AAK91523	Human digestive sy	c 506	46	1.6	141589	21	AAK35005	Human adenosine re
434	46	1.6	2844	22	AAK32177	Human liver associ	c 507	46	1.6	141589	21	AAK35030	Human adenosine re
435	46	1.6	2844	24	ABN90532	Human liver outlq	c 508	46	1.6	145831	24	ABI82309	Human adenosine re
436	46	1.6	2844	24	ABU34326	Human zinc finger	c 509	46	1.6	145831	24	ABL86806	Colon adenocarcino
437	46	1.6	2876	22	AAK69707	Human immune/haema	c 510	46	1.6	145831	24	ABL86806	Lung cancer relate
438	46	1.6	3116	22	AAK39688	Genomic sequence #	c 511	46	1.6	145831	24	ABL69213	Kidney cancer rela
439	46	1.6	3116	22	AAK90041	Human digestive sy	c 512	46	1.6	145831	24	ABL69213	Prostate cancer re
440	46	1.6	3185	22	AAH57528	Human pancreas cel	c 513	46	1.6	145831	21	AAK21442	Human ELAM-1 polyn
441	46	1.6	3512	23	ABK43087	Genomic sequence #	c 514	46	1.6	147708	24	ABQ88154	Human osteoblast d
442	46	1.6	3753	22	AAI04946	Human reproductive	c 515	46	1.6	201143	24	ABK83568	Human DNA differe
443	46	1.6	3753	23	AAH197840	Human testicular a	c 516	46	1.6	209273	21	AAK21437	Human factor-relat
444	46	1.6	3917	22	AAH18646	Human cDNA sequence	c 517	46	1.6	224930	24	ABK84349	Human cDNA differe
445	46	1.6	4412	22	AAH57372	Human heart cells	c 518	46	1.6	101	22	AAI36545	Human musculoskele
446	46	1.6	4727	22	AAK65762	Human immune/haema	c 519	46	1.6	116	22	AAK82023	Human immune/haema
447	46	1.6	5032	22	AAK90709	Human digestive sy	c 520	46	1.6	116	22	AAI35886	Human reproductive

c 521	1.6	118	23	ABL98449	Human testicular a	594	45	1.6	1701	20	AAV83945	Bacterial artificial
c 522	1.6	118	23	ABL98450	Human testicular a	595	45	1.6	1837	24	ABA94430	Human Pp1345 prote
c 523	1.6	122	22	ABA16055	Human testicular a	596	45	1.6	1926	24	ABK69884	Human secreted pro
c 524	1.6	137	22	AAI04408	Human reproductive	c 597	45	1.6	2121	24	ABA96972	DNA encoding novel
c 525	1.6	138	22	AAK76081	Human immune/haema	c 598	45	1.6	2173	23	AAK72272	Human L-3-phospho
c 526	1.6	153	17	AAI31589	Probe (BLUR) for	c 599	45	1.6	2566	22	AAH17845	Human cDNA sequenc
c 527	1.6	156	22	AAK76634	Human immune/haema	c 600	45	1.6	2579	22	AAH15692	Human cDNA sequenc
c 528	1.6	166	21	AAK22006	Human secreted pro	c 601	45	1.6	2585	21	AAK64476	Prostate tumour as
c 529	1.6	168	22	AAI06104	Human reproductive	c 602	45	1.6	2648	24	AAK35108	Human cDNA encodin
c 530	1.6	168	23	ABL98669	Human testicular a	603	45	1.6	2716	23	ABV22030	Human prostate exp
c 531	1.6	193	21	AAI16209	Human secreted pro	604	45	1.6	2716	23	ABV25415	Human prostate exp
c 532	1.6	228	22	AAK76633	Human immune/haema	605	45	1.6	2716	23	ABV27864	Human prostate exp
c 533	1.6	234	22	AAK80238	Human immune/haema	606	45	1.6	2797	22	AAH18187	Human cDNA sequenc
c 534	1.6	234	22	AAK80241	Human immune/haema	607	45	1.6	2843	22	AAK32907	Human genomic DNA
c 535	1.6	264	22	AAI62911	Human immune/haema	c 608	45	1.6	2863	22	AAK07837	Human secreted pro
c 536	1.6	273	22	AAK03866	Human nervous syst	609	45	1.6	2903	24	ABA93808	Human zcytor17 CDN
c 537	1.6	282	21	AAK30399	Human secreted pro	c 610	45	1.6	2958	22	AAK81424	Human immune/haema
c 538	1.6	288	22	AAK55522	Human immune/haema	c 611	45	1.6	3011	22	AAK41928	Genomic sequence #
c 539	1.6	295	22	AAK82995	Human immune/haema	c 612	45	1.6	3011	22	AAK35102	DNA #52 encoding h
c 540	1.6	298	21	AAK12082	Human secreted pro	c 613	45	1.6	3091	22	AAK28567	Genomic sequence #
c 541	1.6	298	22	AAK73170	Human immune/haema	c 614	45	1.6	3091	22	AAK28568	Genomic sequence #
c 542	1.6	320	22	AAI85946	Human polynucleoti	c 615	45	1.6	3486	22	AAK52890	Human polynucleoti
c 543	1.6	361	21	AAK45315	Human secreted exp	c 616	45	1.6	3516	22	AAK85421	Human immune/haema
c 544	1.6	372	23	AAV49560	Human prostate exp	c 617	45	1.6	3563	22	AAK14352	Human manganese su
c 545	1.6	414	23	ABV12901	Human prostate exp	618	45	1.6	3783	22	AAK71130	Human immune/haema
c 546	1.6	415	22	AAI84196	Human polynucleoti	619	45	1.6	3788	22	AAK71131	Human immune/haema
c 547	1.6	425	22	AAI89685	Human polynucleoti	620	45	1.6	3844	22	AAK80274	Nucleotide sequenc
c 548	1.6	428	22	AAI85512	Human polynucleoti	621	45	1.6	4079	22	AAK82384	Human immune/haema
c 549	1.6	433	23	ABV04732	Human prostate exp	c 622	45	1.6	4502	22	AAK72445	Human immune/haema
c 550	1.6	438	21	AAK23431	Human secreted pro	c 623	45	1.6	5071	22	AAK74516	Human immune/haema
c 551	1.6	443	22	AAI00868	Human reproductive	c 624	45	1.6	5071	22	ABK69831	Human secreted pro
c 552	1.6	443	23	ABV59216	Human prostate exp	c 625	45	1.6	5072	22	AAK74517	Human immune/haema
c 553	1.6	448	23	AAK87410	DNA encoding novel	c 626	45	1.6	5072	24	ABK69833	Human secreted pro
c 554	1.6	449	22	AAK72847	Human immune/haema	c 627	45	1.6	5318	22	AAK55961	Human eukaryotic p
c 555	1.6	458	23	ABV50873	Human prostate exp	c 628	45	1.6	5581	18	AAI48737	Human leucocyte sp
c 556	1.6	480	23	ABV43027	Human prostate exp	c 629	45	1.6	5581	18	AAI45451	Human LST-1 (leuko
c 557	1.6	480	23	ABV42894	Human prostate exp	c 630	45	1.6	5834	22	AAK40617	DNA encoding human
c 558	1.6	524	23	ABV19795	Human prostate exp	c 631	45	1.6	5834	22	AAK08505	Human reproductive
c 559	1.6	536	24	ABN61361	Human cancer relat	c 632	45	1.6	5834	22	AAK28542	Genomic sequence #
c 560	1.6	542	24	AAH63113	Human cancer relat	c 633	45	1.6	6117	22	AAK68756	Human immune/haema
c 561	1.6	566	22	AAH10559	Human cDNA clone (c 634	45	1.6	6139	19	AAV70354	Coding strand of n
c 562	1.6	574	22	AAI45913	Human musculoskele	c 635	45	1.6	6165	22	AAK75603	Human immune/haema
c 563	1.6	574	22	AAI45914	Human musculoskele	c 636	45	1.6	6191	23	ABK42222	Genomic sequence #
c 564	1.6	600	23	ABV53773	Human prostate exp	c 637	45	1.6	6194	23	ABK42223	Genomic sequence #
c 565	1.6	607	24	ABQ89177	Human prostate exp	638	45	1.6	6455	22	ABA17328	Human nervous syst
c 566	1.6	610	22	AAK77666	Human immune/haema	c 639	45	1.6	6455	22	AAK34621	Human DNA for a no
c 567	1.6	612	22	AAK77665	Human immune/haema	c 640	45	1.6	6411	16	AAQ95493	Human cDNA-2 DNA
c 568	1.6	618	22	ABA18304	Human nervous syst	c 641	45	1.6	6782	22	AAK67165	Human immune/haema
c 569	1.6	666	24	ABT04097	Human ovary speci	c 642	45	1.6	7573	22	AAI199080	Human excretory re
c 570	1.6	695	21	AAK81681	N. meningitidis pa	c 643	45	1.6	7573	22	AAI63430	Human kidney relat
c 571	1.6	700	22	AAH92573	Human inflammatory	c 644	45	1.6	7983	22	AAK73139	Human immune/haema
c 572	1.6	700	22	AAH92574	Human inflammatory	c 645	45	1.6	8217	22	AAI07164	Human reproductive
c 573	1.6	709	22	AAK24907	Human breast cancer	c 646	45	1.6	8396	21	AAZ59353	Human SRP2 (phenol
c 574	1.6	739	22	AAK37463	Human musculoskele	c 647	45	1.6	8663	22	AAK30133	Human lung antigen
c 575	1.6	742	22	AAK72035	Human immune/haema	c 648	45	1.6	8841	24	ABK84005	Human cDNA differe
c 576	1.6	767	22	AAI36809	Human musculoskele	c 649	45	1.6	8841	24	ABL64081	Breast cancer rela
c 577	1.6	798	22	AAK71964	Human immune/haema	c 650	45	1.6	8918	22	AAK26708	Human genomic DNA
c 578	1.6	868	22	AAH94388	Human fetal cDNA	c 651	45	1.6	8919	22	AAK26709	Human genomic DNA
c 579	1.6	891	20	AAZ40838	Secreted protein E	c 652	45	1.6	9469	22	AAK79514	Human immune/haema
c 580	1.6	963	22	AAI04364	Human reproductive	c 653	45	1.6	9475	22	AAK72443	Human immune/haema
c 581	1.6	963	22	AAI04365	Human reproductive	c 654	45	1.6	9507	22	AAK07097	Human reproductive
c 582	1.6	1040	20	AAK79016	Human secreted pro	c 655	45	1.6	10093	22	AAK07184	Human pancreatic c
c 583	1.6	1089	22	AAK07902	Human secreted pro	656	45	1.6	10093	22	AAK35890	Human cardiovascular
c 584	1.6	1383	21	ABI90401	Human polynucleoti	657	45	1.6	10093	22	AAK89816	Human digestive sy
c 585	1.6	1395	24	AAZ64955	Methyane-bound pro	c 658	45	1.6	10420	22	ABA16598	Human nervous syst
c 586	1.6	1395	22	AAK92062	Human PR874 cDNA	c 659	45	1.6	10885	22	AAI37478	Human musculoskele
c 587	1.6	1395	22	AAK44103	Human PR874 (JN04	c 660	45	1.6	12163	22	ABA14697	Human nervous syst
c 588	1.6	1424	20	AAK89611	Human secreted pro	661	45	1.6	12221	22	AAK71585	Human immune/haema
c 589	1.6	1424	22	AAK55242	Human cDNA encodin	c 662	45	1.6	12500	22	AAK77971	Human immune/haema
c 590	1.6	1424	24	ABA90911	Human polynucleoti	663	45	1.6	12665	22	AAK71602	Human immune/haema
c 591	1.6	1513	21	AAH18303	Human nervous syst	664	45	1.6	12667	22	AAK71604	Human immune/haema
c 592	1.6	1538	22	AAK93347	Human secreted pro	c 665	45	1.6	13058	22	AAK29194	Genomic sequence #
c 593	1.6	1560	21	AAK79746	Human secreted pro	666	45	1.6	13058	22	AAK79325	Human immune/haema

667	45	1.6	13255	22	AAK76942	Human immune/haema	c 740	45	1.6	122186	22	AAK89560	Human histone deac
668	45	1.6	13670	24	AAI42369	Human Guanine nuc	c 741	45	1.6	122888	24	ABK83569	Human cDNA differe
669	45	1.6	15061	22	AAI04226	Human reproductive	c 742	45	1.6	129722	24	ABK88117	Human cDNA differe
670	45	1.6	15061	23	AAK42104	Genomic sequence #	c 743	45	1.6	165199	24	ABK83460	Stomach cancer rel
671	45	1.6	15651	22	AAK81510	Human immune/haema	744	45	1.6	167343	24	ABL64403	Thyroid cancer rel
672	45	1.6	15714	22	AAK36855	Human cardiovascular	745	45	1.6	167343	24	ABL67239	Human cDNA differe
673	45	1.6	15870	22	AAI16129	Human nervous syst	746	45	1.6	227968	24	ABK3497	Human silent SNP c
674	45	1.6	16299	22	AAK71100	Human immune/haema	747	45	1.5	51	22	AAI75194	Human musculoskele
675	45	1.6	17397	22	AAK36445	Human cardiovascular	c 748	44	1.5	130	22	AAI36471	Human immune/haema
676	45	1.6	17462	22	AAK15655	Human nervous syst	749	44	1.5	144	22	AAK81169	Human reproductive
677	45	1.6	18678	22	AAK32889	Human genomic DNA	c 750	44	1.5	175	22	AAI07200	Human reproductive
678	45	1.6	18678	22	AAK91271	Human digestive sy	c 751	44	1.5	175	22	AAK07201	Human immune/haema
679	45	1.6	18692	23	AAK42795	Genomic sequence #	c 752	44	1.5	193	22	AAK70913	Human immune/haema
680	45	1.6	19334	22	AAK36443	Human cardiovascular	753	44	1.5	215	21	AAK29849	Human secreted pro
681	45	1.6	19345	22	AAK36444	Human cardiovascular	754	44	1.5	312	24	ABN62536	Human cancer relat
682	45	1.6	19407	22	ABAI5979	Human nervous syst	c 755	44	1.5	343	22	AAI25254	Human breast cance
683	45	1.6	19407	22	AAK81438	Human immune/haema	c 756	44	1.5	348	22	AAI16411	Human breast cance
684	45	1.6	21410	22	AAK81290	Human immune/haema	c 757	44	1.5	355	22	AAI84801	Human polynucleoti
685	45	1.6	21596	22	AAK71382	Human immune/haema	758	44	1.5	383	22	AAI90781	Human polynucleoti
686	45	1.6	21724	22	AAK26629	Human genomic DNA	c 759	44	1.5	389	22	AAK64188	Human immune/haema
687	45	1.6	21724	22	AAK86125	Human immune/haema	c 760	44	1.5	389	22	AAK64283	Novel human polynu
688	45	1.6	21727	22	AAK26630	Human genomic DNA	761	44	1.5	395	22	AAI89981	Human polynucleoti
689	45	1.6	21727	22	AAK86126	Human immune/haema	c 762	44	1.5	399	22	AAI92488	Human polynucleoti
690	45	1.6	22161	23	ABK42133	Genomic sequence #	c 763	44	1.5	404	22	AAI85729	Human polynucleoti
691	45	1.6	22467	22	AAK33423	DNA encoding human	c 764	44	1.5	407	22	AAK69316	Human immune/haema
692	45	1.6	22467	22	AAK33425	DNA encoding human	c 765	44	1.5	422	22	AAK77117	Human immune/haema
693	45	1.6	22481	17	AAI11658	FEF full length s	c 766	44	1.5	425	22	AAK77116	Human immune/haema
694	45	1.6	22484	24	ABQ88196	Human osteoblast 3	767	44	1.5	425	24	ABN61884	Human cancer relat
695	45	1.6	22484	24	ABN96844	Gene #332 used to	c 768	44	1.5	435	22	AAK60183	Human immune/haema
696	45	1.6	22484	24	ABN96882	Nucleotide sequen	c 769	44	1.5	439	16	AAI22423	Human gene signatu
697	45	1.6	22484	24	AAK05882	Anticarcinosis inhib	c 770	44	1.5	462	22	AAK58777	Human immune/haema
698	45	1.6	23855	22	AAI19441	Human excretory re	771	44	1.5	469	22	AAI90079	Human polynucleoti
699	45	1.6	23855	22	AAI63761	Human kidney relat	c 772	44	1.5	506	22	AAK68883	Human immune/haema
700	45	1.6	24983	22	AAK63262	Human reproductive	c 773	44	1.5	522	22	AAK70396	Human immune/haema
701	45	1.6	24983	22	AAK63262	Human reproductive	c 774	44	1.5	522	22	AAK70398	Human immune/haema
702	45	1.6	24983	23	ABL98451	Human reproductive	c 775	44	1.5	522	22	AAK70399	Human immune/haema
703	45	1.6	26995	22	AAK29963	Human lung antigen	776	44	1.5	533	24	ABN63875	Human cancer relat
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705	45	1.6	28180	22	AAK68849	Human immune/haema	778	44	1.5	558	22	AAK68819	Human lung tumour
706	45	1.6	30175	24	AAK32742	Human immune/haema	779	44	1.5	558	24	ABK38530	cDNA encoding clon
707	45	1.6	30175	22	AAK68732	Human immune/haema	780	44	1.5	573	24	ABN58977	Human prostate exp
708	45	1.6	30515	22	AAK85029	Human immune/haema	c 781	44	1.5	576	24	ABN61222	Human cancer relat
709	45	1.6	30515	23	ABK42321	Genomic sequence #	782	44	1.5	583	22	AAH12473	Human cDNA clone (
710	45	1.6	30803	22	AAK68410	Human immune/haema	c 783	44	1.5	586	23	ABV51058	Human prostate exp
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712	45	1.6	30826	22	AAK32772	Human genomic DNA	785	44	1.5	671	22	AAK07935	Human cDNA clone (
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714	45	1.6	32176	22	AAK34535	Human cardiovascular	c 787	44	1.5	787	24	ABK89558	Human prostate exp
715	45	1.6	32178	22	AAK36454	Human cardiovascular	c 788	44	1.5	923	21	AAK02633	Human colon cancer
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717	45	1.6	32189	22	AAK40115	Human lung antigen	790	44	1.5	1066	24	AAK52527	cDNA sequence #314
718	45	1.6	32216	22	ABK07741	Human ovarian and	c 791	44	1.5	1094	20	AAK84442	Human secreted pro
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725	45	1.6	57296	22	AAK78170	Human immune/haema	798	44	1.5	1832	22	AAH18103	Human cDNA sequen
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729	45	1.6	65854	22	AAK86282	Human immune/haema	c 802	44	1.5	2056	24	ABK83487	Human cDNA differe
730	45	1.6	74037	24	ABK94412	DNA encoding endo	c 803	44	1.5	2177	22	AAH17283	Human cDNA sequen
731	45	1.6	74962	22	ABK15256	Human phosphatase	c 804	44	1.5	2269	22	ABK14782	Human nervous syst
732	45	1.6	75899	24	ABK45261	Human genomic DNA	805	44	1.5	2510	24	ABK35328	Human cDNA encodin
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737	45	1.6	92638	24	ABK08696	Human osteoblast 3	810	44	1.5	471	22	AAK67524	Human immune/haema
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813	44	1.5	3945	22	AAK83730	Human immune/haema	886	44	1.5	31168	22	AAK89940	Human digestive sy
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829	44	1.5	7703	22	AAH90904	Human digestive sy	902	44	1.5	37449	22	AAH66874	Human immune/haema
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832	44	1.5	10634	22	AAH05488	Human reproductive	905	44	1.5	50000	24	AAH98944	Human asthma-assoc
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835	44	1.5	11942	22	AAH15442	Human CHRNA2 gene	908	44	1.5	84539	24	AAH64158	Stomach cancer rel
836	44	1.5	12931	22	AAH80322	Human immune/haema	909	44	1.5	90220	24	AAH83576	Human cDNA differe
837	44	1.5	15266	22	AAH37432	Human musculoskele	910	44	1.5	103747	24	AAH88139	Human osteoblast d
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860	44	1.5	20966	21	AAH00352	Human APH1 (Adipos	933	44	1.5	309	23	AAH42588	Human reproductive
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862	44	1.5	20966	24	AAH96121	Human nucleic acid	935	44	1.5	324	22	AAH04247	Human reproductive
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864	44	1.5	21423	22	AAH36470	Human musculoskele	937	44	1.5	337	22	AAH76181	Human immune/haema
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866	44	1.5	23130	22	AAH77045	Human immune/haema	939	44	1.5	348	22	AAH88781	Human polynucleoti
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882	44	1.5	31168	22	AAH42115	Human pancreatic c	955	44	1.5	459	22	AAH17152	Human breast cance
883	44	1.5	31168	22	AAH42115	Human pancreatic c	956	44	1.5	471	22	AAH89210	Human polynucleoti
884	44	1.5	31168	22	AAH42115	Human pancreatic c	957	44	1.5	479	24	AAH62597	Human cancer relat
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Db 541 CCCAGCTACTTGGAGGCTAAGGTGGAGGATCGCTTGAGCCCGAGGAGTCAAGTCTACA 600
Qy 601 CTGAGCCATGATGGATCACTGCACTCCAGCCCTGGGTAGACAGCAAGTAAGACACCTGTCTCA 640
Db 601 CTGAGCCATGATGGATCACTGCACTCCAGCCCTGGGTAGACAGCAAGTAAGTGTCTCTCA 680
Qy 661 AAAAAAGAAATGAAGAGAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 AAAAAAGAAATGAAGAGAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 760
Qy 721 GAGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 721 GAGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 740
Qy 781 GATCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 781 GATCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 800
Qy 841 CCCCAAAACCAATTTATGACCAAGGTTATCTTGACCTCAGGTAAGGTAAGGTAAGGTAAG 900
Db 841 CCCCAAAACCAATTTATGACCAAGGTTATCTTGACCTCAGGTAAGGTAAGGTAAGGTAAG 920
Qy 901 CTTGGGCTTTGGGCTTTAGAAAGCTCATCTCTGGGCTTTCTGAGATCCATGCTCTCTCTT 960
Db 901 CTTGGGCTTTGGGCTTTAGAAAGCTCATCTCTGGGCTTTCTGAGATCCATGCTCTCTCTT 980
Qy 961 TTAATTTTCTTGACACGAGTCTGCTCTGCTACATGAGCTGAGCTGAGCTGAGCTGAGCTG 1020
Db 961 TTAATTTTCTTGACACGAGTCTGCTCTGCTACATGAGCTGAGCTGAGCTGAGCTGAGCTG 1040
Qy 1021 TCGACTCACTGTAACTCTGCTCCCGGTTCAAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1021 TCGACTCACTGTAACTCTGCTCCCGGTTCAAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1100
Qy 1081 GATAACAGGCGCGGCCACACATCTGCTTAATTTTGTATTTTGTATTTTGTATTTTGTATTTT 1140
Db 1081 GATAACAGGCGCGGCCACACATCTGCTTAATTTTGTATTTTGTATTTTGTATTTTGTATTTT 1160
Qy 1141 TCATCATGTTGGCCAGGTTGGTTGGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1141 TCATCATGTTGGCCAGGTTGGTTGGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1220
Qy 1201 CTGCAAGTCTGGGATTACAGGATCAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 1260
Db 1201 CTGCAAGTCTGGGATTACAGGATCAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 1280
Qy 1261 CTAGGCGCAACAGTCCATGGTCTAAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1320
Db 1261 CTAGGCGCAACAGTCCATGGTCTAAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1340
Qy 1321 GACTCTAGAAATTCCTTGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Db 1321 GACTCTAGAAATTCCTTGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1400
Qy 1381 TTCTATCGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
Db 1381 TTCTATCGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1460
Qy 1441 GTGGCTGGAGATCCTGTTGACTGTAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
Db 1441 GTGGCTGGAGATCCTGTTGACTGTAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1520
Qy 1501 TGCAGGTGGTGGGAGTTCTGGAATATGATGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
Db 1501 TGCAGGTGGTGGGAGTTCTGGAATATGATGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1580
Qy 1561 GGGCAGCTCTCTATGCCACTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
Db 1561 GGGCAGCTCTCTATGCCACTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1640
Qy 1621 AAATGTGAATCTGCCCTTCAAGGTGGTACAAAGATGATCTTCTGAGGAGGAGGAGGAGGAGGAG 1680
Db 1621 AAATGTGAATCTGCCCTTCAAGGTGGTACAAAGATGATCTTCTGAGGAGGAGGAGGAGGAGGAG 1700
Qy 1681 GTGGCTCCAGCTGCACTTCCAGGCGCTGCTTGGGCGCTTCTTACGGGCTCTGTCTGAGT 1740
Db 1681 GTGGCTCCAGCTGCACTTCCAGGCGCTGCTTGGGCGCTTCTTACGGGCTCTGTCTGAGT 1760
Qy 1741 CTTCTATGAATCTTCCAGGCGAGATTCATATTTAGACTCTTCCACAGTTTGGACCTGAGTTT 1800
Db 1741 CTTCTATGAATCTTCCAGGCGAGATTCATATTTAGACTCTTCCACAGTTTGGACCTGAGTTT 1820
Qy 1801 TGCCAGAAATGAAGTGAATTTAGTTTCTTGCTTGTATGATGATGATGATGATGATGATGATGAT 1860
Db 1801 TGCCAGAAATGAAGTGAATTTAGTTTCTTGCTTGTATGATGATGATGATGATGATGATGATGAT 1880
Qy 1861 TGCTGTGAGGCTGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1920
Db 1861 TGCTGTGAGGCTGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1940
Qy 1921 AGTTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1980
Db 1921 AGTTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2000
Qy 1981 AATTTTACAGACTGCAATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2040
Db 1981 AATTTTACAGACTGCAATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2060
Qy 2041 GTCTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2100
Db 2041 GTCTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2120
Qy 2101 CATATTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2160
Db 2101 CATATTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2180
Qy 2161 TCTT 2220
Db 2161 TCTT 2240
Qy 2221 CTTGGGAGCTCAGGCTGGGATCTCCAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 2280
Db 2221 CTTGGGAGCTCAGGCTGGGATCTCCAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 2300
Qy 2281 CAGGTTTGTGGGGGAGAAACAAACAGCCATTTACCCAGAGGAGTGTCCGCTTCCCTTCCCT 2340
Db 2281 CAGGTTTGTGGGGGAGAAACAAACAGCCATTTACCCAGAGGAGTGTCCGCTTCCCTTCCCT 2360
Qy 2341 CAGCCCAAGTCTAGGCTTGAAGGAGAAACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2400
Db 2341 CAGCCCAAGTCTAGGCTTGAAGGAGAAACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2420
Qy 2401 GAGGAGTCTAGGCTTGAAGGAGAAACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2460
Db 2401 GAGGAGTCTAGGCTTGAAGGAGAAACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2480
Qy 2461 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2520
Db 2461 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2540
Qy 2521 GCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2580
Db 2521 GCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2600
Qy 2581 GCTTCTTAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTTCCGCTT 2640
Db 2581 GCTTCTTAGGCTGAGGCTGAGGCTTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2660
Qy 2641 CTTGCTGTAGGCTTCAAGCTGAGGCTTAAAGGCGGCGGCTTCCAGGCTGCTTCTGCTGCTG 2700
Db 2641 CTTGCTGTAGGCTTCAAGCTGAGGCTTAAAGGCGGCGGCTTCCAGGCTGCTTCTGCTGCTG 2720
Qy 2701 TCGTGGGCTGAGGCTTAAAGCTGAGGCTTAAAGGCGGCGGCTTCCAGGCTGCTTCTGCTGCTG 2760
Db 2701 TCGTGGGCTGAGGCTTAAAGCTGAGGCTTAAAGGCGGCGGCTTCCAGGCTGCTTCTGCTGCTG

Db	1201	CTCCAAAGTGTGGGATTACAGGCAATGAGCCACTGGCCCACTAGATCTCATGCTT	1260
Qy	1261	CTAAGGGCAAAACAGTCCATGGTGTCAAAGGGGCCATGCAACCCAGACATATGAGTACATCTGG	1320
Db	1261	CTAAGGGCAAAACAGTCCATGGTGTCAAAGGGGCCATGCAACCAATATATGATATATCTGG	1320
Qy	1321	GACTTCGGAATTCCTTGCCCTGGTGGCCCTCCACATACATCTGTCAGAGGATCTGTTGGGCTTC	1380
Db	1321	GACTTCGGAATTCCTTGCCCTGGTGGCCCTCCACATACATCTGTCAGAGGATCTGTTGGGCTTC	1380
Qy	1381	TCTATGCGCTGTCTGCTCAGTGTGTGATAGACACACTGATCTGAGTACCTATGAGCTTCAGGCT	1440
Db	1381	TCTATGCGCTGTCTGAGTGTGTGATAGACACACTGATCTGAGTACCTATGAGCTTCAGGCTTC	1440
Qy	1441	GTGGCCCTGGAGATTCCTTGCTTGAGCTGTAGCATGATGAGTGGAGGAGCTTGTGAACTGAATGCTGCA	1500
Db	1441	GTGGCCCTGGAGATTCCTTGCTTGAGCTGTAGCATGATGAGTGGAGGAGCTTGTGAACTGAATGCTGCA	1500
Qy	1501	TGTCAGTGTGTGGAGTCTCTGGAAATGATGTCAGCTTGGAGGTGCTGAACAGAACTAGCTCTTG	1560
Db	1501	TGTCAGTGTGTGGAGTCTCTGGAAATGATGTCAGCTTGGAGGTGCTGAACAGAACTAGCTCTTG	1560
Qy	1561	GGCCAGCTCTCTCATGCCACCTCATCTCTGGCCAAACATCAGTCAAAATCTGTGAAGAGCTCT	1620
Db	1561	GGCCAGCTCTCTCATGCCACCTCATCTCTGGCCAAACATCAGTCAAACTGTGAAGAGCTCT	1620
Qy	1621	AAATGTCAATCTGCCCTTCCAGGTGGCTTACAAGGTATCTCTGTCAAGTATAGAGACCTT	1680
Db	1621	AAATGTCAATCTGCCCTTCCAGGTGGCTTACAAGGTATCTCTGTCAAGTATAGAGACCTT	1680
Qy	1681	GTGGCTCTCAGCTGGCACTTCCAGGCGCTGTCTGGCCCTCTCTCTACAGCTCTGCTTGAGT	1740
Db	1681	GTGGCTCTCAGCTGGCACTTCCAGGCGCTGTCTGGCCCTCTCTCTACAGCTCTGCTTGCTGACT	1740
Qy	1741	CTCTATGAAATCTTCAGGGCAGATTCATATTAGACCTCTCAAGTCTGAGCTGGAGTCTT	1800
Db	1741	CTCTATGAAATCTTCAGGGCAGATTCATATTAGACCTCTTCACAGTCTTCAGCTGAGCTT	1800
Qy	1801	TGGCTACAAATTAAGGTGACATTTAGTTGTGGCTTGATGGATGATTAATATTTACACA	1860
Db	1801	TGGCCACAATAAGGTGACATTTAGTTGTGGCTTGATGGATGACTTAATATTTACACA	1860
Qy	1861	TGGTGTATAGGCTGCAATCTCTACTCTTCCCTTTTCTTTCGCTCTCCAGTCTTCTGGCT	1920
Db	1861	TGGTGTATAGGCTGCAATCTCTACTCTTCCCTTTTCTTTCGCTCTCCAGTCTTCTGGCT	1920
Qy	1921	AGTTTGTCTCCCTACAGCTAAAGCCAACACAGAGTTTGAGTCTGTGACTCTGATACA	1980
Db	1921	AGTTTGTCTCCCTACAGCCAACACAGAGTTTGAGTCTGTGACTCTGATACA	1980
Qy	1981	AAATTTACAGTACGACTGCAATTTCTCTGGCTGCAATCTCAATAAATGATAATTAATACAA	2040
Db	1981	AAATTTACAGGACTGCAATTTCTCTGGCTGCAATCTCAAGAAATGATAATAAATAAATA	2040
Qy	2041	GTCTTGTCTTTTATCACAGGAGGCTGATCAATATATATGAAATTAAGAAATGAGCTCTG	2100
Db	2041	GTCTTGTCTTTTATCACAGGAGGCTGATCAATATATATGAAATTAAGAAATGAGCTCTGAGCT	2100
Qy	2101	CATATGTTCTGTGTTTTGTTTGTGTTTGTGTTGTTGTTTGTGTTTGTGTTTGTGTTGTTG	2160
Db	2101	CATATGTTCTGTGTTTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTGTTG	2160
Qy	2161	TGCTTCTCTCAATTTATGAGAGAGCAGTACGATGTTCTCTCTGGCTCTCTCTGAGGGA	2220
Db	2161	TGCTTCTCTCAATTTATGAGAGAGCAGTAAAGTCTCTCTCTGGCTCTCTCTGAGGGA	2220
Qy	2221	CTCTGGGAGCTCAGGCTGGGAATCTCTCCAGGAGTAGTCTGCTCTATCAAAATCAAAATC	2280
Db	2221	CTCTGGGAGCTCAGGCTGGGAATCTCTCCAGGAGTAGTCTGCTCTATCAAAATCAAAATC	2280
Qy	2281	CAGCTTTGTGGGGGAAAAACAAGACGCTTATTAATACAGAGGACTGTGCTGTATCTCT	2340

Db	2281	CAGGTTTGTGGGGGAAAAACAAGCAGCCCAATTACCCAGGAGACTGTCCGCCCTTCCCTT	2340
Qy	2341	CACCCAGCCCTAGCCCTTTTCAAGAGAAACAAAAGACAAGACAATAATGATTGGCGTCTCTGA	2400
Db	2341	CACCCAGCCCTAGCCCTTTTCAAGAGAAACAAAAGACAAGACAATAATGATTGGCGTCTCTGA	2400
Qy	2401	GGGAGATTCAGCCCTAGAGCTCTCTCTCTCCGCCAATCCCTCCCTCCGGCTGAGGAACCTAAC	2460
Db	2401	GGGAGATTCAGCTTAGAGCTCTCTCTCCGCCAATCCCTCCCTCCGGCTGAGGAACCTAAC	2460
Qy	2461	AAAGGAAAAAATAATTCGGCAAGCAGGATTTTAGAGGAAGCAAAATTCACATGGTCCCTTT	2520
Db	2461	AAAGGAAAAAATAATTCGGCAAGCAGGATTTTAGAGGAAGCAAAATTCACATGGTCCCTTT	2520
Qy	2521	GGCTGCCGGAAATGTGACTTAGAGATCTGCGCGCCAGCCCGAGCCCGAGCGTTCCCGC	2580
Db	2521	GGCTGCCGGAAATGTGACTTAGAGATCTGCGCGCCAGCCCGAGCCCGAGCGTTCCCGC	2580
Qy	2581	CGCTCTTAGCG	2640
Db	2581	CGCTCTTAGCG	2640
Qy	2641	CCTGCTTAGCGCTGACCG	2700
Db	2641	CCTGCTTAGCGCTGACCG	2700
Qy	2701	TCGTGGCGCGCTGAACCTTCGCGCTTAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	2760
Db	2701	TCGTGGCGCGCTGAACCTTCGCGCTTAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	2760
Qy	2761	TGAGTGACTGAACCTACATAACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	2820
Db	2761	TGAGTGACTGAACCTACATAACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	2820
Qy	2821	GCTTTGACCGATAGTAACCTTCGCGCTCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG	2880
Db	2821	GCTTTGACCGATAGTAACCTTCGCGCTCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG	2880
Qy	2881	CGGCAAAAGCGCC 2893	
Db	2881	CGGCAAAAGCGCC 2893	
RESULT 3			
Id	AAF92831	standard; DNA; 183999 bp.	
XX	AAF92831;		
XX	17-MAY-2001 (first entry)		
XX	Human ABC1 genomic DNA.		
KW	High density lipoprotein:cholesterol; HDL-C; cardiovascular; ABC1; ds.		
OS	Homo sapiens.		
XX	W0200115676-A2.		
XX	08-MAR-2001.		
XX	01-SEP-2000; 2000WO-1B01492.		
XX	01-SEP-1999; 99US-0151977.		
PR	15-MAR-2000; 2000US-0526193.		
PR	23-JUN-2000; 2000US-0213958.		
XX	(UYBR-) UNIV BRITISH COLUMBIA.		
PA	(XENO-) XENON GENETICS INC.		
P1	Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;		
DR	WPI; 2001-244358/25.		

haplotype pair for the RLBPL gene of an individual, a method for identifying an association between a trait and at least one haplotype or haplotype pair of the RLBPL gene, a composition comprising at least one genotyping oligonucleotide for detecting a polymorphism in the RLBPL gene at a PS consisting of PS1-PS24, a kit for genotyping the RLBPL gene of an individual comprising a set of oligonucleotides designed to genotype each of PS1-PS24 recombinant non-human organisms transformed or transfected with the isolated polynucleotide, where the organism expresses a RLBPL protein encoded by the first nucleotide sequence or expresses a RLBPL polypeptide comprising an amino acid sequence that is a polymorphic variant of a reference sequence for the RLBPL protein or its fragment, an anti-RLBPL antibody, a method for screening for drugs targeting the isolated polypeptide, and a computer system for storing and analysing polymorphism data for the RLBPL oncogene gene.

The polynucleotide comprising polymorphisms in the RLBPL gene is useful in studying the expression and function of RLBPL, and in expressing RLBPL protein for use in screening candidate drugs to treat diseases related to RLBPL activity (e.g. autosomal recessive retinitis pigmentosa (arRP)). The methods and haplotypes are useful in improving the efficiency and output of several steps in the drug discovery and development process, including target validation, identifying lead compounds, and early phase clinical trials. These are also useful for designing clinical trials of candidate drugs for treating a specific condition or disease, as well as for screening compounds targeting RLBPL to treat a specific condition or disease predicted to be associated with RLBPL activity. The kit and method are useful for determining whether an individual has one of the haplotypes or haplotype pairs cited above. The transgenic animals are useful for studying expression of the RLBPL isoforms *in vivo*, for *in vivo* screening and testing of drugs targeted against RLBPL protein, and for testing the efficacy of therapeutic agents and compounds for retinal diseases in a biological system. The gene for RLBPL is located on chromosome 15q26. The present sequence is a representation of the gene for RLBPL encompassing all the single nucleotide polymorphisms in the gene.

XX Sequence 13646 BP; 3373 A; 3254 C; 3459 G; 3525 T; 24 other;

Query Match 1.9%; Score 55; DB 24; Length 13646;
Best Local Similarity 100.0%; Pred. No. 8.3e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTTGGCTCCCAAGTCTGGGATTACAGCATGACCTGCGCCAGC 1244
|||||
Db 13646 CCCACCTTGGCTCCCAAGTCTGGGATTACAGCATGACCTGCGCCAGC 13646

RESULT 10

AAV57926
ID AAV57926 standard; DNA; 235033 BP.

XX AAV57926;

XX 23-DEC-1998 (first entry)

XX Hereditary haemochromatosis subregion from an unaffected individual.

XX Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;
KW diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3;
KW BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
KW type 1 sodium transport gene; ss.

XX Homo sapiens.

XX W09814466-A1.

XX 09-APR-1998.

XX 30-SEP-1997; 97WO-US17658.

XX 07-MAY-1997; 97US-0852495.

XX 01-OCT-1996; 96US-0724394.

XX (PROG-) PROGENTIOR INC.
PA Feder JN, Kronmal GS, Lauer PM, Kuddy DA, Thomas WJ;
PI Tsuchihashi Z, Wolitt HK;
XX WPI; 1998-240014/21.
DK Hereditary haemochromatosis gene products - used to develop products
PT for the diagnosis and treatment of hereditary disorders in iron
PI metabolism
XX Example 2; Fig 8; 209pp; English.
XX The present invention describes hereditary haemochromatosis gene
CC products from the human haemochromatosis gene. The present sequence
CC represents a hereditary haemochromatosis subregion from an individual
CC unaffected by hereditary haemochromatosis (HH). Also described is a
CC method to determine the presence or absence of the common hereditary
CC haemochromatosis (HFE) gene mutation in an individual comprising:
CC (a) providing DNA or RNA from the individual; and (b) assessing the
CC DNA or RNA for the presence or absence of a haplotype or genotype where
CC the presence or absence of the haplotype genotype indicates the likely
CC presence of the HFE gene mutation in the genome of the individual. The
CC HFE gene sequences from the present invention can be used to develop
CC products for use in the diagnosis and treatment of HFE. The present
CC invention also describes BTF genes, which are homologues of the milk
CC protein butyrophilin (BT), and can be used in the production of agonists
CC and antagonists of BT function. Also described are: (1) a RoRet gene
CC which can be used to develop products for the study, diagnosis and
CC treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes
CC which are homologues of a type 1 sodium transport gene, and can
CC similarly be used for hypophosphatemia.
XX Sequence 235033 BP; 68786 A; 48466 C; 49441 G; 68340 T; 0 other;

Query Match 1.9%; Score 55; DB 19; Length 235033;
Best Local Similarity 100.0%; Pred. No. 8.3e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTTGGCTCCCAAGTCTGGGATTACAGCATGACCTGCGCCAGC 1244
|||||
Db 225009 CCCACCTTGGCTCCCAAGTCTGGGATTACAGCATGACCTGCGCCAGC 225063

RESULT 11

AAV57903
ID AAV57903 standard; DNA; 247326 BP.

XX AAV57903;

XX 21-DEC-1998 (first entry)

XX Hereditary haemochromatosis subregion from an HH affected individual.

XX Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;
KW diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3;
KW BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
KW type 1 sodium transport gene; ss.

XX Homo sapiens.

XX W09814466-A1.

XX 09-APR-1998.

XX 30-SEP-1997; 97WO-US17658.

XX 07-MAY-1997; 97US-0852495.

XX 01-OCT-1996; 96US-0724394.

XX (PROG-) PROGENTIOR INC.

PI Feder JN, Kronmal GS, Iauer PM, Ruddy DA, Thomas WJ.
XX Tsuchihashi Z, Wolff RK.
XX WPI: 1998-240014/21.
XX Hereditary haemochromatosis gene products used to develop products
PT for the diagnosis and treatment of hereditary disorders in iron
PT metabolism
XX Claim 1: Fig 9: 209pp; English.
XX The present invention describes hereditary haemochromatosis gene
CC products from the human haemochromatosis gene. The present sequence
CC represents a hereditary haemochromatosis subregion from at hereditary
CC haemochromatosis (HH) affected individual. Also described is a
CC method to determine the presence or absence of the common hereditary
CC haemochromatosis (HFE) gene mutation in an individual; comprising:
CC (a) providing DNA or RNA from the individual; and (b) assessing the
CC DNA or RNA for the presence or absence of a haplotype or genotype where
CC the presence or absence of the haplotype/genotype indicates the likely
CC presence of the HFE gene mutation in the genome of the individual. The
CC HFE gene sequences from the present invention can be used to develop
CC products for use in the diagnosis and treatment of HFE. The present
CC invention also describes Bf genes, which are homologues of the milk
CC protein butyrophilin (BT), and can be used in the production of agonists
CC and antagonists of Bf function. Also described are: (1) a kit for the
CC which can be used to develop products for the study, diagnosis and
CC treatment of lupus and Sjogren's syndrome; and (2) NPI3 and NPI4 genes
CC which are homologues of a type 1 sodium transport gene, and can
CC similarly be used for hypophosphatemia.
XX Sequence 237426 BP; 69596 A; 48904 C; 48217 G; 70509 T; 0 other;
SQ

Query Match 1.9%; Score 55; DB 19; Length 237426;
Best Local Similarity 100.0%; Pred. No. 8,30-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCATCGGCGACG 1244
|||||
DB 227302 CCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCATCGGCGACG 227456
|||||

RESULT 12
ABN65629
ID ABN65629 standard; cDNA: 475 BP.
XX
AC ABN65629;
XX
DT 28-JUN-2002 (first entry)
XX
DE Human cancer related polynucleotide SEQ ID NO: 55
XX
KW Human; cytostatic; gene expression; gene mapping; tissue proteins;
KW gene therapy; cancer; tumour; gene; ss.
XX
OS Homo sapiens.
XX
FH Key location/qualifiers
FT CDS /aa: 195
FT /product: "ribosomal S11 protein 12"
FT /note: "claimed in claim 6"
XX
PN W0200172801 A1
XX
XX 04-OCT-2001.
XX
XX 26-MAR-2001; 2003WO CN00438.
XX
XX 27-MAR-2000; 2000CN-0115182.
XX
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
XX Mao Y, Xie Y;
XX
XX WPI: 2001-597134/67.
XX P-PSDH; AAG78169.
XX
XX New human ribosomal S11 protein 12 and encoded polynucleotide,
PI applicable in diabetes and treatment of malignant tumour, haemopathy,
PI human immunodeficiency virus infection, immunological diseases and
XX inflammation
XX
XX Claim 6, Page 29 to 43p; Chinese.
XX

PT New nucleic acid for producing a polypeptide, detecting differentially
PT expressed genes correlated with a cancerous state of a mammalian cell,
PT and inhibiting tumor growth.
XX
XX Claim 1: SEQ ID NO 5596; 883pp * Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (ABN27253-ABN3262)
CC with cytostatic activity. The polynucleotide is used to produce a
CC polypeptide, to detect differentially expressed genes correlated with a
CC cancerous state of a mammalian cell and to inhibit tumour growth. The
CC polynucleotide is used as a probe in mapping and tissue profiling. The
CC encoded polypeptide and antibodies to the polypeptide can also be used
CC for therapeutic and diagnostic purposes. The polynucleotide is useful for
CC gene therapy.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 475 BP; 143 A; 107 C; 91 G; 134 T; 0 other;
SQ

Query Match 1.8%; Score 52; DB 24; Length 475;
Best Local Similarity 100.0%; Pred. No. 20-13;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCATCGGCGACG 1241
|||||
DB 212 CCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCATCGGCGACG 263
|||||

RESULT 13
AA164613
ID AA164613 standard; cDNA: 1316 BP.
XX
AC AA164613;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human ribosomal S11 protein 12 encoding cDNA.
XX
XX Human; ribosomal S11 protein 12; cytostatic; virucidal;
KW immunomodulatory; antiinflammatory; haemostatic; malignant tumour;
KW human immunodeficiency virus; HIV; infection; immunological disease;
KW gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key location/qualifiers
FT CDS /aa: 95
FT /product: "ribosomal S11 protein 12"
FT /note: "claimed in claim 6"
XX
PN W0200172801 A1
XX
XX 04-OCT-2001.
XX
XX 26-MAR-2001; 2003WO CN00438.
XX
XX 27-MAR-2000; 2000CN-0115182.
XX
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
XX Mao Y, Xie Y;
XX
XX WPI: 2001-597134/67.
XX P-PSDH; AAG78169.
XX
XX New human ribosomal S11 protein 12 and encoded polynucleotide,
PI applicable in diabetes and treatment of malignant tumour, haemopathy,
PI human immunodeficiency virus infection, immunological diseases and
XX inflammation
XX
XX Claim 6, Page 29 to 43p; Chinese.
XX

PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
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PR 17-NOV-2000; 2000US-0246207.
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PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
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PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249267.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI: 2001-465572/50.

Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers

Claim 1: SEQ ID NO 545; 577pp; English.

The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SEPs), the polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SEPs. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SEPs by binding with the cells own genes and preventing their expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The SEPs may also be used as antigens to produce antibodies and to identify modulators (agonists and antagonists) of the SEPs. The anti-SEP antibodies and antagonists may also be used to down regulate expression and activity of SEPs and as diagnostic agents for detecting the presence of SEPs in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease) cardio-/cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections), other uses

CC Include wound healing, maintenance of organs before transplantation, support of cell culture of primary tissues, modulation of for example

Query Match 1.8%; Score 52; DB 22; Length 5351;
Best Local Similarity 100.0%; Pred No. 1.9e-13;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1193 ACCITGGCTCCCAAGTGTGGATTACAGGATGAGCCACTGCGCCGACG 1244
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DB 989 ACCITGGCTCCCAAGTGTGGATTACAGGATGAGCCACTGCGCCGACG 938
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RESULT 15
AHQ66790/c
ID AHQ66790 standard; DNA: 5351 BP.
XX AC ABQ66790;
XX DT 23-AUG-2002 (first entry)
XX DE Human polynucleotide SEQ ID NO 545.
XX KW Human; nontropic; neuroprotective; cytostatic; dermatological; viricide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antistickling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX OS Homo sapiens.
XX PN US2002042386-A1.
XX PD 11-APR-2002.
XX PE 17-JAN-2001; 2001US-0764870.
XX PR 31-JAN-2000; 2000US-179065P.
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PR 13-OCT-2000; 2000US-0239937.
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PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
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PR 17-NOV-2000; 2000US-0249297.
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PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001:483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure: SEQ ID NO 20009; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAK62170 to AAK61921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/hematopoietic-related diseases, especially cancers and cancer metastases of hematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/hematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAK82169 represent sequences used in the exemplification of the present invention.

Sequence 8319 BP; 2521 A; 1610 C; 1560 G; 2628 T; 0 other;

PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
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PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
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PR 20-OCT-2000; 2000US-0241785.
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PR 26-OCT-2000; 2000US-0241787.
PR 26-OCT-2000; 2000US-0241808.
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PR 26-OCT-2000; 2000US-0241826.
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PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
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PR 17-NOV-2000; 2000US-0249244.
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PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
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PR 17-NOV-2000; 2000US-0249299.
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PR 01-DEC-2000; 2000US-0250391.
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PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Barash SC, Ruben SM:
XX WPI: 2001-541565/60.
XX

PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
XX cancers and metastases
PS Disclosure; SEQ ID NO 10357; 1701pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
XX
SQ Sequence 29329 BP; 6864 A; 6756 C; 7225 G; 8484 T; 0 other;

Query Match i.8%; Score 52; DB 22; Length 29329;
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGCATGAGCCACTGCG 1238
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DB 22210 CTGCCACCTTGGCTCCCAAGTCTGGGATTACAGCATGAGCCACTGCG 22159

RESULT 21
ABA20511/C
ID ABA20511 standard; IMA: 29329 BP.
XX
AC ABA20511;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 1284.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antischizoid; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
XX WO200159063-A2.
XX
PD 16-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01334.
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XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
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PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05 JAN-2001; 2001US-0259678.
(HUMAN) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-541565/56.
Nucleic acids encoding 324 human nervous system antigen polypeptides,
useful for preventing, diagnosing and/or treating nervous system
cancers and metastases.
Disclosure: SEQ ID NO 12842; 1701pp + Sequence Listing; English.
The invention relates to novel genes (AB11004-AB21534) and proteins
(AB14678-AB18001) useful for preventing, treating or ameliorating
medical conditions e.g. by protein or gene therapy. The genes are
isolated from a range of human tissues disclosed in the specification.
The nucleic acids, proteins, antibodies and (antagonists are useful
in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
and ovarian cancer and other cancers of the adrenal gland, bone, bone
marrow, breast, gastrointestinal tract, liver, lung, or urogenita.;

PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 05-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI: 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure: SEQ ID NO 25603; 307lpp + Sequence Listing: English.

AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or (I) supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/hematopoietic-related diseases, especially cancers and cancer metastases of hematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/hematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK64702 and AAK82169 represent sequences used in the exemplification of the present invention.

Sequence 29329 BP; 6864 A; 6756 C; 7225 G; 8484 T; 0 other;

Query Match 1.8%; Score 52; BB 22; Length 29329;
Best local Similarity 100.0%; Pred. No. 1-5e 13;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CIGCCACCTTGGCGCTCCCAAGTGGGATACAGGATGAGAGGACTGCTG 1248

|||||
1187 CIGCCACCTTGGCGCTCCCAAGTGGGATACAGGATGAGAGGACTGCTG 1248

DB 22210 CIGCCACCTTGGCGCTCCCAAGTGGGATACAGGATGAGAGGACTGCTG 22159

RESULT 23

AAK78512/C

1D AAK78512 standard; DNA; 29329 BP.

XX

AC AAK78512;

XX

07-NOV-2001 (first entry)

DT

Human immune/hematopoietic antigen genomic sequence SEQ ID NO:13124.

DE

Human; immune; haematopoietic; immune/hematopoietic antigen; cancer;

KW

cytostatic; gene therapy; vaccine; metastasis; ds.

XX

OS Homo sapiens.

XX

PN W0200157182-A2.

XX

09-AUG-2001.

PD

17-JAN-2001; 2001WO-US01354.

XX

31-JAN-2000; 2000US-0179065.

PR

04-FEB-2000; 2000US-0180628.

PR

24-FEB-2000; 2000US-0184664.

PR

02-MAR-2000; 2000US-0186350.

PR

16-MAR-2000; 2000US-0189874.

PR

17-MAR-2000; 2000US-0190076.

PR

18-APR-2000; 2000US-0198123.

PR

19-MAY-2000; 2000US-0205515.

PR

07-JUN-2000; 2000US-0209467.

PR

28-JUN-2000; 2000US-0214886.

PR

30-JUN-2000; 2000US-0215135.

PR

07-JUL-2000; 2000US-0216647.

PR

07-JUL-2000; 2000US-0216880.

PR

11-JUL-2000; 2000US-0217487.

PR

11-JUL-2000; 2000US-0217496.

PR

14-JUL-2000; 2000US-0218290.

PR

26-JUL-2000; 2000US-0220963.

PR

26-JUL-2000; 2000US-0220964.

PR

14-AUG-2000; 2000US-0224518.

PR

14-AUG-2000; 2000US-0224519.

PR

14-AUG-2000; 2000US-0225213.

PR

14-AUG-2000; 2000US-0225214.

PR

14-AUG-2000; 2000US-0225266.

PR

14-AUG-2000; 2000US-0225267.

PR

14-AUG-2000; 2000US-0225270.

PR

14-AUG-2000; 2000US-0225447.

PR

14-AUG-2000; 2000US-0225757.

PR

14-AUG-2000; 2000US-0225758.

PR

14-AUG-2000; 2000US-0225759.

PR

18-AUG-2000; 2000US-0226279.

PR

22-AUG-2000; 2000US-0226681.

PR

22-AUG-2000; 2000US-0226868.

PR

23-AUG-2000; 2000US-0227182.

PR

23-AUG-2000; 2000US-0227009.

PR

30-AUG-2000; 2000US-0228924.

PR

01-SEP-2000; 2000US-0229287.

PR

01-SEP-2000; 2000US-0229343.

PR

01-SEP-2000; 2000US-0229344.

PR

01-SEP-2000; 2000US-0229345.

PR

05-SEP-2000; 2000US-0229509.

PR

05-SEP-2000; 2000US-0229513.

PR

06-SEP-2000; 2000US-0230437.

PR

06-SEP-2000; 2000US-0230438.

PR

08-SEP-2000; 2000US-0231242.

PR

08-SEP-2000; 2000US-0231243.

PR

08-SEP-2000; 2000US-0231244.

PR

08-SEP-2000; 2000US-0231413.

PR

08-SEP-2000; 2000US-0231414.

PR

08-SEP-2000; 2000US-0232080.

PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249219.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249246.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.

PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 06-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 PI WPI; 2001-483426/52.
 DR
 XX
 XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis.
 PT
 XX
 PS Disclosure: SEQ ID NO 33324; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 29329 BP; 6864 A; 6756 C; 7225 G; 8484 T; 0 other;
 Query Match 1.8%; Score 52; DB 22; Length 29329;
 Best Local Similarity 100.0%; Pred. No. 1.9e-13;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1187 CTGCCACCTTAACTTCCAAAGTCTGGATTACAGGCATGAGCCACTGG 1238
 DB 22210 CTGCCACCTTGGCTCCAAAGTCTGGATTACAGGCATGAGCCACTGG 22159
 RESULT 24
 AAC25949/c
 ID AAC25949 standard; cDNA: 149 BP.
 XX
 AC AAC25949;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein 5' EST, SEQ ID NO: 30024.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EF1033401-A2.
 XX
 PD 06-SEP-2000.

XX 21 FEB-2000; 2000EP-0200610.
PF 26 FEB-1999; 99US-0122487.
XX (GUEST) GENSET.
XX Dumas Milne Edwards J, Duclert A, Giordano J;
PI WP1: 2000-500381/45.
XX
XX New nucleic acid that is a 5' expressed sequence tag (EST) for
PI obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PI diagnostic, forensic, gene therapy and chromosome mapping procedures
XX
XX Claim 1: SEQ ID 30024; 71pp * CD-ROM; English.
PS
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX
SQ Sequence 149 BP; 37 A; 43 C; 40 G; 28 T; 1 other;
Query Match 1.8%; Score 51; DB 21; Length 149;
Best Local Similarity 100.0%; Pred No. 5.6e-13; Mismatches 0; Gaps 0;
Matches 51; Conservative 0; Indels 0; Gaps 0;
QY 1194 CCTTGGCTCCCAAGTGGGATTACAGGCATGAGCCACTGGCCAGC 1244
DB 66 CTTTGGCTCCCAAGTGGGATTACAGGCATGAGCCACTGGCCAGC 16
RESULT 25
ABV03782
ID ABV03782 standard; cDNA; 358 BP.
XX
AC AHV03782;
XX
XX 13-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 1773.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX
XX Schlegel R, Endege WO, Monahan JE;
PI WP1: 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful

PI Schlegel R, Endege WO, Monahan JE;
DR WP1: 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer .
XX
XX Claim 1: Page 674; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV6221) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 358 BP; 87 A; 73 C; 69 G; 128 T; 1 other;
Query Match 1.8%; Score 51; DB 23; Length 358;
Best Local Similarity 100.0%; Pred No. 5.6e-13; Mismatches 0; Gaps 0;
Matches 51; Conservative 0; Indels 0; Gaps 0;
QY 1194 CCTTGGCTCCCAAGTGGGATTACAGGCATGAGCCACTGGCCAGC 1244
DB 105 CCTTGGCTCCCAAGTGGGATTACAGGCATGAGCCACTGGCCAGC 155
RESULT 26
ABV12951
ID ABV12951 standard; cDNA; 459 BP.
XX
AC ABV12951;
XX
XX 13-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 12942.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX
XX Schlegel R, Endege WO, Monahan JE;
PI WP1: 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful

CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 381 BP; 81 A; 103 C; 86 G; 111 T; 0 other;

Query Match 1.8%; Score 51; DB 23; Length 396;
 Best Local Similarity 100.0%; Prod. No. 5.6e-13;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1194 CTTGGGCTCCCAAAGTCTGGGATTACAGGCATGACGACCTGGGCTAG 1244

DB 217 CTTGGGCTCCCAAAGTCTGGGATTACAGGCATGACGACCTGGGCTAG 267

RESULT 29

AA181653/C
 ID AA181653 standard; cDNA; 396 BP.

XX AC AA181653;

XX DT 06-NOV-2001 (first entry)

XX DE Human polynucleotide SEQ ID NO 1713

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation; ss.

XX OS Homo sapiens.

XX PN W0200164835-A2.

XX PD 07-SEP-2001.

XX PF 26-FEB-2001; 2001WO-US04927.

XX PR 28-FEB-2000; 2000US-0515126.

XX DR 18-MAY-2000; 2000US-0577459.

XX PA (HYSEQ) HYSEQ INC.

XX PI Tang YL, Liu C, Drmanac RT;

XX PS WPI: 2001 514838/56.

XX DR P PSDB: AA001722.

XX PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders.

XX PS Claim 1: SEQ ID NO 1713; 1399pp + Sequence List(s), Fig. 1(a).

XX CC The invention relates to human polynucleotides (AA17943-AA19484) and
 CC the encoded proteins (AA00010-AA01916) that exhibit activity related to
 CC cytokine, cell proliferation or cell differentiation of which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis-inducing
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.

XX CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WPI
 CC at http://wipo.int/pub/published_pot_sequences.

XX

SQ Sequence 396 BP; 124 A; 75 C; 87 G; 110 T; 0 other;

Query Match 1.8%; Score 51; DB 22; Length 396;
 Best Local Similarity 100.0%; Prod. No. 5.6e-13;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1187 CTGCCACCTTGGGCTCCCAAAGTCTGGGATTACAGGCATGACCCACTGC 1237

DB 378 CTGCCACCTTGGGCTCCCAAAGTCTGGGATTACAGGCATGACCCACTGC 328

RESULT 30

ABV34857
 ID ABV34857 standard; cDNA; 406 BP.

XX AC ABV34857;

XX DT 16-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 34848.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN W0200150860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US05171.

XX PR 17-FEB-2000; 2000US 183119P.

XX PR 16-MAR-2000; 2000US-189862P.

XX PR 25-MAY-2000; 2000US-207454P.

XX PR 09-JUN-2000; 2000US-211314P.

XX PR 18-JUL-2000; 2000US-219007P.

XX PR 13-DEC-2000; 2000US-255281P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX DR WPI: 2001-662795/76.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.

XX PS Claim 1: Page 7240-7291; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (i) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV02213) of the
 CC specification or its complement. (i) is useful for:

XX CC (a) assessing whether a patient is afflicted with prostate cancer;

XX CC (b) monitoring the progression of prostate cancer in a patient;

XX CC (c) assessing the efficacy of a test compound to inhibit prostate
 XX cancer in a patient;

XX CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 XX in a patient;

XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;

XX CC (f) assessing the prostate cell carcinogenic potential of a compound;

XX CC (g) determining whether prostate cancer has metastasized in a patient;

XX CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 XX patient;

XX CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX SQ Sequence 406 BP; 86 A; 108 C; 93 G; 117 T; 0 other;

Query Match 1.8%; Score 51; DB 23; Length 406;
 Best Local Similarity 100.0%; Prod. No. 5.6e-13;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGACG 1244
ID AAV34074
DB 242 CCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGACG 292

RESULT 3:

ABV34074
ID ABV34074 standard: cDNA: 412 BP.
XX AC ABV34074;
XX DT 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 34064.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN W0200160860 A2.
XX PD 21-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US05171.
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX DR WPI: 2001-662795/76.
XX PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -

Claim 1: Page 7178; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (1) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
CC (1) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 412 BP: 98 A; 88 C; 89 G; 137 T; 0 other;

Query Match 1.8%; Score 51; DB 23; Length 412;
Best Local Similarity 100.0%; Pred. No. 5,6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGACG 1244
ID AAV34074
DB 158 CCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGACG 298

RESULT 12

ABV42939
ID ABV42939 standard: cDNA: 412 BP.
XX AC ABV42939;
XX DT 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 42930.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN W0200160860 A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US05171.
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX DR WPI: 2001-662795/76.
XX PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -

Claim 1: Page 8579; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (1) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
CC (1) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 412 BP: 98 A; 88 C; 89 G; 137 T; 0 other;

Query Match 1.8%; Score 51; DB 23; Length 412;
Best Local Similarity 100.0%; Pred. No. 5,6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGACG 1244
ID AAV42939
DB 158 CCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGACG 208

RESULT 33

AA187958/c
ID AA187958 standard: cDNA: 425 BP.
XX AC AA187958;
XX DT 06-NOV-2001 (first entry)


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PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Endege WO, Monahan JE;
XX WPI: 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1: Page 799; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (1) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (1) is useful for:
XX (a) assessing whether a patient is afflicted with prostate cancer;
XX (b) monitoring the progression of prostate cancer in a patient;
XX (c) assessing the efficacy of a test compound to inhibit prostate
XX cancer in a patient;
XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound;
XX (g) determining whether prostate cancer has metastasized in a patient;
XX (h) assessing the aggressiveness or indolence of prostate cancer in a
XX patient;
XX (i) is also useful as a pharmacodynamic or pharmacogenetic marker.
XX
XX Sequence 446 BP: 108 A; 112 C; 96 G; 127 T; 3 other;
XX
XX Query Match 1.8%; Score 51; DB 23; Length 446;
XX Best Local Similarity 100.0%; Pred. No. 5.6e-13;
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1194 CTTGGCTGCTCCAAAGTCTGGGATTACAGGCATGAGCCACTGGGCGCAAT 244
XX |||||
XX 212 CTTGGCTGCTCCAAAGTCTGGGATTACAGGCATGAGCCACTGGGCGCAAT 262
XX
XX RESULT 46
XX ABV02959
XX ID ABV02959 standard: cDNA; 459 BP.
XX
XX AC ABV02959;
XX
XX DT 14-SEP-2002 (first entry)
XX
XX DE Human prostate expression marker cDNA 2959.
XX
XX KW Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200160860-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 20-FEB-2001; 2001WO-US05171.
XX
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX
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XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Endege WO, Monahan JE;
XX WPI: 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1: Page 549; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (1) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (1) is useful for:
XX (a) assessing whether a patient is afflicted with prostate cancer;
XX (b) monitoring the progression of prostate cancer in a patient;
XX (c) assessing the efficacy of a test compound to inhibit prostate
XX cancer in a patient;
XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound;
XX (g) determining whether prostate cancer has metastasized in a patient;
XX (h) assessing the aggressiveness or indolence of prostate cancer in a
XX patient;
XX (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 459 BP: 106 A; 118 C; 100 G; 135 T; 0 other;
XX
XX Query Match 1.8%; Score 51; DB 23; Length 459;
XX Best Local Similarity 100.0%; Pred. No. 5.6e-13;
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1194 CTTGGCTGCTCCAAAGTCTGGGATTACAGGCATGAGCCACTGGGCGCAAT 1244
XX |||||
XX 210 CTTGGCTGCTCCAAAGTCTGGGATTACAGGCATGAGCCACTGGGCGCAAT 260
XX
XX RESULT 37
XX ABV34901
XX ID ABV34901 standard: cDNA; 512 BP.
XX
XX AC ABV34901;
XX
XX DT 16-SEP-2002 (first entry)
XX
XX DE Human prostate expression marker cDNA 34892.
XX
XX KW Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200160860-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 20-FEB-2001; 2001WO-US05171.
XX
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Endege WO, Monahan JE;
XX WPI: 2001-662795/76.
XX
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XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer;
 XX Claim 1: Page 7297-7298; 11750pp; English.
 XX The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification of its complement. (1) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (1) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX Sequence 512 BP; 118 A; 136 C; 114 G; 144 T; 0 other;

Query Match 1.8%; Score 51; DB 24; Length 512;
 Best Local Similarity 100.0%; Pred. No. 5.6e-13;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1194 CTTTGGCTCCCAAGTCTGGATTACAGGATGAGCCATGCGCCAGC 1244
 |||||||
 DB 250 CTTTGGCTCCCAAGTCTGGATTACAGGATGAGCCATGCGCCAGC 300

RESULT 38

ABV33273
 ID ABV33273 standard; cDNA; 515 BP.
 AC ABV33273;
 XX
 XX 16-SEP-2002 (first entry)
 XX Human prostate expression marker cDNA 33264.
 XX Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX Homo sapiens.
 XX WO200160860-A2.
 XX 23-AUG-2001.
 XX 20-FEB-2001; 2001WO-US05171.
 XX 17-FEB-2000; 2000US-183319P.
 XX 16-MAR-2000; 2000US-189862P.
 XX 25-MAY-2000; 2000US-207454P.
 XX 09-JUN-2000; 2000US-211314P.
 XX 18-JUL-2000; 2000US-219007P.
 XX 13-DEC-2000; 2000US-255281P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA Schlegel R, Endege WO, Monahan JE;
 P1 WPI: 2001-662795/76.
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer;
 XX Claim 1: Page 7053; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification of its complement. (1) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (1) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX Sequence 515 BP; 118 A; 135 C; 115 G; 146 T; 1 other;

Query Match 1.8%; Score 51; DB 23; Length 515;
 Best Local Similarity 100.0%; Pred. No. 5.6e-13;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1194 CTTTGGCTCCCAAGTCTGGATTACAGGATGAGCCATGCGCCAGC 1244
 |||||||
 DB 255 CTTTGGCTCCCAAGTCTGGATTACAGGATGAGCCATGCGCCAGC 305

RESULT 39

ABV43707
 ID ABV43707 standard; cDNA; 515 BP.
 AC ABV43707;
 XX
 XX 16-SEP-2002 (first entry)
 XX Human prostate expression marker cDNA 43698.
 XX Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX Homo sapiens.
 XX WO200160860-A2.
 XX 23-AUG-2001.
 XX 20-FEB-2001; 2001WO-US05171.
 XX 17-FEB-2000; 2000US-183319P.
 XX 16-MAR-2000; 2000US-189862P.
 XX 25-MAY-2000; 2000US-207454P.
 XX 09-JUN-2000; 2000US-211314P.
 XX 18-JUL-2000; 2000US-219007P.
 XX 13-DEC-2000; 2000US-255281P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA Schlegel R, Endege WO, Monahan JE;
 P1 WPI: 2001-662795/76.
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer;
 XX Claim 1: Page 8698; 11750pp; English.
 XX The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification of its complement. (1) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX Sequence 515 BP: 118 A; 135 C; 115 G; 146 T; 1 other;
SQ

Query Match 1.8%; Score 51; DB 23; Length 115;
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1194 CTTGGCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGCGCCAGC 1244
|||||
DB 255 CTTGGCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGCGCCAGC 305
|||||

RESULT 4C
ABV32646
ID ABV32646 standard; cDNA: 521 BP.
XX
AC ABV32646;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 32637.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI: 2001-662795/76.
XX

Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 6956; 11750pp; English.
XX

The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX Sequence 521 BP: 119 A; 138 C; 118 G; 146 T; 0 other;
SQ

CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX Sequence 521 BP: 119 A; 138 C; 118 G; 146 T; 0 other;
SQ

Query Match 1.8%; Score 51; DB 23; Length 521;
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1194 CTTGGCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGCGCCAGC 1244
|||||
DB 250 CTTGGCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGCGCCAGC 300
|||||

RESULT 4I
ABV41571
ID ABV41571 standard; cDNA: 521 BP.
XX
AC ABV41571;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 41562.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI: 2001-662795/76.
XX

Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 8451; 11750pp; English.
XX

The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX Sequence 521 BP: 119 A; 138 C; 118 G; 146 T; 0 other;
SQ

Query Match 1.8%; Score 51; DB 23; Length 521;
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1194 CCTTGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 1244
|||||
DB 250 CCTTGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 300
|||||

RESULT 42
ABV42196
ID ABV42196 standard: cDNA; 521 BP.
XX AC ABV42196;
XX CT 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 42187.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN W0200160860-A2.
XX PU 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US05171.
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX PA (MILL) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX PI WPI: 2001-662795/76.
XX DR
XX PT Novel isolated nucleic acid molecule associated with cancerous state of
XX PT prostate cells and correlating with presence of prostate cancer, useful
XX PT for detecting presence of prostate cancer, stage of prostate cancer;
XX PS Claim 1: Page 8456; 11750pp; English.
XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
XX CC a nucleotide sequence given in Tables 1-4 (ABV0010-ABV4213) of the
XX CC specification or its complement. (I) is useful for:
XX CC (a) assessing whether a patient is afflicted with prostate cancer;
XX CC (b) monitoring the progression of prostate cancer in a patient;
XX CC (c) assessing the efficacy of a test compound to inhibit prostate
XX CC cancer in a patient;
XX CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX CC in a patient;
XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;
XX CC (f) assessing the prostate cell carcinogenic potential of a compound;
XX CC (g) determining whether prostate cancer has metastasized in a patient;
XX CC (h) assessing the aggressiveness or indolence of prostate cancer in a
XX CC patient;
XX CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX SQ Sequence 521 BP; 119 A; 138 C; 118 G; 146 T; 0 other;

Query Match 1.8%; Score 51; DB 23; Length 521;
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1194 CCTTGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 1244
|||||

DB 250 CCTTGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 300
|||||

RESULT 43
ABV43750
ID ABV43750 standard: cDNA; 521 BP.
XX AC ABV43750;
XX CT 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 43741.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN W0200160860-A2.
XX PU 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US05171.
XX PR 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX PA (MILL) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX PI WPI: 2001-662795/76.
XX DR
XX PT Novel isolated nucleic acid molecule associated with cancerous state of
XX PT prostate cells and correlating with presence of prostate cancer, useful
XX PT for detecting presence of prostate cancer, stage of prostate cancer;
XX PS Claim 1: Page 8705-8706; 11750pp; English.
XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
XX CC a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the
XX CC specification or its complement. (I) is useful for:
XX CC (a) assessing whether a patient is afflicted with prostate cancer;
XX CC (b) monitoring the progression of prostate cancer in a patient;
XX CC (c) assessing the efficacy of a test compound to inhibit prostate
XX CC cancer in a patient;
XX CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX CC in a patient;
XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;
XX CC (f) assessing the prostate cell carcinogenic potential of a compound;
XX CC (g) determining whether prostate cancer has metastasized in a patient;
XX CC (h) assessing the aggressiveness or indolence of prostate cancer in a
XX CC patient;
XX CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX SQ Sequence 521 BP; 119 A; 138 C; 118 G; 146 T; 0 other;

Query Match 1.8%; Score 51; DB 23; Length 521;
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1194 CCTTGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 1244
|||||

DB 250 CCTTGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCAGC 300
|||||

RESULT 44
ABV21487

ID ARV21487 standard; cDNA: 670 BP.
 XX
 AC ARV21487;
 XX
 DT 13-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 21478.
 XX
 KW Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 OS Homo sapiens.
 XX
 XX WC200160860-A2.
 XX
 XX 23-AUG-2001.
 XX
 XX 20-FEB-2001; 2001WO-US05171.
 XX
 XX 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer;
 XX
 PS (Claim 1; Page 3588; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-9 (ARV00000-ARV62213) of the
 CC specification or its complement. (1) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 670 BP; 164 A; 167 C; 146 G; 190 T; 3 other;
 XX
 Query Match 1.8%; Score 51; DB 23; Length 670;
 Best Local Similarity 100.0%; Pred. No. 5.6e-13; Indels 0; Gaps 0;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1194 CCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCATGAGCCACTGCGCCAGC 1244
 ID ABV21910
 DB 198 CCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCATGAGCCACTGCGCCAGC 248
 XX
 AC ARV21910;
 XX
 XX 13-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 21478.
 XX
 KW Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 OS Homo sapiens.
 XX
 XX WC200160860-A2.
 XX
 XX 23-AUG-2001.
 XX
 XX 20-FEB-2001; 2001WO-US05171.
 XX
 XX 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer;
 XX
 PS (Claim 1; Page 3588; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-9 (ARV00000-ARV62213) of the
 CC specification or its complement. (1) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 670 BP; 164 A; 167 C; 146 G; 190 T; 3 other;
 XX
 Query Match 1.8%; Score 51; DB 23; Length 670;
 Best Local Similarity 100.0%; Pred. No. 5.6e-13; Indels 0; Gaps 0;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1194 CCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCATGAGCCACTGCGCCAGC 1244
 ID ABV21910
 DB 198 CCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCATGAGCCACTGCGCCAGC 248
 XX
 AC ARV21910;
 XX
 XX 13-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 21478.
 XX
 KW Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 OS Homo sapiens.
 XX

DE Human prostate expression marker cDNA 21901.
 XX
 KW Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX WC200160860-A2.
 XX
 XX 23-AUG-2001.
 XX
 XX 20-FEB-2001; 2001WO-US05171.
 XX
 XX 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer;
 XX
 PS (Claim 1; Page 3730-3731; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (1) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 670 BP; 164 A; 167 C; 146 G; 190 T; 3 other;
 XX
 Query Match 1.8%; Score 51; DB 23; Length 670;
 Best Local Similarity 100.0%; Pred. No. 5.6e-13; Indels 0; Gaps 0;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1194 CCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCATGAGCCACTGCGCCAGC 1244
 ID ABV22485
 DB 198 CCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCCACTGCGCCAGC 248
 XX
 AC ARV22485;
 XX
 XX 13-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 22476.
 XX
 KW Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 OS Homo sapiens.
 XX

PR 13-DEC-2000; 2000US-255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI: 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1: Page 5550; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (1) is useful for:
XX (a) assessing whether a patient is afflicted with prostate cancer;
XX (b) monitoring the progression of prostate cancer in a patient;
XX (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound;
XX (g) determining whether prostate cancer has metastasized in a patient;
XX (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
XX (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 670 BP; 164 A; 167 C; 146 G; 190 T; 3 other:

Query Match 1.8%; Score 51; DB 23; Length 670;
Best Local Similarity 100.0%; Pred. No. 5,6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CCTTGGCTCCCAAAAGTGTGGGATTACAGGCATGAGCCACTGGCCCGC 1244
|||||
DB 198 CCTTGGCTCCCAAAAGTGTGGGATTACAGGCATGAGCCACTGGCCCGC 248

RESULT 49
ABV27742
ID ABV27742 standard; cDNA; 670 BP.
XX
XX AC ABV27742;
XX
XX 16-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 27742.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX W0200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
XX 16-MAR-2000; 2000US-189862P.
XX 25-MAY-2000; 2000US-207454P.
XX 09-JUN-2000; 2000US-211314P.
XX 18-JUL-2000; 2000US-219007P.
XX 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI: 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

DR WPI: 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1: Page 5697 5698; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (1) is useful for:
XX (a) assessing whether a patient is afflicted with prostate cancer;
XX (b) monitoring the progression of prostate cancer in a patient;
XX (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound;
XX (g) determining whether prostate cancer has metastasized in a patient;
XX (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
XX (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 670 BP; 164 A; 167 C; 146 G; 190 T; 3 other:

Query Match 1.8%; Score 51; DB 23; Length 670;
Best Local Similarity 100.0%; Pred. No. 5,6e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CCTTGGCTCCCAAAAGTGTGGGATTACAGGCATGAGCCACTGGCCCGC 1244
|||||
DB 198 CCTTGGCTCCCAAAAGTGTGGGATTACAGGCATGAGCCACTGGCCCGC 248

RESULT 50
ABV28300
ID ABV28300 standard; cDNA; 670 BP.
XX
XX AC ABV28300;
XX
XX 16-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 28291.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX W0200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
XX 16-MAR-2000; 2000US-189862P.
XX 25-MAY-2000; 2000US-207454P.
XX 09-JUN-2000; 2000US-211314P.
XX 18-JUL-2000; 2000US-219007P.
XX 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI: 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

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PS Claim 1: Page 5888: 11750pp: English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in tables 1-9 (ABV00010-ABV0213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacokinetic marker.
XX
SQ Sequence 670 BP: 164 A; 167 C; 146 G; 190 T; 4 other:

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Query Match 1.98; Score 51; LH 23; Length 232;
Host Local Similarity 100.08; Pred No. 5,68 13;
Matches 5: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1164 CTTGGCCCTCCCAAGTCTGGGATTACAGGATGAGGCACTGCTGTAGT 1244
    |||||
DB 198 CTTGGCCCTCCCAAGTCTGGGATTACAGGATGAGGCACTGCTGTAGT 248

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Search completed: May 9, 2003, 19:01:43
Job Time : 1790.62 secs

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81	49	1.7	259	9	A1281111	A1281111 qm53cc01.x	c 154	49	1.7	856	17	A0750004	A0750004 HS_5574_A
82	49	1.7	260	9	A1283111	A1283111 qm53cc01.x	c 155	49	1.7	888	14	B0876371	B0876371 AGENCOURT
83	49	1.7	270	12	B0329774	B0329774 qm1556685	c 156	49	1.7	930	13	B1861454	B1861454 qm3386687
84	49	1.7	271	9	AF529772	AF529772 qp29411.x	c 157	49	1.7	936	17	A0747363	A0747363 HS_5536_A
85	49	1.7	271	10	B168893	B168893 QV1_H1051	c 158	49	1.7	945	12	BF125568	BF125568 601763322
86	49	1.7	280	12	BF962210	BF962210 K55_NMI55	c 159	49	1.7	1030	14	B0942185	B0942185 AGENCOURT
87	49	1.7	306	17	A0313177	A0313177 qp1111110	c 160	49	1.7	1037	13	HM557577	HM557577 AGENCOURT
88	49	1.7	328	14	H86301	H86301 Y104322.S1	c 161	49	1.7	1128	13	B1087374	B1087374 602851883
89	49	1.7	330	17	A0310071	A0310071 C1TH1_E1-	c 162	48	1.7	1133	14	T25753	T25753 ESTD18184_C
90	49	1.7	336	10	AW194192	AW194192 X070381.x	c 163	48	1.7	196	17	A0543332	A0543332 RPT1-11-3
91	49	1.7	366	14	H85616	H85616 Y105111.S1	c 164	48	1.7	225	10	HE148791	HE148791 CM4-HT024
92	49	1.7	372	9	A1445088	A1445088 T194q04.x	c 165	48	1.7	250	13	B1040758	B1040758 PM2-NT023
93	49	1.7	377	9	AQ138696	AQ138696 HS_6035_A	c 166	48	1.7	263	13	BG949199	BG949199 CM2-HB000
94	49	1.7	379	9	AQ15387	AQ15387 qp24121.x	c 167	48	1.7	263	17	AQ376001	AQ376001 RPT111-16
95	49	1.7	380	9	AA613624	AA613624 ncl3803.S	c 168	48	1.7	270	13	B1055218	B1055218 PM2-GN049
96	49	1.7	386	17	AQ038958	AQ038958 CIT-HSP-2	c 169	48	1.7	286	14	W47055	W47055 X23810.S1
97	49	1.7	386	17	AQ216195	AQ216195 HS_5252_B	c 170	48	1.7	288	10	AW750725	AW750725 CM1-CN004
98	49	1.7	388	17	AQ123840	AQ123840 HS_5985_B	c 171	48	1.7	295	17	AQ085609	AQ085609 HS_2167_B
99	49	1.7	389	17	AG050505	AG050505 RPT1-11-2	c 172	48	1.7	299	17	AQ252895	AQ252895 HS_3029_A
100	49	1.7	390	17	BF9179	BF9179 C17987814	c 173	48	1.7	309	10	AW518364	AW518364 X44308_X
101	49	1.7	394	12	BF857377	BF857377 QV1-17620	c 174	48	1.7	314	12	BF741659	BF741659 CM4-HB002
102	49	1.7	401	9	A1635819	A1635819 tz81c12.x	c 175	48	1.7	316	10	AA772696	AA772696 hmo5904.x
103	49	1.7	403	17	AQ059217	AQ059217 CIT-HSP-2	c 176	48	1.7	335	9	AA300052	AA300052 EST12659
104	49	1.7	404	10	B2153364	B2153364 PM4-H1033	c 177	48	1.7	339	12	BF382977	BF382977 601816729
105	49	1.7	405	17	AQ017686	AQ017686 CIT-HSP-2	c 178	48	1.7	346	9	AA993165	AA993165 qt77c09.S
106	49	1.7	411	10	AV764334	AV764334 AV764334	c 179	48	1.7	349	9	AA084676	AA084676 zn20q03.S
107	49	1.7	413	12	BF808698	BF808698 PM4-C1015	c 180	48	1.7	351	10	AW750527	AW750527 RPT1-CN001
108	49	1.7	414	17	B05097	B05097 CIT-HSP-203	c 181	48	1.7	356	17	AQ318671	AQ318671 RPT

C 226	48	1.7	494	10	BE148337	US148337 MO0-H1024	C 299	48	1.7	726	17	AG187206	AG187206 Pan trogl
C 227	48	1.7	499	14	H73306	H73306 US27c12.r1	C 300	48	1.7	746	17	AG104781	AG104781 Pan trogl
C 228	48	1.7	500	17	AQ215816	AQ215816 HS_3238_F	C 301	48	1.7	741	17	HU021064	HU021064
C 229	48	1.7	501	17	AQ040260	AQ040260 CIT-HSP-2	C 302	48	1.7	745	17	AG029705	AG029705 Pan trogl
C 230	48	1.7	507	9	AL013893	AL013893 no81h09.s	C 303	48	1.7	777	12	BQ565021	BQ565021
C 231	48	1.7	510	9	AL070901	AL070901 DKFZp6858	C 304	48	1.7	784	14	BQ429000	BQ429000 ACNCOURT
C 232	48	1.7	513	10	AW174443	AW174443 x106q07.x	C 305	48	1.7	797	12	BG743440	BG743440 G12634956
C 233	48	1.7	515	14	N20867	N20867 YX52412.s1	C 306	48	1.7	802	10	HK300400	HK300400 G60944523
C 234	48	1.7	516	17	AO616105	AO616105 HS_5147_A	C 307	48	1.7	805	12	BG776292	BG776292 G62663360
C 235	48	1.7	518	9	AA765173	AA765173 n275022.s	C 308	48	1.7	817	17	AG894273	AG894273 HS_3100_B
C 236	48	1.7	518	10	AV719687	AV719687 AV719687	C 309	48	1.7	819	12	BF541930	BF541930 G62068433
C 237	48	1.7	519	10	AW902110	AW902110 CV3-NK102	C 310	48	1.7	822	12	BG105498	BG105498 G62312585
C 238	48	1.7	523	12	BF724849	BF724849 BX9608_Y	C 311	48	1.7	832	17	AQ743503	AQ743503 HS_5482_B
C 239	48	1.7	525	17	AQ0505403	AQ0505403 RPT111-4	C 312	48	1.7	848	14	BQ881909	BQ881909 ACNCOURT
C 240	48	1.7	529	17	AQ012840	AQ012840 HS_5165_B	C 313	48	1.7	854	12	BG697926	BG697926 G62661359
C 241	48	1.7	530	10	BE180767	BE180767 R31-HT562	C 314	48	1.7	894	10	BE548613	BE548613 G61074087
C 242	48	1.7	532	10	BE019370	BE019370 BE50633_Y	C 315	48	1.7	914	10	BE564637	BE564637 G61136476
C 243	48	1.7	532	17	AO831058	AO831058 HS_5411_H	C 316	48	1.7	916	12	HE742399	HE742399 G611575949
C 244	48	1.7	534	17	AQ636175	AQ636175 RPT111-4	C 317	48	1.7	922	12	BG755473	BG755473 G62713846
C 245	48	1.7	535	17	AQ118105	AQ118105 HS_3101_A	C 318	48	1.7	938	12	BG828741	BG828741 G62752757
C 246	48	1.7	538	17	AQ675788	AQ675788 HS_2145_A	C 319	48	1.7	940	12	BF304788	BF304788 G61888124
C 247	48	1.7	541	10	BE245107	BE245107 TCBAP-D25	C 320	48	1.7	954	12	RG387907	RG387907 G62412928
C 248	48	1.7	543	17	AQ415818	AQ415818 RPT111-2	C 321	48	1.7	955	9	AL518143	AL518143
C 249	48	1.7	548	9	AL711524	AL711524 DKFZp686E	C 322	48	1.7	957	12	BE742779	BE742779 G61574389
C 250	48	1.7	549	10	AW577917	AW577917 RPT111-3	C 323	48	1.7	983	10	BE300452	BE300452 G60944190
C 251	48	1.7	549	17	AQ529507	AQ529507 RPT111-3	C 324	48	1.7	984	12	BG679183	BG679183 G62627259
C 252	48	1.7	552	9	AI669485	AI669485 TY294-2.x	C 325	48	1.7	991	12	BF304111	BF304111 G61886924
C 253	48	1.7	555	17	AQ384299	AQ384299 RPT111-13	C 326	48	1.7	1045	13	BM558258	BM558258 ACNCOURT
C 254	48	1.7	555	17	AQ485647	AQ485647 RPT111-2	C 327	48	1.7	1049	14	BM905988	BM905988 ACNCOURT
C 255	48	1.7	561	9	A1076609	A1076609 OZ31008.x	C 328	48	1.7	1072	14	BM905516	BM905516 ACNCOURT
C 256	48	1.7	564	10	AW379447	AW379447 C84-H1024	C 329	48	1.7	1072	14	BM905516	BM905516 ACNCOURT
C 257	48	1.7	573	17	AQ676078	AQ676078 HS_5325_B	C 330	48	1.7	1072	14	BM905516	BM905516 ACNCOURT
C 258	48	1.7	574	17	AQ530043	AQ530043 RPT111-3	C 331	48	1.7	1129	13	BM480344	BM480344 ACNCOURT
C 259	48	1.7	575	14	BM979245	BM979245 UT-CE-DU1	C 332	48	1.7	108	17	B74379	B74379 CIT-HSP-202
C 260	48	1.7	576	10	BE142930	BE142930 MFG-BF015	C 333	48	1.7	143	17	AQ471444	AQ471444 CITBI-E1-
C 261	48	1.7	583	10	AW577913	AW577913 RPT111-3	C 334	48	1.7	205	13	BM510118	BM510118 i358b02.x
C 262	48	1.7	592	10	AV718792	AV718792 AV718792	C 335	48	1.7	205	13	BM510118	BM510118 i358b02.x
C 263	48	1.7	601	10	AV719326	AV719326 AV719326	C 336	48	1.7	241	9	AA372590	AA372590 ES164774.x
C 264	48	1.7	601	12	RG349386	RG349386 G62457327	C 337	48	1.7	246	9	AA078384	AA078384 7P02F07.C
C 265	48	1.7	604	10	AV720014	AV720014 AV720014	C 338	48	1.7	247	13	BG960713	BG960713 CMO-CT081
C 266	48	1.7	613	10	AV720842	AV720842 AV720842	C 339	48	1.7	259	9	AA287502	AA287502 z550c02.r
C 267	48	1.7	613	13	BF194113	BF194113 G6245812	C 340	48	1.7	259	9	AA287502	AA287502 z550c02.r
C 268	48	1.7	622	12	BF724838	BF724838 BX09028.x	C 341	48	1.7	269	9	A1648558	A1648558 t255f08.x
C 269	48	1.7	630	17	AG088067	AG088067 Pan trogl	C 342	48	1.7	269	9	A1648558	A1648558 t255f08.x
C 270	48	1.7	631	17	AQ423832	AQ423832 CITBI-E1	C 343	48	1.7	281	13	B1019636	B1019636 IL13-MT026
C 271	48	1.7	634	17	AQ414084	AQ414084 RPT111-2	C 344	48	1.7	288	9	A1493828	A1493828 q253d09.x
C 272	48	1.7	639	17	AG095412	AG095412 Pan trogl	C 345	48	1.7	295	14	N84156	N84156 KR6515F Hum
C 273	48	1.7	642	12	BG365387	BG365387 G2457934	C 346	48	1.7	299	17	AQ057900	AQ057900 CIT-HSP-2
C 274	48	1.7	648	17	AG065044	AG065044 RPT111-15	C 347	48	1.7	305	9	AA488004	AA488004 ab12607.r
C 275	48	1.7	650	17	AQ385940	AQ385940 RPT111-15	C 348	48	1.7	314	10	AW804477	AW804477 QV5-UM009
C 276	48	1.7	659	17	AG149814	AG149814 Pan trogl	C 349	48	1.7	315	10	AW591754	AW591754 X8B4d01.x
C 277	48	1.7	660	12	B656611H	B656611H G62547603	C 350	48	1.7	326	9	AL134332	AL134332 DKFZp547N
C 278	48	1.7	661	9	AL710488	AL710488 DKFZp686H	C 351	48	1.7	326	9	AL134332	AL134332 DKFZp547N
C 279	48	1.7	663	17	AG167520	AG167520 Pan trogl	C 352	48	1.7	342	9	AA017240	AA017240 ze52a02.s
C 280	48	1.7	663	17	AG119366	AG119366 Pan trogl	C 353	48	1.7	335	13	AQ072807	AQ072807 HS_2252_B
C 281	48	1.7	666	17	AG091887	AG091887 Pan trogl	C 354	48	1.7	337	13	B1052645	B1052645 RCO-GN027
C 282	48	1.7	670	10	AV705697	AV705697 Pan trogl	C 355	48	1.7	342	12	BE694479	BE694479 RCO-BT071
C 283	48	1.7	671	10	BE254911	BE254911 G61111854	C 356	48	1.7	350	13	B1018461	B1018461 CMI-MT024
C 284	48	1.7	677	17	AG164958	AG164958 Pan trogl	C 357	48	1.7	352	10	AW089016	AW089016 XD34G02.x
C 285	48	1.7	678	17	AG218835	AG218835 RPT111-4	C 358	48	1.7	359	17	AQ123162	AQ123162 HS_3095_B
C 286	48	1.7	681	17	AQ388600	AQ388600 RPT111-15	C 359	48	1.7	361	10	AV762442	AV762442 AV762442
C 287	48	1.7	681	17	AZ081594	AZ081594 RPT111-15	C 360	48	1.7	361	10	R06639	R06639 yf10b08.r1
C 288	48	1.7	681	17	AZ081594	AZ081594 RPT111-15	C 361	48	1.7	361	10	AA084950	AA084950 znl13b11.r
C 289	48	1.7	688	10	AV706016	AV706016 AV706016	C 362	48	1.7	376	12	BF820446	BF820446 MRI-RT004
C 290	48	1.7	688	17	AG128463	AG128463 Pan trogl	C 363	48	1.7	381	17	R40410	R40410 HS-1051-A2-
C 291	48	1.7	689	17	AG105457	AG105457 Pan trogl	C 364	48	1.7	382	17	AZ773460	AZ773460 UP_499-11
C 292	48	1.7	690	10	BE315308	BE315308 G61141857	C 365	48	1.7	383	17	AQ232555	AQ232555 HS_2028_B
C 293	48	1.7	700	17	AG014845	AG014845 Homo sapi	C 366	48	1.7	389	17	AQ715520	AQ715520 HS_5429_B
C 294	48	1.7	701	17	AG065119	AG065119 Pan trogl	C 367	48	1.7	392	9	A1493546	A1493546 th36b01.x
C 295	48	1.7	703	14	BM997575	BM997575 UT-H-DH0	C 368	48	1.7	392	17	AQ715468	AQ715468 HS_5429_B
C 296	48	1.7	704	12	BG827248	BG827248 G6274405	C 369	48	1.7	397	9	AA507692	AA507692 ng88d12.s
C 297	48	1.7	712	13	BF860733	BF860733 G63491158	C 370	48	1.7	398	10	AW341864	AW341864 xu25605.x
C 298	48	1.7	714	14	BQ000785	BQ000785 UT-B-DH1-	C 371	48	1.7	401	9	A1367544	A1367544 kv94d04.x
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C 372	47	1.6	406	10	AW440424	AW440424	bb90c11.x	C 445	47	1.6	679	17	AG049015	*AG049015	Pan trogl
C 373	47	1.6	407	17	AQ047364	AQ047364	CIT-HSP-2	C 446	47	1.6	683	17	AG112753	AG112753	Pan trogl
C 374	47	1.6	409	10	AW770153	AW770153	HK58f03.x	C 447	47	1.6	688	14	BM988443	BM988443	UI-H-DHO-
C 375	47	1.6	410	9	AA568314	AA568314	nfl5c01.s	C 448	47	1.6	691	17	AG001893	AG001893	Homo sapi
C 376	47	1.6	413	10	AW827418	AW827418	hm30h09.x	C 449	47	1.6	694	12	BG28213	BG28213	602753617
C 377	47	1.6	417	14	R06632	R06632		C 450	47	1.6	709	17	AG001891	AG001891	Homo sapi
C 378	47	1.6	421	9	A1521901	A1521901	ti10a0b.r1	C 451	47	1.6	712	17	AG001892	AG001892	Homo sapi
C 379	47	1.6	421	9	AA111881	AA111881	zq84f07.r	C 452	47	1.6	713	12	BE796673	BE796673	601592078
C 380	47	1.6	423	9	AA133550	AA133550		C 453	47	1.6	722	12	BG617782	BG617782	602645311
C 381	47	1.6	423	9	A1610321	A1610321	z014a02.s	C 454	47	1.6	732	13	B1091782	B1091782	602645311
C 382	47	1.6	424	9	AA147102	AA147102		C 455	47	1.6	760	12	BG207240	BG207240	RST26709
C 383	47	1.6	426	9	A1219747	A1219747	q988d07.x	C 456	47	1.6	760	13	BG914229	BG914229	602808455
C 384	47	1.6	426	17	AO553345	AO553345	RPC1-11-4	C 457	47	1.6	769	17	AG185105	AG185105	Pan trogl
C 385	47	1.6	434	10	AV760945	AV760945		C 458	47	1.6	783	12	BE974022	BE974022	601680351
C 386	47	1.6	434	14	B38468	B38468		C 459	47	1.6	796	14	BQ051998	BQ051998	AGENCOURT
C 387	47	1.6	438	17	AO635761	AO635761	RPC1-11-4	C 460	47	1.6	838	12	BG571201	BG571201	602592138
C 388	47	1.6	443	17	AO343649	AO343649	HS-5086_B	C 461	47	1.6	857	12	BF983604	BF983604	602304714
C 389	47	1.6	447	9	AA463831	AA463831	zx57e05.r	C 462	47	1.6	868	17	AQ747663	AQ747663	HS-5533_A
C 390	47	1.6	454	17	AO601236	AO601236		C 463	47	1.6	891	12	BF678918	BF678918	602153543
C 391	47	1.6	455	17	AO146946	AO146946	HS-2248_A	C 464	47	1.6	923	14	BM915281	BM915281	AGENCOURT
C 392	47	1.6	457	17	AQ197732	AQ197732		C 465	47	1.6	1038	13	BM551072	BM551072	AGENCOURT
C 393	47	1.6	459	12	BF805746	BF805746	QV1-C1017	C 466	47	1.6	1058	12	BG036337	BG036337	602326634
C 394	47	1.6	460	12	BF805744	BF805744	QV1-C1017	C 467	47	1.6	1086	11	BC015672	BC015672	Homo sapi
C 395	47	1.6	468	17	AO571846	AO571846	HS-2094_A	C 468	47	1.6	1223	13	BM451554	BM451554	AGENCOURT
C 396	47	1.6	469	17	AO677080	AO677080	HS-5527_A	C 469	47	1.6	1334	10	AV759784	AV759784	AV759784
C 397	47	1.6	471	17	AO317069	AO317069	CIT-HSP-2	C 470	47	1.6	1808	11	AF130050	AF130050	Homo sapi
C 398	47	1.6	473	12	BF514867	BF514867	UI-H-BW1	C 471	47	1.6	4125	11	BC028413	BC028413	Homo sapi
C 399	47	1.6	477	17	AO536394	AO536394	RPC1-11-3	C 472	47	1.6	152	17	AO585086	AO585086	RPC1-11-4
C 400	47	1.6	489	10	BE178244	BE178244	RC3-H-060	C 473	46	1.6	168	17	AO185191	AO185191	CIT-HSP-2
C 401	47	1.6	491	10	AW193512	AW193512	xm17b12.x	C 474	46	1.6	172	10	AO072994	AO072994	x433q08.x
C 402	47	1.6	493	9	AA551170	AA551170	nk76d09.s	C 475	46	1.6	190	17	AO551043	AO551043	RPC1-11-4
C 403	47	1.6	493	17	AO417229	AO417229	RPC1-11-1	C 476	46	1.6	196	17	AO551012	AO551012	RPC1-11-4
C 404	47	1.6	494	10	BM971073	BM971073	EST183159	C 477	46	1.6	214	17	B83900	B83900	RPC111-21B1
C 405	47	1.6	494	10	BE148723	BE148723	CM1-H-024	C 478	46	1.6	215	9	A1753878	A1753878	cr15d12.x
C 406	47	1.6	501	9	AA599749	AA599749	ag11q08.s	C 479	46	1.6	233	14	F34605	F34605	HSP029880.H
C 407	47	1.6	501	17	AO977097	AO977097	EST383184	C 480	46	1.6	278	17	BH861012	BH861012	UP 419-15
C 408	47	1.6	503	10	BE154973	BE154973	PM3-H-034	C 481	46	1.6	279	9	AA605266	AA605266	no83c03.s
C 409	47	1.6	509	17	AO155570	AO155570	HS-3107_B	C 482	46	1.6	287	10	AW836658	AW836658	PM3-LT003
C 410	47	1.6	517	10	BE166690	BE166690	QV0-HT049	C 483	46	1.6	292	9	AA362009	AA362009	EST71352
C 411	47	1.6	530	9	A1683742	A1683742	tw53d11.x	C 484	46	1.6	303	10	AW513905	AW513905	x090b12.x
C 412	47	1.6	531	10	BE157319	BE157319	RC3-H1047	C 485	46	1.6	317	10	BE045105	BE045105	nm28e08.x
C 413	47	1.6	531	17	AQ286075	AQ286075	RPC111-90	C 486	46	1.6	326	17	AQ081931	AQ081931	UP 474-24
C 414	47	1.6	537	17	AO514307	AO514307	HS-5115_B	C 487	46	1.6	331	14	Z30049	Z30049	HFEA21C.A1r
C 415	47	1.6	540	12	BF828758	BF828758	MR2-HM003	C 488	46	1.6	333	10	AW189434	AW189434	x106e04.x
C 416	47	1.6	554	17	AO546291	AO546291	RPC1-11-3	C 489	46	1.6	341	9	AA828145	AA828145	od13c10.s
C 417	47	1.6	560	10	BE674880	BE674880	tw96f10.x	C 490	46	1.6	341	9	AA320095	AA320095	EST22413
C 418	47	1.6	562	17	AO715971	AO715971	HS-543_H	C 491	46	1.6	349	9	AA744175	AA744175	nc79a10.r
C 419	47	1.6	566	10	AV720827	AV720827	AV720827	C 492	46	1.6	349	9	AA468957	AA468957	nc79a10.r
C 420	47	1.6	566	17	AO549290	AO549290	RPC1-11-4	C 493	46	1.6	349	9	AA468957	AA468957	nc79a10.r
C 421	47	1.6	567	12	BF678893	BF678893	602153514	C 494	46	1.6	352	17	AQ307070	AQ307070	HS-2008_A
C 422	47	1.6	571	10	BE544872	BE544872	601678879	C 495	46	1.6	354	14	BQ331932	BQ331932	PM1-ET026
C 423	47	1.6	580	10	AV658841	AV658841	AV658841	C 496	46	1.6	366	9	AA584756	AA584756	no04c01.s
C 424	47	1.6	584	17	AG000686	AG000686	Homo sapi	C 497	46	1.6	366	9	AA632994	AA632994	nq11h10.s
C 425	47	1.6	585	17	AQ549426	AQ549426	RPC1-11-4	C 498	46	1.6	369	10	AW023511	AW023511	df55h11.y
C 426	47	1.6	590	13	BM091350	BM091350	1q21i04.x	C 499	46	1.6	373	17	AQ026253	AQ026253	CITB1-E1-
C 427	47	1.6	593	17	AO420289	AO420289	RPC1-11-1	C 500	46	1.6	377	10	AV708727	AV708727	AV708727
C 428	47	1.6	595	17	AQ267692	AQ267692	RPC111-71	C 501	46	1.6	380	9	AA654968	AA654968	nt61e05.s
C 429	47	1.6	606	17	AQ042325	AQ042325	CIT-HSP-2	C 502	46	1.6	384	9	AA180214	AA180214	zp35901.s
C 430	47	1.6	608	17	AQ196470	AQ196470	CIT-HSP-2	C 503	46	1.6	386	9	AA632994	AA632994	nk48a02.s
C 431	47	1.6	615	9	AL603163	AL603163	DKF2p686g	C 504	46	1.6	387	10	AA438551	AA438551	xu33601.x
C 432	47	1.6	627	17	AG000685	AG000685	Homo sapi	C 505	46	1.6	387	17	AQ0567697	AQ0567697	HS-2118_B
C 433	47	1.6	632	10	BE171849	BE171849	MR0-HT055	C 506	46	1.6	388	9	A1570906	A1570906	tr56g03.x
C 434	47	1.6	635	13	B1916602	B1916602	603178533	C 507	46	1.6	394	9	AA827978	AA827978	od70d06.s
C 435	47	1.6	638	17	AG129313	AG129313	Pan trogl	C 508	46	1.6	396	10	AW502078	AW502078	UI-HF-BRO
C 436	47	1.6	643	10	AV706522	AV706522	AV706522	C 509	46	1.6	396	14	H68120	H68120	yu68b06.s1
C 437	47	1.6	647	12	BF996071	BF996071	MR1-GN017	C 510	46	1.6	398	9	A1587400	A1587400	tr50b03.x
C 438	47	1.6	649	17	AG075635	AG075635	Pan trogl	C 511	46	1.6	398	12	BF878243	BF878243	CM3-ET009
C 439	47	1.6	651	14	BM677523	BM677523	UI-E-B01	C 512	46	1.6	399	14	W45434	W45434	zc83c03.s1
C 440	47	1.6	651	17	AG177756	AG177756	Pan trogl	C 513	46	1.6	400	9	AA449991	AA449991	zx338e12.s
C 441	47	1.6	653	10	BE562953	BE562953	601346394	C 514	46	1.6	400	10	AW169531	AW169531	x127b02.x
C 442	47	1.6	659	14	BM998859	BM998859	UI-H-B1C	C 515	46	1.6	404	9	AA551575	AA551575	nk73b02.s
C 443	47	1.6	669	17	AG176227	AG176227	Pan trogl	C 516	46	1.6	407	17	AQ241984	AQ241984	CITB1-E1-
C 444	47	1.6	672	14	BM975543	BM975543	UI-H-B1C	C 517	46	1.6	408	17	AQ213205	AQ213205	HS-3243_A

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AG749282 HS-5576_A
BF528078 602042825
BQ858891 AGENCOURT
AL567260 AGENCOURT
BF679908 602154609
BE727768 601564103
BQ224699 AGENCOURT
BQ889584 AGENCOURT
BG534648 602564569
BQ669302 AGENCOURT
A0744045 HS-5501_A
BQ668408 AGENCOURT
B1194899 602943879
A0749270 HS-5576_A
BQ480739 602529840
BQ675090 AGENCOURT
AL534620 AL534620

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 4491-4496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-910, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=11&td=113 010115-
C8101-178-H06&t3=2001-01-08&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 568.
Location/Qualifiers
1..569
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UT0115"
/dev_stage="Adult"
/note="Organ: uterus_tumor; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 175 a 114 c 119 g 151 t

ORIGIN

Query Match 1.9%; Score 56; DB 13; Length 569;
Best local Similarity 100.0%; Pred. No. 1.le-10;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCACCTTGGCTCCCAAAGTCTGGGATTACAGGCAATGAGCCACTGCGCCACG 1245
|||||TT
DE 120 CCACCTTGGCTCCCAAAGTCTGGGATTACAGGCAATGAGCCACTGCGCCACG 175

RESULT 8

LOCUS B1015195 600 bp mRNA linear EST 14-JUN-2001

DEFINITION MR4-ET0140-190201-006 e12 ET0140 Homo sapiens cDNA, mRNA sequence.

ACCESSION B1015195

VERSION B1015195.1 GI:14419266

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 600)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Bridges,M.R., Nagai,M.A., da Silva,W. Jr., Zaqui,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baid,R.S., Simpson,A.J.G., Brunstein,A., deOliveira,P.S., Bucher,P., Cocquenet,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 4491-4496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-910, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4-ET0140-190201-006-e12&t3=2001-02-19&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 72.
Location/Qualifiers
1..600
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ET0140"
/dev_stage="Adult"
/note="Organ: lung_tumor; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 208 a 102 c 130 g 160 t

ORIGIN

Query Match 1.9%; Score 56; DB 13; Length 600;
Best local Similarity 100.0%; Pred. No. 1.le-10;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1189 GCCACCTTGGCTCCCAAAGTCTGGGATTACAGGCAATGAGCCACTGCGCCACG 1244
|||||TT
DB 451 GCCACCTTGGCTCCCAAAGTCTGGGATTACAGGCAATGAGCCACTGCGCCACG 396

RESULT 9

LOCUS BG745912 1054 bp mRNA linear EST 15-MAY-2001

DEFINITION 602724092T1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:4850375 3', mRNA sequence.

ACCESSION BG745912 GI:14056565

VERSION BG745912.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1054)

AUTHORS NIH-MGC http://imgc.ncbi.nlm.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs.fmail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory/
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1691 row: h column: 24
High quality sequence stop: 841.
Location/Qualifiers
1..1054
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GG-ACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a

```

BASE COUNT      265 a   270 c   231 g   288 t
ORIGIN

Query Match      1.9%; Score 56; DB 12; Length 1054;
Best Local Similarity 100.0%; Pred. No. 7.7e-11;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1189 GGCACCTTGCCCTCCCAAGTGTGGGATTACAGGCAATGAGCACTGGCTGACG 1244
|||||
Db 188 GGCACCTTGCCCTCCCAAGTGTGGGATTACAGGCAATGAGCACTGGCTGACG 243

RESULT 10
LOCUS      BG014649
DEFINITION 115-GN0239-211200-342-907 GN0239 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG014649
VERSION     BG014649.1 GI:12466063
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 384)
            Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
            20202663
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=115&st2=115-GN0239-
            211200-342-907&st3=2000-12-21&st4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 360.
            Location/Qualifiers
                1..384
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="GN0239"
                /dev_stage="Adult"
                /note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI
                ; Site_2: SmaI; A mini-library was made by cloning
                products derived from ORESTES PCR (U.S. Letters Patent
                application No. 196,716 - Ludwig Institute for Cancer
                Research) profiles into the pUC 18 vector. Reverse
                transcription of tissue mRNA and cDNA amplification were
                performed under low stringency conditions."
                Location/Qualifiers
                    86 a   110 c   87 a   100 t   1 others

BASE COUNT      86 a   110 c   87 a   100 t   1 others
ORIGIN

Query Match      1.9%; Score 55; DB 12; Length 484;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 GGCACCTTGCCCTCCCAAGTGTGGGATTACAGGCAATGAGCACTGGCTGACG 1244
|||||
Db 115 GGCACCTTGCCCTCCCAAGTGTGGGATTACAGGCAATGAGCACTGGCTGACG 169

RESULT 12
LOCUS      AQ056873/c
DEFINITION  CIT-HSP-2339H7.TF CIT-HSP Homo sapiens genomic clone 2339H7, DNA
            sequence.
            AQ056873
            AQ056873.1 GI:3453479
            GSS.
            SOURCE     human.
            ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 387)
            Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
            20202663
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=115&st2=115-GN0239-
            211200-342-907&st3=2000-11-27&st4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 14
            High quality sequence stop: 371.
            Location/Qualifiers
                1..387
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="GN0239"
                /dev_stage="Adult"
                /note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI
                products derived from ORESTES PCR (U.S. Letters Patent
                application No. 196,716 - Ludwig Institute for Cancer
                Research) profiles into the pUC 18 vector. Reverse
                transcription of tissue mRNA and cDNA amplification were
                performed under low stringency conditions."
                Location/Qualifiers
                    86 a   113 c   87 g   99 t   2 others

BASE COUNT      86 a   113 c   87 g   99 t   2 others
ORIGIN

Query Match      1.9%; Score 55; DB 12; Length 387;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCACACTTGCCCTCCCAAGTGTGGGATTACAGGCAATGAGCACTGGCCGACC 1244
|||||
Db 129 CCACACTTGCCCTCCCAAGTGTGGGATTACAGGCAATGAGCACTGGCCGACC 183

RESULT 12
LOCUS      AQ056873
DEFINITION  CIT-HSP-2339H7.TF CIT-HSP Homo sapiens genomic clone 2339H7, DNA
            sequence.
            AQ056873
            AQ056873.1 GI:3453479
            GSS.
            SOURCE     human.
            ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 387)
            Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
            20202663
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=115&st2=115-GN0239-
            211200-342-907&st3=2000-11-27&st4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 14
            High quality sequence stop: 371.
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                /organism="Homo sapiens"
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                /clone_lib="GN0239"
                /dev_stage="Adult"
                /note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI
                products derived from ORESTES PCR (U.S. Letters Patent
                application No. 196,716 - Ludwig Institute for Cancer
                Research) profiles into the pUC 18 vector. Reverse
                transcription of tissue mRNA and cDNA amplification were
                performed under low stringency conditions."
                Location/Qualifiers
                    86 a   113 c   87 g   99 t   2 others

BASE COUNT      86 a   113 c   87 g   99 t   2 others
ORIGIN

```


Hood, L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9749-9754 (1999)
 99380589
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: <http://www.hi-sc.washington.edu>
 Plate: 2151 row: N column: 19
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 453
 Location/Qualifiers
 1..453
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Plate-2151 Col-19 Row-N"
 /clone_lib="CIT Approved Human Genome Sperm Library II"
 /sex="male"
 /note="Organ: sperm; Vector: pBluepAC11; BAC clones in
 E-Coli DH10B"
 BASE COUNT 108 a 114 c 82 g 149 t
 ORIGIN

Query Match 1.88; Score 53; DB 17; Length 453;
 Best Local Similarity 100.0%; Pred. No. 1.4e-09;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1189 GCCACCTTGGCTTCCCAAGTCTGGATTACAGGATGAGCACTGGACCTGCGCC 1241
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 DB 142 GCCACCTTGGCTTCCCAAGTCTGGATTACAGGATGAGCACTGGACCTGCGCC 194
 |||||||

RESULT 18
 A1610607
 LOCUS
 DEFINITION
 t19409.x1 NCI-CGAP-Gas4 Homo sapiens cDNA clone IMAGE:2188288
 Similar to TR099634 099634 RIG-3. [1] contains Alu repetitive
 element.; mRNA sequence.
 A1610607
 A1610607.1 GI:4619774
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 658)
 NC-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap/>
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapb-f@mail.nih.gov
 Tissue procurement: Christopher Moskaluk, M.D., Ph.D., Michael K.
 Emmert-Buck, M.D., Ph.D.
 cDNA library preparation: Life Technologies, Inc.
 cDNA library arrayed by: Greg Leemon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium
www.bio.illinois.gov/brp/image/image.html
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 Seq primer: -400P from Gibco
 High quality sequence stop: 372
 POLYA-No.
 Location/Qualifiers
 1..658

FEATURES
 source

/organism="Homo sapiens"
 /db_xref="taxon:9606"
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 /tissue_type="poorly differentiated adenocarcinoma with
 signet ring cell features"
 /lab_host="DH10B"
 /note="Organ: stomach; Vector: pCMV-SPORT6; Site: 1; Salt;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.69 kb. Life Technologies catalog #:
 21549-011"
 BASE COUNT 110 a 196 c 144 g 187 t 1 others
 ORIGIN

Query Match 1.88; Score 53; DB 9; Length 658;
 Best Local Similarity 100.0%; Pred. No. 1.4e-09;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1189 GCCACCTTGGCTTCCCAAGTCTGGATTACAGGATGAGCACTGGACCTGCGCC 1241
 |||||||
 DB 243 GCCACCTTGGCTTCCCAAGTCTGGATTACAGGATGAGCACTGGACCTGCGCC 295
 |||||||

RESULT 19
 B1062371
 LOCUS
 DEFINITION
 B13-UT0117-160301-502-E10-1 UT0117 Homo sapiens cDNA, mRNA
 sequence.
 ACCESSION
 B1062371
 VERSION
 B1062371.1 GI:14469898
 KEYWORDS
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 233)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Negai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.S.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bal, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, J.V., O'Hare
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202665
 Contact: Simpson, A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3st2-IL3-UT0117-160301-502-E10-1st3-2001-03-16st4-1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 233.
 Location/Qualifiers
 1..233
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="UT0117"
 /dev_stage="Adult"
 /note="Organ: uterus_tumor; Vector: puc18; Site: 1; SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

FEATURES
 source

BASE COUNT 53 a 65 c 53 g 62 t
ORIGIN

Query Match 1.8%; Score 52; DB 13; Length 249;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1189 GCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGCGCC 1240
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DB 137 GCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGCGCC 188
|||||

RESULT 20

B1710918/c

LOCUS B1710918 249 bp mRNA linear EST 11-MAR-2002
DEFINITION 1094904.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:5023662
5' similar to SW:AL07_HUMAN P39194 ALU SUBFAMILY SQ SEQUENCE
CONTAMINATION WARNING ENTRY. [1] ; mRNA sequence.

ACCESSION B1710918

VERSION B1710918.1

KEYWORDS GI:15686613

SOURCE EST.

ORGANISM human.

REFERENCE Homo sapiens

AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 249)

MELTON, D., BROWN, J., KENTY, G., PERMUTT, A., LEE, C., KAESTNER, K.,
LEMISHKA, I., SCARCE, M., BRESTELLI, J., GRADWOHL, G., CLIFTON, S.,
HILLIER, L., MARRA, M., PAPE, D., WYLIE, T., MARTIN, J., BLISTAIN, A.,
SCHMITT, A., THEISING, B., RITTER, E., RONKO, I., BENNETT, J., CARDENAS,
M., GIBBONS, M., MCCANN, R., COLE, R., TSAGAREISHVILI, R., WILLIAMS, T.,
JACKSON, Y., and BOWERS, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Harvard University, Howard Hughes Medical Institute,
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohpc.harvard.edu

Library was constructed by Dr. J. Ferrer in vivo mass-excised to

pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington

University Genome Sequencing Center For information on obtaining a

clone please contact: Dr. Hiroshi Inoue (hinoue@mol.wustl.edu)

Seq primer: -40BP from Gibco

High quality sequence stop: 190

Location/Qualifiers

1..249

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5023662"

/tissue_type="Insulinoma"

/lab_host="Human insulinoma"

/note="Organ: pancreas; Vector: pBluescript SK-; Site: 1;
XhoI; Site: 2; EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

BASE COUNT 69 a 59 c 57 g 64 t

ORIGIN

Query Match 1.8%; Score 52; DB 14; Length 249;

Best Local Similarity 100.0%; Pred. No. 5.9e-09;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

Best Local Similarity

Matches 52; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 1189 GCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGCGCC 1240
|||||
DB 120 GCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGCGCC 69
|||||

RESULT 21

B1711369

LOCUS B1711369

DEFINITION 1094904.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:5023662

3' similar to SW:AL07_HUMAN P39194 ALU SUBFAMILY SQ SEQUENCE

CONTAMINATION WARNING ENTRY. [1] ; mRNA sequence.

ACCESSION B1711369

VERSION B1711369.1

KEYWORDS GI:15687064

SOURCE EST.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 348)

MELTON, D., BROWN, J., KENTY, G., PERMUTT, A., LEE, C., KAESTNER, K.,
LEMISHKA, I., SCARCE, M., BRESTELLI, J., GRADWOHL, G., CLIFTON, S.,
HILLIER, L., MARRA, M., PAPE, D., WYLIE, T., MARTIN, J., BLISTAIN, A.,
SCHMITT, A., THEISING, B., RITTER, E., RONKO, I., BENNETT, J., CARDENAS,
M., GIBBONS, M., MCCANN, R., COLE, R., TSAGAREISHVILI, R., WILLIAMS, T.,
JACKSON, Y., and BOWERS, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Harvard University, Howard Hughes Medical Institute,
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohpc.harvard.edu

Library was constructed by Dr. J. Ferrer in vivo mass-excised to

pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington

University Genome Sequencing Center For information on obtaining a

clone please contact: Dr. Hiroshi Inoue (hinoue@mol.wustl.edu)

Seq primer: -40BP from Gibco

High quality sequence stop: 316

Location/Qualifiers

1..348

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5023662"

/tissue_type="Human insulinoma"

/lab_host="Human insulinoma"

/note="Organ: pancreas; Vector: pBluescript SK-; Site: 1;
XhoI; Site: 2; EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

BASE COUNT 80 a 89 c 79 g 100 t

ORIGIN

Query Match 1.8%; Score 52; DB 13; Length 348;

Best Local Similarity 100.0%; Pred. No. 4.8e-09;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1189 GCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGCGCC 1240

|||||

DB 246 GCCACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGCGCC 297

|||||


```

Query Match      1.88; Score 52; DB 9; Length 417
Best Local Similarity 100.0%; Pred. No. 4.1e-09;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1189 GCCCAGCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCATGCGGC 1240
|||||
DB 423 GCCCAGCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCATGCGGC 374

RESULT 27
LOCUS      A1679952      417 bp      mRNA      linear      EST 26-MAY-1999
DEFINITION tu67h07.x1 NCI-CCAF_Gas4 Homo sapiens cDNA clone IMAGE:2256157 3'
similar to contains Alu repetitive element.; mRNA sequence.
ACCESSION  A1679952
VERSION    A1679952.1 GI:4890134
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 417)
NCI-CCAF http://www.ncbi.nlm.nih.gov/ncicaf.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgafts@mail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAF clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: -400P from Gibco
High quality sequence stop: 409.
Location/Qualifiers
1. 417
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2256157"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="DH10B"
/Note="Organ: stomach; Vector: pCMV-SP66; Site: 1; Salt:
Site 2: Not1; Cloned unidirectionally. Primers: 5' end at
Average insert size 1.69 kb. Life Technologies catalog #
11549-011"
BASE COUNT      83 a 106 c 102 g 125 t
ORIGIN

Query Match      1.88; Score 52; DB 9; Length 417
Best Local Similarity 100.0%; Pred. No. 4.1e-09;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 GCCACCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCATGCGGC 1241
|||||
DB 210 GCCACCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCATGCGGC 261

RESULT 28
LOCUS      B1062368      450 bp      mRNA      linear      EST 15-JUN-2001
DEFINITION IL4-UT0117-160301-502-G10 UT0117 Homo sapiens cDNA, mRNA sequence.
ACCESSION  B1062368
VERSION    B1062368.1 GI:14469895
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 450)
NCI-CCAF http://www.ncbi.nlm.nih.gov/ncicaf.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgafts@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 450)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Naqai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsumura,A., Bala,G.S., Simpson,D.H.,
Brustein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,J.M., Soares,F., Brentani,R.R., Reis,L.F., de Souza S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with OAT expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202653
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=IL36t2=IL3-UT0117-
160301-502-G106t3=2001-03-16st4=1)
Seq primer: puc 18 forward
High quality sequence stop: 450.
Location/Qualifiers
1. 450
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="cG0117"
/dev_stage="Adult"
/Note="Organ: uterus_tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      111 a 122 c 97 g 120 t
ORIGIN

Query Match      1.88; Score 52; DB 13; Length 450;
Best Local Similarity 100.0%; Pred. No. 4.1e-09;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1189 GCCCAGCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCATGCGGC 1240
|||||
DB 157 GCCCAGCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCATGCGGC 208

RESULT 29
LOCUS      A1089524/c      455 bp      mRNA      linear      EST 01-OCT-1998
DEFINITION oz22a01.x1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:1676040 3' similar to contains Alu repetitive element.; mRNA
sequence.
ACCESSION  A1089524
VERSION    A1089524.1 GI:3428583
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 455)
NCI-CCAF http://www.ncbi.nlm.nih.gov/ncicaf.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgafts@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the

```

IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert length: 761 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 444.
 Location/Qualifiers

FEATURES

1. .455
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:1676040"
 /dev_stage="8-9 weeks"
 /lab_host="DH10B"

/note="Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - oligo(dT) primer (5'-TGTTCAATCTGAATGGGAGCGCGGCTTAATTTTCTTTTCTTTT-3'). Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Ronaldo."
 136 a 105 c 111 g 103 t

BASE COUNT

ORIGIN
 Query Match 1.8%; Score 52; DB 9; Length 484;
 Best local Similarity 100.0%; Pred. No. 4; 10-09;
 Mismatches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1193 ACCTTGCTCCCAAGTCTGGGATTACAGGATGAGGACATGAGCCAGTCCGCCC 1244
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 359 ACCTTGCTCCCAAGTCTGGGATTACAGGATGAGGACATGAGCCAGTCCGCCC 308

RESULT 30

A1002969 484 bp mRNA linear: EST 09-JUN-1998
 LOCUS
 DEFINITION
 IMAGE:1699540 3' similar to contains Alu repetitive element
 ; contains element MER22 repetitive element 1; mRNA sequence.

ACCESSION

VERSION
 A1002969
 KEYWORDS
 EST.
 SOURCE
 human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
 1 (bases 1 to 484)
 Hallier L., Allen M., Howles L., Dubouque T., Geisler G., Jost S.,
 Krizman D., Kucaba T., Lacy M., Le N., Lennon G., Martin M.,
 Moore B., Schellenberg K., Steptoe M., Tan E., Theisohn R.,
 White Y., Wyllie T., Waterston R. and Wilson R.

TITLE

WashU-NCI human EST Project
 Unpublished (1997)
 Contact: Willson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8401, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

COMMENT

Email: est@wustl.edu.
 This clone is available royalty free through IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 444.

FEATURES

Location/Qualifiers
 1. .484
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:1699540"
 /clone_lib="Gessler Wilms tumor"
 /sex="pooled (6)"
 /lab_host="DH10B"
 /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; RNA

was prepared from a pool of 6 anonymous Wilms' tumor RNAs. RNA was prepared by acid-phenol, followed by one round of oligo dT selection. cDNA library preparation was with the BRL/Life Tech. Superscript Plasmid system. An oligo-dT NotI primer for first strand synthesis generated gggccacccc(t)n at the 3' end of the clones. A 5' SalI adaptor was used with sequence 5'-gtcgaccacgcgcg-3'. Resulting cDNAs were size selected (average size 2 kb), NotI digested, and ligated into NotI/SalI-cut pSPORT1. Library was constructed by Dr. Manfred Gessler."

BASE COUNT 126 a 131 c 103 g 124 t
 ORIGIN

Query Match 1.8%; Score 52; DB 9; Length 484;
 Best local Similarity 100.0%; Pred. No. 3; 9e-09;
 Mismatches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCACCTTGCTCCCAAGTCTGGGATTACAGGATGAGCCAGTCCGCCC 1241
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 227 CCACCTTGCTCCCAAGTCTGGGATTACAGGATGAGCCAGTCCGCCC 278

RESULT 31

BQ007739/c 493 bp mRNA linear EST 26-MAR-2002
 LOCUS
 DEFINITION
 UI-H-E10-ayh k-22-0-UI.s1 NCI_CGAP_E10 Homo sapiens cDNA clone
 IMAGE:5838861 3', mRNA sequence.

ACCESSION

VERSION
 BQ007739
 KEYWORDS
 EST.
 SOURCE
 human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
 1 (bases 1 to 493)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS

TITLE
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL

COMMENT
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapb@fmail.nih.gov

Tissue Procurement: Dr. Jose Mercuendo
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

The following repetitive elements were found in this cDNA
 sequence: 310-440, >ALU
 Seq primer: M13 FORWARD
 POLYA+Yes.

FEATURES

Location/Qualifiers
 1. .493
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:5838861"
 /clone_lib="NCI_CGAP_E10"
 /tissue_type="Chondrosarcoma"
 /dev_host="Adult"

/lab_host="DH10B (Life Technologies)"
 /note="Orphan: left pelvis; Vector: pT73-Pac (Pharmacia)
 with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
 NCI_CGAP_E10 is a cDNA library containing the following

tissue(s): Chondrosarcoma. The library was constructed
 according to Ronaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac

vector. The oligonucleotide used to prime the synthesis of
 first strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is ACACTTGAC.

```

TAG-UI-H-E10
TAG-TISSUE=Chondrosarcoma
TAG-SEQ=ACACTTGCAC
BASE COUNT      152 a   116 c   116 g   109 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 52; DB 14; Length 144;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1193 ACCTTGCGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGAG 1244
|||||
DB 362 ACCTTGCGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGAG 312

RESULT 32
AQ489571
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Other_GSSs: RPCI-11-230P5.TJ
Contact: Shaying Zhao, William Niernman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Peter de Jong
(peter@dejong.med.buffalo.edu). Clones may be purchased from
BACpac Resources (http://bacpac.med.buffalo.edu/~peter/) or from
Research Genet cs (http://resgen.com). BAC clone search page:
http://www.tigr.org/tdb/human/genetcs/seq.html
Seq primer: T7
Class: BAC ends.
FEATURES
source
location/Qualifiers
1..501
/organism="Homo sapiens"
/db_xref="GDB:7588100"
/db_xref="taxon:9606"
/clone="RPCI-11-230P5"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC4.6; Site 1: BAC1; Site 2: EMB1;
RPCI11 Human Male BAC Library"
BASE COUNT      196 a   123 c   107 g   165 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 52; DB 17; Length 144;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 119 ACCTTGCGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGAG 1244
|||||
DB 495 ACCTTGCGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGAG 444

RESULT 33

```

```

AW971724
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 294
Seq primer: Forward
location/Qualifiers
1..530
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGL"
/note="Vector: pBluescriptSKm"
BASE COUNT      135 a   139 c   111 g   145 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 52; DB 10; Length 530;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTTGGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGC 1242
|||||
DB 227 CCCACCTTGGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACTGGCCGC 278

RESULT 34
AQ623696
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Mahairas G. Wallace JC, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3687
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(peter@dejong.med.buffalo.edu). Clones may be purchased from

```

BACPAC Resources (http://bacpac.med.buffalo.edu/submiting_bac.htm)
or from Research Genetics (info@resgen.com) BAC End Web Server:
<http://www.hsc.washington.edu>
Plate: 895 row: E column: 20
Seq primer: 17
Class: BAC ends
High quality sequence stop: 545.
Location/Qualifiers

FEATURES

Source

1. 545
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-895 Col-20 Row-E"
/clone_lib="RPC1-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBAC3.6 vector at EcoRI sites"

BASE COUNT 117 a 139 c 139 g 144 t 6 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 52; DB 17; Length 545;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CCTTGGCTCCCAAGTCTGGGATACAGGATGAGCCACTGCGCCAGC 1245

DB 349 CCTTGGCTCCCAAGTCTGGGATACAGGATGAGCCACTGCGCCAGC 402

RESULT 35

LOCUS A1084593.1

DEFINITION ox63f01.s1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE166107
3' similar to contains Alu repetitive element; mRNA sequence.

ACCESSION A1084593

VERSION A1084593.1

KEYWORDS EST;

SOURCE human.

ORGANISM Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cqabp-r@mail.nih.gov
This clone is available royalty-free through LNCX; contact the
IMAGE Consortium (<http://image.llnl.gov>) for further information.
Insert Length: 470 Std Error: 0.00
Seq primer: -40m13 fwd. E1 from Aresnas
High quality sequence stop: 411.
Location/Qualifiers

FEATURES

Source

1. 583
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:166107"
/clone_lib="Soares_NIHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pTZ19 Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NHM, pregnant uterus
NDHPu, and fetal heart NDHPu) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR amplified cDNAs from pools of
5,000 clones made from the same 4 libraries. The pools

consisted of 1. M.A.G.E. clones 260232-265223,
340488-345479, and 484479-489479.
BASE COUNT 165 a 138 c 139 g 140 t 1 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 52; DB 9; Length 583;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1193 ACCTTGGCTCCCAAGTCTGGGATACAGGATGAGCCACTGCGCCAGC 1244

DB 346 ACCTTGGCTCCCAAGTCTGGGATACAGGATGAGCCACTGCGCCAGC 295

RESULT 36

LOCUS A0589333

DEFINITION C:TR1-El-2645K6.TF C:TR1-El Homo sapiens genomic clone 2645K6, DNA
sequence.

ACCESSION A0589333

VERSION A0589333.1

KEYWORDS GSS;

SOURCE human.

ORGANISM Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hue@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M14-21
Class: BAC ends.
Location/Qualifiers

FEATURES

Source

1. 717
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2645K6"
/clone_lib="C:TR1-El"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"

BASE COUNT 222 a 175 c 140 g 180 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 52; DB 17; Length 717;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1025 CTCACGTGAATCTGCTCCGGGTTCAAGCGATTCTCTCGCTCAGCCCTC 1076

DB 464 CTCACGTGAATCTGCTCCGGGTTCAAGCGATTCTCTCGCTCAGCCCTC 413

RESULT 37

LOCUS AV718287

DEFINITION AV718287 FHTB Homo sapiens cDNA clone FHTB202 5', mRNA sequence.

ACCESSION AV718287

VERSION AV718287

KEYWORDS EST.

IMAGE:841103 5' similar to contains Alu repetitive element;; mRNA sequence.

AA460970.1 GI:2217134
 EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 469)
 REFERENCE

AUTHORS

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., White, T., Waterston, R. and Wilson, R.

TITLE	COMMENT
WashU-NCI human EST Project Unpublished (1997)	Watson, R. and Wilson, R. WashU-NCI human EST Project Unpublished (1997)
Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu	Watson, R. and Wilson, R. Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu

```

FEATURES
  source
    1..369
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:841103"
      /clone_lib="Stratagene lung (#937210)"

  High quality sequence stop: 361.
  Location/Qualifiers
    Insert Length: 2381 Std Error: 0.00
    Seq primer: -28ml3 rev1 ET from Amersham
    This feature is available only free through EMBL. Contact the
    IMAGE Consortium (info@image.llnl.gov) for further information.

```

```

/sex="male"
/dec_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: lung; Vector: pBluescript SK-; Site: 1: EcoRI; Site: 2: XhoI; Cloned unidirectionally; Primer: Oligo dT; normal lung. Average insert size: 1.6 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' CAATTGGCAGAC 3' -3'

```

```

vector: 3 adaptor sequence: 3 GATTTGGCAGCAG 3
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'
BASE COUNT      96 a      77 c      96 g      100 t
ORIGIN
Query Match      1.8% Score 51; DB 9; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1190 CCACCTTTCGCTCTCTCAAGTCTGGATTACAGGCATGAGCCACTGCGCC 1240
      |||||
Db 321 CCACCTTTCGCTCTCCANAGTCTGGATTACAGGCATGAGCCACTGCGCC 271
      |||||

RESULT 42      BF924753/c
LOCUS          BF924753
DEFINITION     CM1-NT0209-281100-609-c10 NT0209 Homo sapiens cDNA, mRNA sequence
ACCESSION      BF924753

```

accession BF924773.1
 version 1
 keywords EST
 source human
 organism Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 375)

Dias Neto, E., Garcia Correa, R., Vertovski-Almeida, S., Priones, M. R.
Nagai, M. A., da Silva, W. Jr, Zago, M. A., Bordin, S., Costa, F. F.

TITLE
Shotgun sequencing of the human transcriptome with 98F expressed
sequence tags

JOURNAL
MEDLINE
COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000).
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-900, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR BAC Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM1812-031-NT0209-231100-609-cl08t3-2000-11-28&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 374.

FEATURES
SOURCE

Location/Qualifiers
1..375
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0209"
/dev_stage="Adult"

/note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORFESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
99 a 94 c 113 g 69 t

BASE COUNT
ORIGIN

Query Match 1.8%; Score 51; DB 12; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCCACCTGGCCCTCCCAAGTGTGGGATTACAGCATGAGCCACCTGCCGC 1240
|||||
DB 165 CCCACCTGGCCCTCCCAAGTGTGGGATTACAGCATGAGCCACCTGCCGC 115

RESULT 43

AQ280600 375 bp DNA linear GSS 22-Nov-1998
LOCUS CITB1-EL-2516H22.1R CITB1-EL Homo sapiens genomic clone 2516H22.
DEFINITION DNA sequence.

ACCESSION AQ280600.1 GI:3906419
VERSION
KEYWORDS GSS.
SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 375)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Lin,M., K., Golden,K.,
Berry,K., Granger,D., Suh,E., Witte,D., Shikuya,B., Simon,M. and
Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building

Unpublished (1998)
Other_GSSs: CITB1-EL-2516H22.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse

FEATURES
SOURCE

Location/Qualifiers
1..379
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="2516H22"
/clone_lib="CITB1-EL"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelOBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
85 a 98 c 111 q 85 t

Query Match 1.8%; Score 51; DB 17; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CCTTGGCTCCCAAGTGTGGGATTACAGCATGAGCCACCTGCCCCAGC 1244
|||||
DB 174 CCTTGGCTCCCAAGTGTGGGATTACAGCATGAGCCACCTGCCCCAGC 224

RESULT 44

AQ178114 394 bp DNA linear GSS 17-OCT-1998
LOCUS HS-2217-B2_F01_MF CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate-2217 Col-2 Row-L. DNA sequence.
ACCESSION AQ178114
VERSION AQ178114.1 GI:3575481
KEYWORDS GSS.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 394)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas G.G., Wallace J.C., Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-4887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2217 row: L column: 2
Class: BAC ends
High quality sequence stop: 394.

JOURNAL

MEDLINE

COMMENT

FEATURES
SOURCE

Location/Qualifiers
1..394
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_plate="2217 Col-2 Row-L"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in
F-Coli DH10B"

BASE COUNT

71 a 104 c 78 g 137 t 4 others

Query Match 1.8%; Score 51; DB 17; Length 394;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CCTTGGCTCCCAAGTGTGGGATTACAGCATGAGCCACCTGCCCCAGC 1244
|||||
DB 252 CCTTGGCTCCCAAGTGTGGGATTACAGCATGAGCCACCTGCCCCAGC 302

Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: <http://www.htsc.washington.edu>.
 Plate: 587 row: 1 column: 15
 Seq primer: 17
 Class: BAC ends
 High quality sequence stop: 479.

FEATURES

Location/Qualifiers
 1..479

Source
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate-587 Col-15 Row-1"
 /clone_lib="RPC111 Human Male BAC Library"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBACe3.6; RPC111 Human Male BAC Library"

BASE COUNT 149 a 99 c 113 g 117 t 1 others
 ORIGIN
 Query Match 1.8%; Score 51; DB 17; Length 479;
 Best Local Similarity 100.0%; Pred. No. 9.4e-09;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 CTGACACCTGGCTCCCAAGTCTGGGATTACAGGCATGAGCACTGG 1237

Db 342 CTGCCACCTGGCTCCCAAGTCTGGGATTACAGGCATGAGCACTGG 292

RESULT 48

AQ342716/c

LOCUS AQ342716 498 bp DNA linear GSS 06-MAY-1999
 DEFINITION RPC111-113P19.TJ RPC111 Homo sapiens genomic clone RPC111-113P19,
 DNA sequence.

ACCESSION AQ342716

VERSION AQ342716.1 GI:4167612

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
 1 (bases 1 to 498)

REFERENCE Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jesus,P. and Venter
 J.C.

AUTHORS Use of BAC End Sequences from Library RPC111-113P19 Sequence Ready

TITLE Map Building

JOURNAL Unpublished (1997)

COMMENT Other_GSSs: RPC111-113P19.TJ

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbeettgr.org

Clones are derived from the human BAC library RPC111. For BAC
 library availability, please contact Dieter de Jager
 (pieteradejong.med.buhalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buhalo.edu/buhalo/>) or from
 Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/human/bac_end_search/bac_end_search.htm

Seq primer: SP6

Class: BAC ends.

FEATURES

Location/Qualifiers

1..498

/organism="Homo sapiens"

/db_xref="GDB:7543386"

/db_xref="taxon:9606"

/clone="RPC111-113P19"

/clone_lib="RPC111"

/sex="Male"

/cell_type="Lymphocytes"

/note="Vector: pBACe3.6; Site_1: EORI; Site_2: EORI;

BASE COUNT 146 a 114 c 122 g 115 t 1 others
 ORIGIN

Query Match 1.8%; Score 51; DB 17; Length 498;

Best Local Similarity 100.0%; Pred. No. 9.1e-09;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CCGACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCACTGGCC 1240

Db 210 CCGACCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCACTGGCC 159

similar to contains Alu repetitive element; contains L1.t3 L1

repetitive element ;, mRNA sequence.

RESULT 49

A1912862

LOCUS A1912862 531 bp mRNA linear EST 16-DEC-1999

DEFINITION A1912862.1 GI:5632717

ACCESSION A1912862

VERSION A1912862.1 GI:5632717

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 531)

REFERENCE NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

TITLE Tumor Gene Index

UNPUBLISHED (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cygbps@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CCGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert length: 1410 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 415.

Location/Qualifiers

1..531

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2289101"

/clone_lib="NCI-CCGAP.Ut2"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="DH10B"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.85 kb. Life Technologies catalog #:

11539-012"

BASE COUNT 152 a 141 c 106 g 131 t 1 others

ORIGIN

Query Match

Best Local Similarity 1.8%; Score 51; DB 9; Length 531;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 CCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCACTGGCCCGC 1244

Db 230 CCTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCACTGGCCCGC 280

similar to contains Alu repetitive element; contains L1.t3 L1

repetitive element ;, mRNA sequence.

RESULT 50

AQ395413

LOCUS AQ395413 539 bp DNA linear GSS 06-MAR-1999

DEFINITION C17B1 E1-2546N10.1H C17B1-E1 Homo sapiens genomic clone 2546N10,

